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(54) Title: MANIPULATION OF ORGANIC ACID BIOSYNTHESIS AND SECRETION

(57) Abstract: The present invention relates to nucleic acid fragments encoding amino acid sequences for organic acid biosynthetic enzymes in plants, and the use thereof for the modification of, for example, organic acid biosynthesis and secretion in plants. In particularly preferred embodiments, the invention relates to the combinatorial expression of citrate synthase (CS) and/or malate dehydrogenase (MDH) and/or phosphoenolpyruvate carboxylase (PEPC) in plants to modify, for example, organic acid synthesis and secretion.



MANIPULATION OF ORGANIC ACID BIOSYNTHESIS AND SECRETION

The present invention relates to nucleic acid fragments encoding amino acid sequences for organic acid biosynthetic enzyme polypeptides in plants, and the use thereof for the modification of organic acid biosynthesis and secretion in plants. In particularly preferred embodiments, the invention relates to the combinatorial expression of malate dehydrogenase (MDH) and/or phosphoenolpyruvate carboxylase (PEPC) and/or citrate synthase (CS) in plants to modify organic acid biosynthesis and secretion.

Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

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Organic acids, such as citrate and malate, are key metabolites in plants. They are involved in numerous processes, including C4 and Crassulacean acid metabolism (CAM) photosynthesis, stomatal and pulvinual movement, nutrient uptake, respiration, nitrogen assimilation, fatty acid oxidation, and providing energy to bacteroids in root nodules. For example, malate plays a key role in root nodule metabolism and nitrogen fixation, serving as the primary carbon source for bacteroid maintenance and nitrogenase activity, and is also tightly linked to nodule nitrogen assimilation. Furthermore, the complexing role of organic acids produced and excreted from plant roots has also been associated with tolerance to the aluminium cation Al³⁺ which is toxic to many plants at micromolar concentrations. Aluminium toxicity has been recognized as a major limiting factor of plant productivity on acidic soils, which account for approximately 40% of the earth's arable land.

The tricarboxylic acid cycle (TCA), also known as Krebs cycle (after its discoverer Hans Krebs) or citric acid cycle, moves electrons from organic acids to the oxidized redox cofactors NAD⁺ and FAD, forming NADH, FADH₂, and carbon dioxide (CO₂). The reaction sequence of the TCA cycle involves: in a reaction catalysed by citrate synthase (CS), acetyl-CoA formed by the pyruvate dehydrogenase complex combines with oxaloacetate to produce the C₆ tricarboxylic acid, citrate. In the overall cycle, the citrate is oxidized to produce two molecules of CO₂ in a series of reactions that leads to the formation of one oxaloacetate, three NADH, one FADH₂, and one ATP. The resulting oxaloacetate

2

reacts with another molecule of acetyl-CoA to continue the cycle. The oxidative decarboxylation of pyruvate yields an additional CO₂ and NADH. Thus the TCA cycle brings about the complete oxidation of pyruvate to three CO₂ plus 10 electrons, which are stored temporarily as 4 NADH and 1 FADH₂.

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Cytosolic reactions generate products that are transported into the mitochondria to feed the TCA cycle. The nature of the end product of the glycolytic reactions in the cytosol of plants is determined by the relative activities of the three enzymes that can utilize phosphoenol-pyruvate (PEP) as substrate. Both pyruvate kinase and PEP-phosphatase form pyruvate; while PEP-carboxylase (PEPC) generates oxaloacetate. Pyruvate is transported directly into the mitochondrion. Oxaloacetate is either transported directly into the mitochondrion or first reduced to malate by cytosolic malate dehydrogenase (MDH).

Before entering the TCA cycle proper, pyruvate is oxidised and decarboxylated by the pyruvate dehydrogenase enzyme complex to form CO_2 , acetyl-CoA, and NADH. The pyruvate dehydrogenase enzyme complex, which requires the bound cofactors thiamine pyrophosphate, lipoic acid, and FAD as well as free coenzyme A (CoASH) and NAD $^+$, links the TCA cycle to glycolysis.

It is known that the TCA cycle includes the following enzymes: pyruvate dehydrogenase, citrate synthase, citrate hydrolase, isocitrate dehydrogenase, oxoglutarate dehydrogenase, succinyl-CoA synthetase, succinate dehydrogenase, fumarase, malate dehydrogenase, NAD-malic enzyme and phosphoenolpyruvate carboxylase.

In particular, citrate synthase (CS) catalyses the condensation of acetyl-CoA and oxaloacetate to form the C6 molecule citrate and free CoASH, as the TCA cycle proper begins.

Malate dehydrogenase (MDH) catalyses the final step of the TCA cycle, oxidizing malate to oxaloacetate and producing NADH. This reaction catalysed by MDH is reversible, thus allowing also for the reversible reduction of oxaloacetate to malate. The enzyme MDH is important in several metabolic pathways, and higher plants contain multiple forms that differ in co-enzyme specificity and subcellular localization. Chloroplasts contain an NADP*-dependent MDH that plays a critical role in balancing reducing equivalents between the cytosol and

stroma. Plants also contain NAD-dependent MDHs which are found in a) mitochondria as part of the TCA cycle; b) cytosol and peroxisomes involved in malate-aspartate shuttles; and c) glyoxisomes functioning in β-oxidation. In root nodules of nitrogen-fixing legumes, such as white clover (*Trifolium repens*) and alfalfa (*Medicago sativa*), malate serves as the primary carbon source to support the respiratory needs of the bacterial microsymbiont and the fixation of N₂ by nitrogenase, and a nodule-enhanced MDH is thus critical for nodule function.

Phosphoenolpyruvate carboxylase (PEPC) catalyses the reaction of phosphoenol-pyruvate with HCO3⁻ releasing the phosphate and producing the C4 product, oxaloacetate. Oxaloacetate is commonly reduced to malate by NADH through the action of malate dehydrogenase (MDH). PEPC is a homotetrameric enzyme widely distributed in most plant tissues. In plants, PEPC fulfils various physiological roles such as the photosynthetic CO₂ fixation in C₄ and Crassulacean Acid Metabolism (CAM) plants, and the anaplerotic pathway.

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While nucleic acid sequences encoding some organic acid biosynthetic enzymes have been isolated for certain species of plants, there remains a need for materials useful in modifying organic acid biosynthesis; in modifying organic acid secretion; in modifying phosphorus acquisition efficiency in plants; in modifying aluminium and acid soil tolerance in plants; in modifying nitrogen fixation and nodule function, particularly in forage legumes and grasses, including alfalfa, medics, clovers, ryegrasses and fescues, and for methods for their use.

This invention is directed towards overcoming, or at least alleviating, one or more of the difficulties or deficiencies associated with the prior art.

In one aspect, the present invention provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding the organic acid biosynthetic polypeptides CS, MDH and PEPC, from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, or functionally active fragments or variants of these polypeptides.

The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of polypeptides which are related to CS, MDH and PEPC (from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species) of CS, MDH

4

and PEPC, or functionally active fragments or variants of CS, MDH and PEPC. Such polypeptides are referred to herein as CS-like, MDH-like and PEPC-like respectively and include polypeptides having similar functional activity.

The present invention also relates to individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene activities in plants to enhance or otherwise alter organic acid biosynthesis; to enhance or reduce or otherwise alter organic acid secretion; to enhance or reduce or otherwise alter phosphorous acquisition efficiency in plants; to enhance or reduce or otherwise alter aluminium and acid soil tolerance in plants; and/or to enhance or reduce or otherwise alter nitrogen fixation and nodule function in legumes.

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The individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene activities in plants has significant consequences for a range of applications in, for example, plant production, plant performance, plant nutrition and plant tolerance. For example, it has applications in increasing plant tolerance to aluminium-toxic acid soils; in improving plant nutrient acquisition efficiency for example in increasing acquisition of phosphorus from soils; in increasing nodule function in nitrogen-fixing legumes for example leading to enhanced nitrogen fixation; in modifying the accumulation of organic acids such as citrate in fruits; in modifying the secretion of organic acids for example citrate and/or malate from plant roots.

Manipulation of CS, MDH and/or PEPC or like gene activities in plants, including legumes such as clovers (*Trifolium* species), lucerne (*Medicago sativa*) and grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species) may be used to facilitate the production of, for example, forage legumes and forage grasses and other crops with enhanced tolerance to aluminium toxic soils; enhanced nutrient acquisition efficiency; forage legumes with enhanced nitrogen fixation; fruits with enhanced organic acid content leading to enhanced flavour and health benefits.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium*)

5

multiflorum), perennial ryegrass (Lolium perenne), tall fescue (Festuca arundinacea), meadow fescue (Festuca pratensis) and red fescue (Festuca rubra). Preferably the species is a clover or a ryegrass, more preferably white clover (T. repens) or perennial ryegrass (L. perenne). White clover (Trifolium repens L.) and perennial ryegrass (Lolium perenne L.) are key pasture legumes and grasses, respectively, in temperate climates throughout the world. Perennial ryegrass is also an important turf grass.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof. The RNA is readily obtainable, for example, by transcription of a DNA sequence according to the present invention, to produce a RNA corresponding to the DNA sequence. The RNA may be synthesised *in vivo* or *in vitro* or by chemical synthesis to produce a sequence corresponding to a DNA sequence by methods well known in the art. In this specification, where the degree of sequence similarity between an RNA and DNA is such that the strand of the DNA could encode the RNA, then the RNA is said to "correspond" to that DNA.

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The term "isolated" means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid or polypeptide present in a living plant is not isolated, but the same nucleic acid or polypeptide separated from some or all of the coexisting materials in the natural system, is isolated. Such an isolated nucleic acid could be part of a vector and/or such a nucleic acid could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment. An isolated polypeptide could be part of a composition and still be isolated in that such a composition is not part of its natural environment.

By "functionally active" in respect of a nucleic acid it is meant that the fragment or variant is capable of modifying organic acid biosynthesis in a plant. A variant in this context can be an analogue, derivative or mutant and includes naturally occurring allelic variants and non-naturally occurring variants. Additions, deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity

6

of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the functional part of the above mentioned sequence, more preferably at least approximately 90% identity, most preferably at least approximately 95% identity. Such functionally active variants and fragments include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 30 nucleotides, more preferably at least 45 nucleotides, most preferably at least 60 nucleotides.

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By "functionally active" in respect of a polypeptide it is meant that the fragment or variant has one or more of the biological properties of the proteins CS, CS-like, MDH, MDH-like, PEPC and PEPC-like. A variant in this context includes additions, deletions, substitutions and derivatizations of one or more of the amino acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 60% identity to the functional part of the above mentioned sequence, more preferably at least approximately 80% identity, most preferably at least approximately 90% identity. Such functionally active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, most preferably at least 20 amino acids.

The term "construct" as used herein refers to an artificially assembled or isolated nucleic acid molecule which includes the gene of interest. In general a construct may include the gene or genes of interest, a marker gene which in some cases can also be the gene of interest and appropriate regulatory sequences. It should be appreciated that the inclusion of regulatory sequences in a construct is optional, for example, such sequences may not be required in situations where the regulatory sequences of a host cell are to be used. The term construct includes vectors but should not be seen as being limited thereto.

The term "vector" as used herein encompasses both cloning and expression vectors. Vectors are often recombinant molecules containing nucleic acid molecules from several sources.

7

By "operatively linked" in respect of a regulatory element, nucleic acid or nucleic acid fragment and terminator, it meant that the regulatory element is capable of causing expression of said nucleic acid or nucleic acid fragment in a plant cell and said terminator is capable of terminating expression of said nucleic acid or nucleic acid fragment in a plant cell. Preferably, said regulatory element is upstream of said nucleic acid or nucleic acid fragment and said terminator is downstream of said nucleic acid or nucleic acid fragment.

By "an effective amount" of a nucleic acid or nucleic acid fragment it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, 10 or a plant, plant seed or other plant part derived therefrom. Such amounts can be readily determined by an appropriately skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is incorporated herein by reference.

It will also be understood that the term "comprises" (or its grammatical variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

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Such nucleic acids or nucleic acid fragments could be assembled to form a consensus contig. As used herein, the term "consensus contig" refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acids or nucleic acid 25 fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acids or nucleic acid fragments, the sequences (and thus their corresponding nucleic acids or nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encodes a CS or CS-like polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102, 104, 114, 118 and 122 hereto (SEQ ID NOS 1, 3 to 10, 11, 13 to 16, 17, 19, 327, 329 to 335, 336, 338 to 344, 349, 351, 353 respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encodes a MDH or MDH-like polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequence shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and 84 hereto (SEQ ID NOS. 21, 23 to 29; 30, 32 to 33, 34, 36, 38, 40, 42 to 43, 44, 46, 48 to 110, 111, 113, 115, 117 to 182, 183, 185, 205, 207 to 217, 218, 220 to 251, 252, 254 to 270, 271, 273 to 275, 276, 278 to 287, 288, 290 to 292, 293, 295 to 296, 297, 299 to 301, 304 to 305, 306, 308); (b) complements of the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).

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In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encodes a PEPC or PEPC-like polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86, 88, 89, 91, 92, 94, 95, 97 and 110 hereto (SEQ ID NOS 187, 189, 191 to 197, 199, 201, 203, 310, 312 to 314, 315, 317 to 318, 319, 321 to 322, 323, 325 and 347 respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).

Nucleic acids or nucleic acid fragments encoding at least a portion of several CS, MDH and PEPC polypeptides have been isolated and identified. Genes encoding other CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins, either as cDNAs or genomic DNAs, may be isolated directly by using all

9

or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant employing the methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labelling, nick translation, or end-labelling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers may be designed and used to amplify a part or all of the sequences of the present invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full-length cDNA or genomic fragments under conditions of appropriate stringency.

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In addition, short segments of the nucleic acids or nucleic acid fragments of the present invention may be used in protocols to amplify longer nucleic acids or nucleic acid fragments encoding homologous genes from DNA or RNA. For example, polymerase chain reaction may be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol (Frohman et al. (1988) Proc. Natl. Acad Sci. USA 85:8998, the entire disclosure of which is incorporated herein by reference) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or 5' cDNA fragments may be isolated (Ohara et al. (1989) Proc. Natl. Acad Sci USA 86:5673; Loh et al. (1989) Science 243:217, the entire disclosures of which are incorporated herein by reference). Products generated by the 3' and 5' RACE procedures may be combined to generate full-length cDNAs.

In a further aspect of the present invention there is provided a substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*),

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ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like polypeptides; and functionally active fragments and variants of these polypeptides.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*).

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated CS or CS-like polypeptide includes an amino acid sequence selected from the group consisting of sequences shown in Figures 2, 5, 8, 10, 100, 103, 115, 119, 123 hereto (SEQ ID NOS 2, 12, 18, 20, 328, 337, 350, 352 and 354 respectively); and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated MDH or MDH-like polypeptide includes an amino acid sequence selected from the group consisting of sequences shown in Figures 12, 15, 18, 20, 22, 24, 27, 29, 32, 34, 36, 39, 41, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83 and 85 hereto (SEQ ID NOS 22, 31, 35, 37, 39, 41, 45, 47, 112, 114, 116, 184, 186, 206, 219, 253, 272, 277, 289, 294, 297, 303, 307 and 309, respectively) and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated PEPC or PEPC-like polypeptide includes an amino acid sequence selected from the group consisting of sequences shown in Figures 43, 45, 48, 50, 52, 54, 87, 90, 93, 96, 98 and 111 hereto (SEQ ID NOS 188, 190, 198, 200, 202, 204, 311, 316, 320, 324, 326, and 348 ,respectively); and functionally active fragments and variants thereof.

In a further embodiment of this aspect of the invention, there is provided a polypeptide produced (e.g. recombinantly) from a nucleic acid or nucleic acid

11

fragment according to the present invention. Techniques for recombinantly producing polypeptides are known to those skilled in the art.

Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins including the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.

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A genotype is the genetic constitution of an individual or group. Variations in genotype are important in commercial breeding programs, in determining parentage, in diagnostics and fingerprinting, and the like. Genotypes can be readily described in terms of genetic markers. A genetic marker identifies a specific region or locus in the genome. The more genetic markers, the finer defined is the genotype. A genetic marker becomes particularly useful when it is allelic between organisms because it then may serve to unambiguously identify an individual. Furthermore, a genetic marker becomes particularly useful when it is based on nucleic acid sequence information that can unambiguously establish a genotype of an individual and when the function encoded by such nucleic acid is known and is associated with a specific trait. Such nucleic acids and/or nucleotide sequence information including single nucleotide polymorphisms (SNPs), variations in single nucleotides between allelic forms of such nucleotide sequence, may be used as perfect markers or candidate genes for the given trait.

Applicants have identified a number of SNPs of the nucleic acids or nucleic acid fragments of the present invention. These are indicated (marked with grey on the black background) in the figures that show multiple alignments of nucleotide sequences of nucleic acid fragments contributing to consensus contig sequences. See for example, Figures 3, 6, 9, 13, 16, 30, 37, 57, 60, 63, 79, 89, 92 and 104 hereto.

Accordingly, in a further aspect of the present invention, there is provided a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid or nucleic acid fragment

according to the present invention, for example a SNP from a nucleic acid sequence shown in Figures 3, 6, 9, 13, 16, 30, 37, 57, 60, 63, 66, 67, 72, 78, 88, 94, 101 and 104 hereto; or complements or sequences antisense thereto, and functionally active fragments and variants thereof. The invention further provides a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) isolated by the method of this invention.

In a still further aspect of the present invention there is provided a method of isolating a nucleic acid or nucleic acid fragment of the present invention including a SNP, said method including sequencing nucleic acid fragments from a nucleic acid library. The method includes the step of identifying the SNP.

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The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid or nucleic acid fragment may be isolated from a recombinant plasmid or may be amplified, for example using polymerase chain reaction.

The sequencing may be performed by techniques known to those skilled in the art.

In a still further aspect of the present invention, there is provided use of the nucleic acids or nucleic acid fragments of the present invention including SNPs, and/or nucleotide sequence information thereof, as molecular genetic markers.

In a still further aspect of the present invention there is provided use of a nucleic acid or nucleic acid fragment of the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers in plant improvement in relation to plant tolerance to abiotic stresses such aluminium toxic acid soils; in relation to nutrient acquisition efficiency including phosphorus; in

13

relation to nitrogen fixation; in relation to nodulation. Even more particularly, sequence information revealing SNPs in allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging and mapping and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues.

In a still further aspect of the present invention there is provided a construct or vector including a nucleic acid or nucleic acid fragment according to the present invention.

In a particularly preferred embodiment the construct or vector may include nucleic acids or nucleic acid fragments encoding both CS or CS-like and MDH or MDH-like polypeptides.

In yet another preferred embodiment the construct or vector may include nucleic acids or nucleic acid fragments encoding both MDH or MDH-like and PEPC or PEPC-like polypeptides.

In yet another preferred embodiment the construct or vector may include both CS or CS-like and PEPC or PEPC-like polypeptides.

In another preferred embodiment the construct or vector may include nucleic acids or nucleic acid fragments encoding all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like polypeptides.

In a preferred embodiment of this aspect of the invention, the vector may include one or more regulatory element such as a promoter, one or more nucleic acids or nucleic acid fragments according to the present invention and one or more terminators; said one or more regulatory elements, one or more nucleic acids or nucleic acid fragments and one or more terminators being operatively linked.

In a preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding both CS or CS-like and MDH or MDH-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both CS or CS-like and MDH or MDH-like polypeptides are expressed.

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In another preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding both CS or CS-like and PEPC or PEPC-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both CS or CS-like and PEPC or PEPC-like polypeptides are expressed.

In yet another particularly preferred embodiment of the present invention the vector or construct may contain nucleic acids or nucleic acid fragments encoding both MDH or MDH-like and PEPC or PEPC-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both MDH or MDH-like and PEPC or PEPC-like polypeptides are expressed.

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In another particularly preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like, operatively linked to a regulatory element or regulatory elements, such that all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like polypeptides are expressed.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, non-chromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from *Agrobacterium tumefaciens*, derivatives of the Ri plasmid from *Agrobacterium rhizogenes*; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable, integrative or viable in the plant cell.

The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they are functional in the target plant cell.

Preferably the regulatory element is a promoter. A variety of promoters which may be employed in the vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the desired tissue specificity of the vector, and whether constitutive or inducible expression is desired and the nature of the plant cell to be transformed (eg.

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monocotyledon or dicotyledon). Particularly suitable constitutive promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) promoter, the maize Ubiquitin promoter, and the rice Actin promoter. Particularly suitable tissue-specific promoters include root-prevalent promoters.

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A variety of terminators which may be employed in the vectors of the present invention are also well known to those skilled in the art. The terminator may be from the same gene as the promoter sequence or a different gene. Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (nos) and the octopine synthase (ocs) genes.

The vector, in addition to the regulatory element, the nucleic acid or nucleic acid fragment of the present invention and the terminator, may include further elements necessary for expression of the nucleic acid or nucleic acid fragment, in different combinations, for example vector backbone, origin of replication (ori), multiple cloning sites, spacer sequences, enhancers, introns (such as the maize Ubiquitin *Ubi* intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (*npt2*) gene, the hygromycin phosphotransferase (*hph*) gene, the phosphinothricin acetyltransferase (*bar* or *pat*) gene, the phospho-mannose isomerase (*pmi*) gene], and reporter genes (such as beta-glucuronidase (GUS) gene (*gusA*)]. The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, northern and Western blot hybridisation analyses.

Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid or nucleic acid fragment. Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such techniques include the use of linkers, such as synthetic linkers, for example including one or more restriction enzyme sites.

PCT/AU2004/000493 WO 2004/089066

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The vectors of the present invention may be incorporated into a variety of plants, including monocotyledons (such as grasses from the genera Lolium, Festuca, Paspalum, Pennisetum, Panicum and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley), dicotyledons (such as Arabidopsis, tobacco, 5 clovers, medics, eucalyptus, potato, sugarbeet, canola, soybean, chickpea) and gymnosperms. In a preferred embodiment, the vectors may be used to transform monocotyledons, preferably grass species such as ryegrasses (Lolium species) and fescues (Festuca species), more preferably perennial ryegrass, including forage- and turf-type cultivars. In an alternate preferred embodiment, the vectors may be used to transform dicotyledons, preferably forage legume species such as clovers (Trifolium species) and medics (Medicago species), more preferably white clover (Trifolium repens), red clover (Trifolium pratense), subterranean clover (Trifolium subterraneum) and alfalfa (Medicago sativa). Clovers, alfalfa and medics are key pasture legumes in temperate climates throughout the world.

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Techniques for incorporating the vectors of the present invention into plant cells (for example by transduction, transfection or transformation) are known to those skilled in the art. Such techniques include Agrobacterium mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into immature embryos and high velocity projectile introduction to cells, tissues, calli, immature and mature embryos. The choice of technique will depend largely on the type of plant to be transformed.

Cells incorporating the vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to regenerate transformed plants, using techniques well known in the art. The culture conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

In a further aspect of the present invention there is provided a plant cell, plant, plant seed or other plant part, including, e.g. transformed with, a vector, nucleic acid or nucleic acid fragment of the present invention.

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The plant cell, plant, plant seed or other plant part may be from any suitable species, including monocotyledons, dicotyledons and gymnosperms. In a preferred embodiment the plant cell, plant, plant seed or other plant part may be from a monocotyledon, preferably a grass species, more preferably a ryegrass (Lolium species) or fescue (Festuca species), more preferably perennial ryegrass, including both forage- and turf-type cultivars. In an alternate preferred embodiment the plant cell, plant, plant seed or other plant part may be from a dicotyledon, preferably forage legume species such as clovers (Trifolium species) and medics (Medicago species), more preferably white clover (Trifolium repens), red clover (Trifolium pratense), subterranean clover (Trifolium subterraneum) and alfalfa (Medicago sativa).

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant cell of the present invention.

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant of the present invention.

In a further aspect of the present invention there is provided a method of modifying organic acid biosynthesis; of modifying organic acid secretion; of modifying phosphorous and other nutrients acquisition efficiency in plants; of modifying aluminium and acid soil tolerance in plants; of modifying nitrogen fixation and nodule function, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to the present invention. Preferably the nucleic acid or nucleic acid fragment is part of a vector.

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Using the methods and products of the present invention, organic acid biosynthesis; organic acid secretion; phosphorous and other plant nutrient acquisition efficiency; aluminium and acid soil tolerance; nitrogen fixation and nodule function, may be increased or otherwise altered, for example by incorporating additional copies of a sense nucleic acid or nucleic acid fragment of the present invention. They may be decreased or otherwise altered, for example by incorporating an antisense nucleic acid or nucleic acid fragment of the present invention.

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In a particularly preferred embodiment the method may include introducing into said plant nucleic acids or nucleic acid fragments encoding both CS or CS-like and MDH or MDH-like polypeptides.

In another preferred embodiment the method may include introducing into said plant nucleic acids or nucleic acid fragments encoding both CS or CS-like and PEPC or PEPC polypeptides.

In yet another preferred embodiment the method may include introducing into said plant nucleic acids or nucleic acid fragments encoding both MDH or MDH-like and PEPC or PEPC-like polypeptides.

In an even more preferred embodiment the method may include introducing into said plant nucleic acids or nucleic acid fragments encoding all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like polypeptides.

The present invention will now be more fully described with reference to the accompanying Examples and drawings. It should be understood, however, that the description following is illustrative only and should not be taken in any way as a restriction on the generality of the invention described above.

In the Figures

Figure 1 shows the consensus contig nucleotide sequence of LpCSa.

Figure 2 shows the deduced amino acid sequence of LpCSa.

20 Figure 3 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSa.

Figure 4 shows the consensus contig nucleotide sequence of LpCSb.

Figure 5 shows the deduced amino acid sequence of LpCSb.

Figure 6 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSb.

Figure 7 shows the nucleotide sequence of LpCSc.

Figure 8 shows the deduced amino acid sequence of LpCSc.

Figure 9 shows the nucleotide sequence of LpCSd.

Figure 10 shows the deduced amino acid sequence of LpCSd.

Figure 11 shows the consensus contig nucleotide sequence of LpMDHa.

Figure 12 shows the deduced amino acid sequence of LpMDHa.

Figure 13 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHa.

Figure 14 shows the consensus contig nucleotide sequence of LpMDHb. 5

Figure 15 shows the deduced amino acid sequence of LpMDHb.

Figure 16 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHb.

Figure 17 shows the nucleotide sequence of LpMDHc.

Figure 18 shows the deduced amino acid sequence of LpMDHc. 10

Figure 19 shows the nucleotide sequence of LpMDHd.

Figure 20 shows the deduced amino acid sequence of LpMDHd.

Figure 21 shows the nucleotide sequence of LpMDHe.

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Figure 22 shows the deduced amino acid sequence of LpMDHe.

Figure 23 shows the consensus contig nucleotide sequence of LpMDHf.

Figure 24 shows the deduced amino acid sequence of LpMDHf.

Figure 25 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHf.

Figure 26 shows the nucleotide sequence of LpMDHg.

Figure 27 shows the deduced amino acid sequence of LpMDHg. 20

Figure 28 shows the consensus contig nucleotide sequence of LpMDHh.

Figure 29 shows the deduced amino acid sequence of LpMDHh.

Figure 30 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHh.

Figure 31 shows the nucleotide sequence of LpMDHi. 25

Figure 32 shows the deduced amino acid sequence of LpMDHi.

Figure 33 shows the nucleotide sequence of LpMDHj.

Figure 34 shows the deduced amino acid sequence of LpMDHj.

Figure 35 shows the consensus contig nucleotide sequence of LpMDHk.

Figure 36 shows the deduced amino acid sequence of LpMDHk.

Figure 37 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHk.

Figure 38 shows the nucleotide sequence of LpMDHI.

Figure 39 shows the deduced amino acid sequence of LpMDHI.

Figure 40 shows the nucleotide sequence of LpMDHm.

Figure 41 shows the deduced amino acid sequence of LpMDHm.

10 Figure 42 shows the nucleotide sequence of LpPEPCa.

Figure 43 shows the deduced amino acid sequence of LpPEPCa.

Figure 44 shows the consensus contig nucleotide sequence of LpPEPCb.

Figure 45 shows the deduced amino acid sequence of LpPEPCb.

Figure 46 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpPEPCb.

Figure 47 shows the nucleotide sequence of LpPEPCc.

Figure 48 shows the deduced amino acid sequence of LpPEPCc.

Figure 49 shows the nucleotide sequence of LpPEPCd.

Figure 50 shows the deduced amino acid sequence of LpPEPCd.

20 Figure 51 shows the nucleotide sequence of LpPEPCe.

Figure 52 shows the deduced amino acid sequence of LpPEPCe.

Figure 53 shows the nucleotide sequence of LpPEPCf.

Figure 54 shows the deduced amino acid sequence of LpPEPCf.

Figure 55 shows the consensus contig nucleotide sequence of TrMDHa.

25 Figure 56 shows the deduced amino acid sequence of TrMDHa.

Figure 57 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHa.

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Figure 58 shows the consensus contig nucleotide sequence of TrMDHb.

Figure 59 shows the deduced amino acid sequence of TrMDHb.

Figure 60 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHb.

Figure 61 shows the consensus contig nucleotide sequence of TrMDHc.

Figure 62 shows the deduced amino acid sequence of TrMDHc.

Figure 63 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHc.

Figure 64 shows the consensus contig nucleotide sequence of TrMDHd.

Figure 65 shows the deduced amino acid sequence of TrMDHd.

Figure 66 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHd.

Figure 67 shows the consensus contig nucleotide sequence of TrMDHe.

Figure 68 shows the deduced amino acid sequence of TrMDHe.

Figure 69 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHe.

Figure 70 shows the consensus contig nucleotide sequence of TrMDHf.

Figure 71 shows the deduced amino acid sequence of TrMDHf.

Figure 72 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHf.

Figure 73 shows the consensus contig nucleotide sequence of TrMDHg.

Figure 74 shows the deduced amino acid sequence of TrMDHg.

Figure 75 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHg.

Figure 76 shows the consensus contig nucleotide sequence of TrMDHh.

Figure 77 shows the deduced amino acid sequence of TrMDHh.

Figure 78 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHh.

Figure 79 shows the consensus contig nucleotide sequence of TrMDHi.

Figure 80 shows the deduced amino acid sequence of TrMDHi.

Figure 81 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHi.

Figure 82 shows the nucleotide sequence of TrMDHj. 5

Figure 83 shows the deduced amino acid sequence of TrMDHj.

Figure 84 shows the nucleotide sequence of TrMDHk.

Figure 85 shows the deduced amino acid sequence of TrMDHk.

Figure 86 shows the consensus contig nucleotide sequence of TrPEPCa.

Figure 87 shows the deduced amino acid sequence of TrPEPCa. 10

Figure 88 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCa.

Figure 89 shows the consensus contig nucleotide sequence of TrPEPCb.

Figure 90 shows the deduced amino acid sequence of TrPEPCb.

Figure 91 shows the nucleotide sequences of the nucleic acid fragments 15 contributing to the consensus contig sequence TrPEPCb.

Figure 92 shows the consensus contig nucleotide sequence of TrPEPCc.

Figure 93 shows the deduced amino acid sequence of TrPEPCc.

Figure 94 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCc. 20

Figure 95 shows the nucleotide sequence of TrPEPCd.

Figure 96 shows the deduced amino acid sequence of TrPEPCd.

Figure 97 shows the nucleotide sequence of TrPEPCe.

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Figure 98 shows the deduced amino acid sequence of TrPEPCe.

Figure 99 shows the consensus contig nucleotide sequence of TrCSa.

Figure 100 shows the deduced amino acid sequence of TrCSa.

Figure 101 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSa.

Figure 102 shows the consensus contig nucleotide sequence of TrCSb.

Figure 103 shows the deduced amino acid sequence of TrCSb.

Figure 104 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSb.

Figure 105 shows the plasmid map in pGEM-T Easy of TrMDH.

Figure 106 shows the nucleotide sequence of TrMDH.

Figure 107 shows the deduced amino acid sequence of TrMDH.

10 Figure 108 shows the plasmid map of sense construct of TrMDH in the binary vector pPZP221:35S².

Figure 109 shows the plasmid map in pGEM-T Easy of TrPEPC.

Figure 110 shows the nucleotide sequence of TrPEPC.

Figure 111 shows the deduced amino acid sequence of TrPEPC.

15 Figure 112 shows the plasmid map of sense construct of TrPEPC in the binary vector pPZP221:35S².

Figure 113 shows the plasmid map in pGEM-T Easy of TrCSa.

Figure 114 shows the nucleotide sequence of TrCSa.

Figure 115 shows the deduced amino acid sequence of TrCSa.

20 Figure 116 shows the plasmid map of sense construct of TrCSa in the binary vector pPZP221:35S².

Figure 117 shows the plasmid map in pGEM-T Easy of TrCSb.

Figure 118 shows the nucleotide sequence of TrCSb.

Figure 119 shows the deduced amino acid sequence of TrCSb.

25 Figure 120 shows the plasmid map of sense construct of TrCSb in the binary vector pPZP221:35S².

Figure 121 shows the plasmid map in pGEM-T Easy of TrCSd.

Figure 122 shows the nucleotide sequence of TrCSd.

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Figure 123 shows the deduced amino acid sequence of TrCSd.

Figure 124 shows the plasmid map of sense construct of TrCSd in the binary vector pPZP221:35S².

Figure 125 shows the plasmid maps of the modular vector system comprising a binary base vector and 7 auxiliary vectors.

Figure 126 shows an example of the modular binary transformation vector system comprising plasmid maps of the binary transformation vector backbone and 4 expression cassettes for combinatorial expression of chimeric CS and MDH and PEPC genes in auxiliary vectors (A) and the plasmid map of the T-DNA region of the final binary transformation vector (B).

Figure 127 shows the results of RT-PCR experiments performed as described in Example 6. Samples were isolated from: L, leaf; S, stolon; St, stolon tip; R, root; Rt, root tip. –C: negative (no reverse transcriptase) control; +C, positive (plasmid) control. The numbers indicate cycle numbers. A: phosphate transporter homolog; B: root iron transporter homolog.

Figure 128 shows the screening of a white clover BAC library using the phosphate transporter cDNA as a probe (A); Southern hybridisation blot of six BAC clones identified in A using the same probe (B); physical map of the phosphate transporter genomic region including the coding region and the promoter region (C).

Figure 129 shows white clover cotyledons, various stages of selection of plantlets transformed with a binary transformation vector constructed as described in Examples 4 and 5, transgenic white clover on root-inducing medium, and white clover plants transformed with genes involved in organic acid biosynthesis.

25 Figure 130 shows the molecular analysis of transgenic white clover plants for the presence of the chimeric MDH gene with real time PCR amplification plot and agarose gel of PCR product.

Figure 131 shows the molecular analysis of transgenic white clover plants for the presence of the chimeric PEPC gene with real time PCR amplification plot and agarose gel of PCR product.

Figure 132 shows the molecular analysis of transgenic white clover plants for the presence of the chimeric CS gene with real time PCR amplification plot and agarose gel of PCR product.

EXAMPLE 1

Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for CS, CS-like, MDH, MDH-like, PEPC and PEPC-like polypeptides from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*)

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cDNA libraries representing mRNAs from various organs and tissues of white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*) were prepared. The characteristics of the white clover and perennial ryegrass libraries, respectively, are described below (Tables 1 and 2).

TABLE 1 cDNA libraries from white clover (*Trifolium repens*)

Library Organ/Tissue		
Library		
01wc	Whole seedling, light grown	
02wc	Nodulated root 3, 5, 10, 14, 21 &28 day old seedling	
03wc	Nodules pinched off roots of 42 day old rhizobium inoculated white	
	clover	
04wc	Nodulated white clover cut leaf and stem collected after 0, 1, 4, 6 &14	
	h after cutting	
05wc	Non-nodulated Inflorescences: <50% open, not fully open and fully	
	open	
06wc	Dark grown etiolated	
07wc	Inflorescence – very early stages, stem elongation, < 15 petals, 15-20	
	petals	
08wc	seed frozen at –80°C, imbibed in dark overnight at 10°C	
09wc	Drought stressed plants	
10wc	AMV infected leaf	
11wc	WCMV infected leaf	

Organ/Tissue		
Phosphorus starved plants		
Vegetative stolon tip		
stolon root initials		
Senescing stolon		
Senescing leaf		

TABLE 2
cDNA libraries from perennial ryegrass (*Lolium perenne*)

Library	Organ/Tissue		
01rg	Roots from 3-4 day old light-grown seedlings		
02rg	Leaves from 3-4 day old light-grown seedlings		
03rg	Etiolated 3-4 day old dark-grown seedlings		
04rg	Whole etiolated seedlings (1-5 day old and 17 days old)		
05rg	Senescing leaves from mature plants		
06rg	Whole etiolated seedlings (1-5 day old and 17 days old)		
07rg	Roots from mature plants grown in hydroponic culture		
08rg	Senescent leaf tissue		
09rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)		
10rg	Embryogenic suspension-cultured cells		
11rg	Non-embryogenic suspension-cultured cells		
12rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)		
13rg	Shoot apices including vegetative apical meristems		
14rg	Immature inflorescences including different stages of inflorescence		

Library	Organ/Tissue		
	meristem and inflorescence development		
15rg	Defatted pollen		
16rg	Leaf blades and leaf sheaths (rbcL, rbcS, cab, wir2A subtracted)		
17rg	Senescing leaves and tillers		
18rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)		
19rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with half-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)		
20rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with double-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)		
21rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)		
22rg	Spikelets with open and maturing florets		
23rg	Mature roots (specific subtraction with leaf tissue)		

The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the manufacturers' instructions. cDNAs may be generated using the SMART PCR cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into Escherichia coli Epicurian coli XL10-Gold

ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.

Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into *E. coli* DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).

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Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analysed using an Applied Biosystems ABI 3700 sequence analyser.

EXAMPLE 2 DNA sequence analyses

The cDNA clones encoding CS, CS-like, MDH, MDH-like, PEPC and PEPC-like polypeptides were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul *et al.* (1993) *J. Mol. Biol.* 215:403-410) searches. The cDNA sequences obtained were analysed for similarity to all publicly available DNA sequences contained in the eBioinformatics nucleotide database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the SWISS-PROT protein sequence database using BLASTx algorithm (v 2.0.1) (Gish and States (1993) *Nature Genetics* 3:266-272) provided by the NCBI.

The cDNA sequences obtained and identified were then used to identify additional identical and/or overlapping cDNA sequences generated using the BLASTN algorithm. The identical and/or overlapping sequences were subjected to a multiple alignment using the CLUSTALw algorithm, and to generate a consensus contig sequence derived from this multiple sequence alignment. The consensus contig sequence was then used as a query for a search against the SWISS-PROT protein sequence database using the BLASTx algorithm to confirm the initial identification.

EXAMPLE 3

10 Identification and full-length sequencing of cDNAs encoding CS, MDH and PEPC polypeptides

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To fully characterise for the purposes of the generation of probes for hybridisation experiments and the generation of transformation vectors, a set of cDNAs encoding white clover CS, MDH and PEPC polypeptides was identified and fully sequenced.

Full-length cDNAs were identified from our EST sequence database using relevant published sequences (NCBI databank) as queries for BLAST searches. Full-length cDNAs were identified by alignment of the query and hit sequences using Sequencher (Gene Codes Corp., Ann Arbor, MI 48108, USA). The original plasmid was then used to transform chemically competent XL-1 cells (prepared inhouse, CaCl₂ protocol). After colony PCR (using HotStarTaq, Qiagen) a minimum of three PCR-positive colonies per transformation were picked for initial sequencing with M13F and M13R primers. The resulting sequences were aligned with the original EST sequence using Sequencher to confirm identity and one of the three clones was picked for full-length sequencing, usually the one with the best initial sequencing result.

Sequencing of all cDNAs was completed by primer walking, i.e. oligonucleotide primers were designed to the initial sequence obtained using M13F and M13R oligonucleotide primers and used for further sequencing. The sequences of the oligonucleotide primers are shown in Table 2.

Contigs were then assembled in Sequencher. The contigs include the sequences of the SMART primers used to generate the initial cDNA library as well

as pGEM-T Easy vector sequence up to the EcoRI cut site both at the 5' and 3' end.

Plasmid maps and the full cDNA sequences of TrCSa, TrCSb, TrCSd, TrMDH and TrPEPC polypeptides were obtained (Figures 1, 2, 5, 6, 9, 10, 13, 14, 17, 18, 21, 22, 25, 26, 29 and 30).

TABLE 3

List of primers used for sequencing of the full-length cDNAs encoding CS,

MDH and PEPC

gene name	clone ID	sequencing primer	primer sequence (5'>3')
TrCSa	05wc1HsB08	05wc1HsB08.f1	TTGCCCGAGGCTATACTGTGGC
	 	05wc1HsB08.f2	CAGCTCACCTAGTTGCTAG
		05wc1HsB08.f3	CCATGGCCTAATGTTGATGC
		05wc1HsB08.r1	TTGGCCTTTCAAGTGGCATTCC
		05wc1HsB08.r2	CAGAATGGGAGGCACGACTTC
		05wc1HsB08.r3	ATGTGAGCATAGTTTGCACC
TrCSb	05wc2HsD09	05wc2HsD09.f1	GACTGCCAGAAAACACTTCCAGG
		05wc2HsD09.f2	ATGACTGCTTTAGTGTGG
		05wc2HsD09.r1	CTCAAGTTTCTCCAGTGTGACAC
		05wc2HsD09.r2	TGACTTATGTATCCCACC
		05wc2HsD09.r3	GCTCTGAATGGTTTAGCTGG
TrCSd	10wc1BsF10	10wc1BsF10.f1	GCACTGCCTGTTTCTGCTCATCC
11000		10wc1BsF10.f2	AGCCAACTTATGAGGATAGC
		10wc1BsF10.r1	CTCCAATACTCCTCGCGACGCC
		10wc1BsF10.r2	AGGCACAACCTGGCCACTG
		10wc1BsF10.r3	ACGTTGCCACCTTCATGATC
TrMDH	13wc1NsD01	13wc1NsD01.f1	GTTGTTATACCTGCTGGTGTT
	100000000000000000000000000000000000000	13wc1NsD01.r1	CTCACTCAACCCTTGGAGAT
TrPEPC	15wc1DsH12	15wc1DsH12.f1	TCCTAAGAAACTTGAAGAGCTCGG
	10001201112	15wc1DsH12.f2	AGATGTTTGCTTACTAGC
		15wc1DsH12.r1	GCCAGCAGCAATACCCTTCATGG
		15wc1DsH12.r2	TTGCTTCTCAACTGTTCC
		10001031112.12	

EXAMPLE 4

Development of binary transformation vectors containing chimeric genes with cDNA sequences encoding CS, MDH and PEPC

To alter the expression of the polypeptides involved in organic acid biosynthesis to improve phosphorus acquisition efficiency as well as aluminium and acid soil tolerance in forage plants, a set of sense binary transformation vectors was produced.

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The pPZP221 binary transformation vector (Hajdukiewicz *et al.*, 1994) was modified to contain the 35S² cassette from pKYLX71:35S² (Schardl *et al.*, 1987) as follows: pKYLX71:35S² was cut with Clal. The 5' overhang was filled in using Klenow and the blunt end was A-tailed with Taq polymerase. After cutting with EcoRI, the 2kb fragment with an EcoRI-compatible and a 3'-A tail was gel-purified. pPZP221 was cut with HindIII and the resulting 5' overhang filled in and T-tailed with Taq polymerase. The remainder of the original pPZP221 multi-cloning site was removed by digestion with EcoRI, and the expression cassette cloned into the EcoRI site and the 3' T overhang restoring the HindIII site. This binary vector contains between the left and right border the plant selectable marker gene aacC1 under the control of the 35S promoter and 35S terminator and the pKYLX71:35S²-derived expression cassette with a CaMV 35S promoter with a duplicated enhancer region and an rbcS terminator.

A GATEWAY® cloning cassette (Invitrogen) was introduced into the multicloning site of the pPZP221:35S² vector obtained as described following the manufacturer's protocol.

cDNA fragments were generated by high fidelity PCR with a proofreading DNA polymerase using the original pGEM-T Easy plasmid cDNA as a template. The primers used (Table 3) contained *att*B sequences for use with recombinases utilising the GATEWAY® system (Invitrogen). The resulting PCR fragments were used in a recombination reaction with pDONR® vector (Invitrogen) to generate entry vectors. In a further recombination reaction, the cDNAs encoding the open reading frame sequences were transferred from the entry vector to the GATEWAY®-enabled pPZP221:35S² vector.

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The orientation of the constructs (sense or antisense) was checked by restriction enzyme digest and sequencing which also confirmed the correctness of the sequence. Transformation vectors containing chimeric genes using full-length open reading frame cDNAs encoding white clover TrCSa, TrCSb, TrCSd, TrMDH and TrPEPC proteins in sense orientation under the control of the CaMV 35S² promoter were generated (Figures 4, 8, 12, 16, 20, 24, 28 and 32).

TABLE 4

List of primers used to PCR-amplify the open reading frames of cDNAs encoding CS, MDH and PEPC

gene name	clone ID	primer	primer sequence (5'>3')
ГгСSа	05wc1HsB08	05wc1HsB08f	GGGGACAAGTTTGTACAAAAAAGC AGGCTTGATCTTAATGGCGTTCTT TCG
		05wc1HsB08r	GGGGACCACTTTGTACAAGAAAGC TGGGTTTTCAATTTTAGGACGATG CG
TrCSb	05wc2HsD09	05wc2HsD09f	GGGGACAAGTTTGTACAAAAAAGC AGGCTTTGTTGATTGATCTTAATG GC
		05wc2HsD09r	GGGGACCACTTTGTACAAGAAAGC TGGGTTAGTAATCCACAGATAACC G
TrCSd	10wc1BsF10	10wc1BsF10f	GGGGACAAGTTTGTACAAAAAAGC AGGCTCTAGATTGTTGATTGATCT AAATGGC
		10wc1BsF10r	GGGGACCACTTTGTACAAGAAAGC TGGGTCTAGATTCAATTTTAGGAT GATGCACC
TrMDH	13wc1NsD01	13wc1NsD01f	GGGGACAAGTTTGTACAAAAAAGC AGGCTCTAGAAATTCCCATTACCA TTCATTCC
		13wc1NsD01r	GGGGACCACTTTGTACAAGAAAGC TGGGTCTAGATTGACATTCTCTCG CATGGACGC
TrPEPC	15wc1DsH12	15wc1DsH12f	GGGGACAAGTTTGTACAAAAAAGC AGGCTTGAGAAGGAGTGAATTGCT CC
		15wc1DsH12r	GGGGACCACTTTGTACAAGAAAGC TGGGTATGATATCTTAGCACACAC TTAAC

5 EXAMPLE 5

Development of binary transformation vectors containing chimeric genes with a combination of 2 or more cDNA sequences encoding CS, MDH and PEPC

To alter the expression of the polypeptides involved in organic acid biosynthesis to improve phosphorus acquisition efficiency as well as aluminium

and acid soil tolerance in forage plants, a modular binary transformation vector system was used (Figure 125). The modular binary vector system enables simultaneous integration of up to seven transgenes the expression of which is controlled by individual promoter and terminator sequences into the plant genome (Goderis *et al.*, 2002).

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The modular binary vector system consists of a pPZP200-derived vector (Hajdukiewicz et al., 1994) backbone containing within the T-DNA a number of unique restriction sites recognised by homing endonucleases. The same restriction sites are present in pUC18-based auxiliary vectors flanking standard multicloning sites. Expression cassettes comprising a selectable marker gene sequence or a cDNA sequence to be introduced into the plant under the control of regulatory sequences like promoter and terminator can be constructed in the auxiliary vectors and then transferred to the binary vector backbone utilising the homing endonuclease restriction sites. Up to seven expression cassettes can thus be integrated into a single binary transformation vector. The system is highly flexible and allows for any combination of cDNA sequence to be introduced into the plant with any regulatory sequence.

For example, a selectable marker cassette comprising the nos promoter and nos terminator regulatory sequences controlling the expression of the nptll gene was PCR-amplified using a proofreading DNA polymerase from the binary vector pKYLX71:35S² and directionally cloned into the Agel and Notl sites of the auxiliary vector pAUX3166. Equally, other selectable marker cassettes can be introduced into any of the auxiliary vectors.

In another example, the expression cassette from the binary vector pWM5 consisting of the ASSU promoter and the tob terminator was PCR-amplified with a proofreading DNA polymerase and directionally cloned into the Agel and Notl sites of the auxiliary vector pAUX3169. Equally, other expression cassettes can be introduced into any of the auxiliary vectors.

In yet another example, the expression cassette from the direct gene transfer vector pDH51 was cut using EcoRI and cloned directly into the EcoRI site of the auxiliary vector pAUX3132.

WO 2004/089066 PCT/AU2004/000493

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TABLE 5

List of primers used to PCR-amplify plant selectable marker cassettes and the regulatory elements used to control the expression of CS, MDH and PEPC genes

expression cassette	primer	primer sequence (5'>3')
nos::nptll-nos	forward	ATAATAACCGGTTGATCATGAGCGGAGAATTAAG GG
	reverse	ATAATAGCGGCCGCTAGTAACATAGATGACACCG CG
35S::aacC1-35S	forward	AATAGCGGCCGCGATTTAGTACTGGATTTTGG
	reverse	AATAACCGGTACCCACGAAGGAGCATCGTGG
35S ² ::rbcS	forward	ATAATAACCGGTGCCCGGGGATCTCCTTTGCC
	reverse	ATAATAGCGGCCGCATGCATGTTGTCAATCAATT
assu::tob	forward	TAATACCGGTAAATTTATTATGRGTTTTTTCCC
	reverse	TAATGCGGCCGCTAAGGGCAGCCCATACAAATGA AGC

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The expression cassettes were further modified by introducing a GATEWAY® cloning cassette (Invitrogen) into the multicloning site of the respective pAUX vector following the manufacturer's protocol. In a recombination reaction, the cDNAs encoding the open reading frame sequences were transferred from the entry vector obtained as described in Example 4 to the GATEWAY®-enabled pAUX vector. Any combination of the regulatory elements with cDNA sequences of TrCSa, TrCSb, TrCSd, TrMDH and TrPEPC can be obtained. One typical example is given in Figure 126 with expression cassettes comprising the nptll plant selectable marker, TrPEPC, TrCSa and TrMDH.

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Complete expression cassettes comprising any combination of regulatory elements and cDNA sequences to be introduced into the plant were then cut from the auxiliary vectors using the respective homing endonuclease and cloned into the respective restriction site on the binary vector backbone. After verification of the construct by nucleotide sequencing, the binary transformation vector

comprising a number of expression cassettes was used to generate transgenic white clover plants.

EXAMPLE 6

Isolation of regulatory elements to direct expression of chimeric genes encoding CS, MDH and PEPC involved in organic acid biosynthesis

To direct the expression of chimeric white clover genes TrCSa, TrCSb, TrCSd, TrMDH and TrPEPC involved in organic acid biosynthesis to specific tissues, regulatory elements showing specificity for expression in root or root tip tissue were identified and isolated.

Using the BLASTn algorithm, white clover EST sequence collections prepared as detailed in Examples 1 and 2 were searched with nucleotide sequences representing genes with known root-specific expression identified in GenBank as queries. Suitable candidate ESTs were identified and oligonucleotide primers for reverse transcription-PCR (RT-PCR) were designed (see Table 4).

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TABLE 6

Oligonucleotide primers used in reverse transcription-PCR to confirm tissue specificity of candidate white clover ESTs

gene	forward primer (5'->3')	reverse primer (5'->3')
histone (internal control)	CCGATTCCGTTTCAATGGCTCGTA	GCCATCCTTAACCCTAAGCACGT
white clover phosphate transporter homolog	TTGCATTTGCTTGGAACAACTAG	GCAAGAGCAAACATGAAACCA
white clover root iron transporter homolog	ATGGGTCTTGGTGGTTGCA	GCAGCAAGAAGATCAACCAAAGCCA

tip, root and root tip of white clover plants grown in the glasshouse using the TRIZOL method. Reverse transcription was performed using SuperScriptII (Invitrogen) following the supplier's instructions. Preliminary PCR reactions using Dynazyme as the DNA polymerase were set up to determine the correct amount of template using the PCR primers for the internal control (histone). The results of this preliminary PCR were used to set up another round of PCR to determine the optimum number of cycles for linear amplification. The final PCR amplifications

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were performed using the following cycling conditions: 94 °C, 4 min., 1 time; 94 °C, 15 sec., 60 °C, 30 sec., 72 °C, 2 min., x times; 72 °C, 10 min., 1 time. The number of cycles in the amplification (x) was found to be dependent on the relative abundance of transcript and had to be optimised for each template.

RT-PCR results using a white clover histone gene as an internal constitutively expressed control confirmed the tissue-specificity of two candidate ESTs to be root-prevalent (Figure 127 A and B). These were a phosphate transporter homolog (clone name 02wc1DsG07) and a root iron transporter homolog (clone name 05wc1lsB11).

A spotted white clover BAC library consisting of 50,304 clones with an estimated 99% genome coverage (6.3 genome equivalents) was screened using the phosphate transporter homolog EST nucleotide sequence as a probe. A number of positive BAC clones could be identified (Figure 128 A). After Southern hybridisation blotting (Figure 128 B) a 7.5 kb EcoRV genomic DNA fragment was selected and fully sequenced. The fragment contained the phosphate transporter 15 homolog open reading frame and 4 kb of upstream sequence including the promoter region. A physical map of the genomic DNA fragment including the promoter region is shown in Figure 128 C.

EXAMPLE 7

Production by Agrobacterium-mediated transformation and analysis of transgenic white clover plants carrying chimeric genes encoding CS, MDH and PEPC involved in organic acid biosynthesis

A set of binary transformation vectors carrying chimeric white clover genes to alter the expression of the polypeptides involved in organic acid biosynthesis to improve phosphorus acquisition efficiency as well as aluminium and acid soil tolerance in forage plants were produced as detailed in Examples 4 and 5.

Agrobacterium-mediated gene transfer experiments were performed using these transformation vectors.

The production of transgenic white clover plants carrying the white clover TrCSa, TrCSb, TrCSd, TrMDH and TrPEPC cDNAs, either singly or in 30 combination, is described here in detail (Table 7).

PCT/AU2004/000493

Preparation of Agrobacterium

Agrobacterium tumefaciens strain AGL-1 transformed with one of the binary vector constructs detailed in Example 6 were streaked on LB medium containing 50 μg/ml rifampicin and 50 μg/ml kanamycin and grown at 27 °C for 48 hours. A single colony was used to inoculate 5 ml of LB medium containing 50 μg/ml rifampicin and 50 μg/ml kanamycin and grown over night at 27 °C and 250 rpm on an orbital shaker. The overnight culture was used as an inoculum for 500 ml of LB medium containing 50 μg/ml kanamycin only. Incubation was over night at 27 °C and 250 rpm on an orbital shaker in a 2 l Erlenmeyer flask.

10 Preparation of white clover seeds

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1 spoon of seeds (ca. 500) was placed into a 280 μ m mesh size sieve and washed for 5 min under running tap water, taking care not to wash seeds out of sieve. In a laminar flow hood, seeds were transferred with the spoon into an autoclaved 100 ml plastic culture vessel. A magnetic stirrer (wiped with 70% EtOH) and ca. 30 ml 70% EtOH were added, and the seeds were stirred for 5 min. The EtOH was discarded and replaced by 50 ml 1.5% sodium hypochlorite. The seeds were stirred for an additional 45 - 60 min on a magnetic stirrer. The sodium hypochlorite was then discarded and the seeds rinsed 3 to 4 times with autoclaved ddH₂O. Finally 30 ml of ddH₂O were added, and seeds incubated over night at 10 - 15°C in an incubator.

Agrobacterium-mediated transformation of white clover

The seed coat and endosperm layer of the white clover seeds prepared as above were removed with a pair of 18 G or 21 G needles. The cotyledons were cut from the hypocotyl leaving a ca. 1.5 mm piece of the cotyledon stalk. The cotyledons were transferred to a petridish containing ddH_2O . After finishing the isolation of clover cotyledons, ddH_2O in the petridish was replaced with Agrobacterium suspension (diluted to an $OD_{600} = 0.2 - 0.4$). The petridish was sealed with its lid and incubated for 40 min at room temperature.

After the incubation period, each cotyledon was transferred to paper towel using the small dissection needle, dried and plated onto regeneration medium RM73. The plates were incubated at 25°C with a 16h light/8h dark photoperiod. On day 4, the explants were transferred to fresh regeneration medium. Cotyledons

PCT/AU2004/000493 WO 2004/089066

39

transformed with Agrobacterium were transferred to RM73 containing cefotaxime (antibacterial agent) and gentamycin. The dishes were sealed with Parafilm and incubated at 25°C under a 16/8 h photoperiod. Explants were subcultured every three weeks for a total of nine weeks onto fresh RM 73 containing cefotaxime and gentamycin. Shoots with a green base were then transferred to root-inducing medium RIM. Roots developed after 1 - 3 weeks, and plantlets were transferred to soil when the roots were well established.

Preparation of genomic DNA for real-time PCR and analysis for the presence of transgenes

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3 - 4 leaves of white clover plants regenerated on selective medium were harvested and freeze-dried. The tissue was homogenised on a Retsch MM300 mixer mill, then centrifuged for 10 min at 1700xg to collect cell debris. Genomic DNA was isolated from the supernatant using Wizard Magnetic 96 DNA Plant System kits (Promega) on a Biomek FX (Beckman Coulter). 5 µl of the sample (50 μl) were then analysed on an agarose gel to check the yield and the quality of the 15 genomic DNA.

Genomic DNA was analysed for the presence of the transgene by real-time PCR using SYBR Green chemistry. PCR primer pairs were designed using MacVector (Accelrys) or PrimerExpress (ABI). The forward primer was located within the 35S² promoter region and the reverse primer within the transgene to amplify products of approximately 150 - 250 bp as recommended. The positioning of the forward primer within the 35S² promoter region guaranteed that endogenous genes in white clover were not detected.

5 μl of each genomic DNA sample was run in a 50 μl PCR reaction including SYBR Green on an ABI 7700 (Applied Biosystems) together with samples containing DNA isolated from wild type white clover plants (negative control), samples containing buffer instead of DNA (buffer control) and samples containing the plasmid used for transformation (positive plasmid control). Cycling conditions used were 2 min. at 50 °C, 10 min. at 95 °C and then 40 cycles of 15 sec. at 95 °C, 1 min. at 60 °C. 30

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Preparation of genomic DNA and analysis of DNA for presence and copy number of transgene by Southern hybridisation blotting

Genomic DNA for Southern hybridisation blotting was obtained from leaf material of white clover plants following the CTAB method. Southern hybridisation blotting experiments were performed following standard protocols as described in Sambrook *et al.* (1989). In brief, genomic DNA samples were digested with appropriate restriction enzymes and the resulting fragments separated on an agarose gel. After transfer to a membrane, a cDNA fragment representing a transgene or selectable marker gene was used to probe the size-fractionated DNA fragments. Hybridisation was performed with either radioactively labelled probes or using the non-radioactive DIG labelling and hybridisation protocol (Boehringer) following the manufacturer's instructions.

Plants were obtained after transformation with all chimeric constructs and selection on medium containing gentamycin. Details of plant analysis are given in Table 5 and Figures 130, 131 and 132.

TABLE 7

Transformation of white clover with binary transformation vectors comprising cDNAs encoding CS, MDH and PEPC involved in organic acid biosyntheses, selection and molecular analysis of regenerated plants.

construct	cotyledons transformed	selection into RIM	llos	QPCR-positive	Southern	copy number range
pPZP221-35S2::TrMDH	2739	72	45	43	p/u	
pPZP221-35S2::TrCS	2550	39	7	pu	p/u	
pPZP221-35S2::TrPEPC	2730	44	10	pu	n/d	

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 - Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as outlined herein.

CLAIMS

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- A substantially purified or isolated nucleic acid or nucleic acid 1. fragment encoding an organic acid biosynthesis enzyme polypeptide selected from the group consisting of a citrate synthase (CS) polypeptide; a CS-like polypeptide; a malate dehydrogenase (MDH) polypeptide; a MDH-like polypeptide; phosphoenolpyruvate carboxylase (PEPC) polypeptide; and a PEPC-like polypeptide; or a functionally active fragment or variant of such a polypeptide, from a clover (Trifolium), medic (Medicago), ryegrass (Lolium) or fescue (Festuca) species.
- A nucleic acid or nucleic acid fragment wherein said nucleic acid or 2. 10 nucleic acid fragment is from white clover (Trifolium repens) or perennial ryegrass (Lolium perenne).
 - A nucleic acid or nucleic acid fragment encoding a CS or CS-like 3. polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102, 104, 114, 118 and 122 hereto (SEQ ID NOS 1, 3 to 10, 11, 13 to 16, 17, 19, 327, 329 to 335, 336, 338 to 344, 349, 351, 353 respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).
- A nucleic acid or nucleic acid fragment encoding a MDH or MDH-like 4. polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequence shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 25 76, 78, 79, 81, 82 and 84 hereto (SEQ ID NOS 21, 23 to 29; 30, 32 to 33, 34, 36, 38, 40, 42 to 43, 44, 46, 48 to 110, 111, 113, 115, 117 to 182, 183, 185, 205, 207 to 217, 218, 220 to 251, 252, 254 to 270, 271, 273 to 275, 276, 278 to 287, 288, 290 to 292, 293, 295 to 296, 297, 299 to 301, 304 to 305, 306, 308); (b) complements of the sequences recited in (a); (c) sequences antisense to the 30 sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).

- 5. A nucleic acid or nucleic acid fragment encoding a PEPC or PEPC-like polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86, 88, 89, 91, 92, 94, 95, 97 and 110 hereto (SEQ ID NOS 187, 189, 191 to 197, 199, 201, 203, 310, 312 to 314, 315, 317 to 318, 319, 321 to 322, 323, 325 and 347 respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).
- 10 6. A construct including one or more nucleic acids or nucleic acid fragments according to any one of claims 1 to 5.
 - 7. A construct according to claim 6 including nucleic acids or nucleic acid fragments encoding both (a) a CS polypeptide or a CS-like polypeptide and (b) a MDH polypeptide or a MDH-like polypeptide.
 - 8. A construct according to claim 6 including nucleic acids or nucleic acid fragments encoding both (a) a CS polypeptide or a CS-like polypeptide and (b) a PEPC polypeptide or a PEPC-like polypeptide.
 - 9. A construct according to claim 6 including nucleic acids or nucleic acid fragments encoding both (a) a MDH polypeptide or a MDH-like polypeptide and (b) a PEPC polypeptide or a PEPC-like polypeptide.
 - 10. A construct according to claim 6 including nucleic acids or nucleic acid fragments encoding all three of (a) a CS polypeptide or a CS-like polypeptide; (b) a MDH polypeptide or a MDH-like polypeptide; and (c) a PEPC polypeptide or a PEPC-like polypeptide.
- 11. A construct according to any one of claims 6 to 10 wherein the one or more nucleic acids or nucleic acid fragments are operably linked to one or more regulatory elements, such that the one or more nucleic acids or nucleic acid fragments are each expressed.
- 12 A construct according to Claim 11, wherein the one or more 30 regulatory elements include a promoter and a terminator, said promoter, nucleic acid or nucleic acid fragment and terminator being operably linked.

- 13. A plant cell, plant, plant seed or other plant part, including a construct according to any one of claims 6 to 12.
- 14. A plant, plant seed or other plant part derived from a plant cell or plant according to Claim 13.
- 5 15. A method of modifying one or more of organic acid synthesis; organic acid secretion; nutrient acquisition; aluminium and acid soil tolerance; or nitrogen fixation and nodule function; in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to any one of claims 1 to 5, or a construct according to any one of claims 6 to 12.
 - 16 A method according to claim 15 wherein said method includes introducing into said plant effective amounts of nucleic acids or nucleic acid fragments encoding both (a) a CS polypeptide or CS-like polypeptide and (b) a MDH polypeptide or MDH-like polypeptide.
- 17. A method according to claim 15 wherein said method includes introducing into said plant effective amounts of nucleic acids or nucleic acid fragments encoding both (a) a CS polypeptide or a CS-like polypeptide and (b) a PEPC polypeptide or a PEPC-like polypeptide
- 18. A method according to claim 15 wherein said method includes 20 introducing into said plant effective amounts of nucleic acids or nucleic acid fragments encoding both (a) a MDH polypeptide or a MDH-like polypeptide and (b) a PEPC polypeptide or a PEPC-like polypeptide.
 - 19. A method according to claim 15 wherein said method includes introducing into said plant effective amounts of nucleic acids or nucleic acid fragments encoding all three of (a) a CS polypeptide or a CS-like polypeptide; (b) a MDH polypeptide or a MDH-like polypeptide; and (c) a PEPC polypeptide or a PEPC-like polypeptide.
 - 20. A method according to any one of claims 15 to 19 wherein the method is modifying nutrient acquisition and the nutrient is phosphorous.

- 21. Use of a nucleic acid or nucleic acid fragment according to any one of claims 1 to 5, and/or nucleotide sequence information thereof, and/or single nucleotide polymorphisms thereof as a molecular genetic marker.
- 22. A substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid fragment according to any one of claims 1 to 5.
 - 23. A nucleic acid or nucleic acid fragment including an SNP according to Claim 22, wherein said nucleic acid or nucleic acid fragment is from white clover (*Trifolium repens*) or perennial ryegrass (*Lolium perenne*).
- 10 24. A substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of CS and CS-like, MDH and MDH-like and PEPC and PEPC-like; and functionally active fragments and variants thereof.
- 25. A polypeptide according to Claim 24, wherein said polypeptide is from white clover (*Trifolium repens*) or perennial ryegrass (*Lolium perenne*).
 - 26. A polypeptide encoded by a nucleic acid or nucleic acid fragment according to any one of claims 1 to 5.
 - 27. A polypeptide according to Claim 24 or 25, wherein said polypeptide is CS or CS-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 2, 5, 8, 10, 100, 103, 115, 119, 123 hereto (SEQ ID NOS 2, 12, 18, 20, 328, 337, 350, 352 and 354 respectively); and functionally active fragments and variants thereof.

- 28. A polypeptide according to Claim 24 or 25, wherein said polypeptide is MDH or MDH-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 12, 15, 18, 20, 22, 24, 27, 29, 32, 34, 36, 39, 41, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83 and 85 hereto (SEQ ID NOS 22, 31, 35, 37, 39, 41, 45, 47, 112, 114, 116, 184, 186, 206, 219, 253, 272, 277, 289, 294, 297, 303, 307 and 309, respectively) and functionally active fragments and variants thereof.
- 30 29. A polypeptide according to Claim 24 or 25, wherein said polypeptide is PEPC or PEPC-like and includes an amino acid sequence selected from the

47

group consisting of sequences shown in Figures 43, 45, 48, 50, 52, 54, 87, 90, 93, 96, 98 and 111 hereto (SEQ ID NOS 188, 190, 198, 200, 202, 204, 311, 316, 320, 324, 326, and 348, respectively); and functionally active fragments and variants thereof.

1/241

LpCSa	:	* GNNTTATAT	rgacggggj	20 ATGAGGGAATTC	* TTCGCTAC	40 CAGAGGCTATCC	* \ATTGAGGA	60 GGT :		60
LpCSa	:	GGCTGAAAG	* CAGCTCGT"	80 FTGTTGAGGTC	* GCTACCT(100 CTTAATGTATGG	* BAATTTGCC	120 CAC	:	120
LpCSa	:	CCAGAGTCA	* ACTGGCAG	140 GCTGGGAGTTT	* GCAATTTC	160 GCAGCACTCTGC		180 AGG	:	180
LpCSa	:	ACTCTTGGA	* TATAATAC	200 AATCAATGCCT	* CATGATGC	220 CCACCCCATGGG	* TGTCCTTGC	240 CAG	:	240
LpCSa	:	TGCAATGAG	* CACACTTI	260 CAGTCTTCCAT	* CCAGATGC	280 AAACCCTGCTCT	* TAGAGGTC!	300 AAGA	:	300
LpCSa	:	TCTATACAA	* \GTCGAAGO	320 AGGTTAGGGAT	* AAGCAAAT	340 TTGTACGAGTTCT	* TGGGAAGG	360 CACC	:	360
LpCSa	. :	agtaatag0	* CAGCTGCAC	380 GCCTATCTGAGA	* TTAGCAGO	400 BAAGGCCCTTTGT	* CCTTCCTT	420 CAAA	:	420
LpCSa	l :	: TAATCTCT(* CTTATTCA	440 BAAAATTTCTTC	* TATATGC!	460 PGGACTCTATGGO	* GTGACAAAG	480 ATTA	:	480
LpCSa	a.	: TAAGCCAA	* ATCCCAGA	500 CTTGCCCGGGT	* CTGGATG	520 FCCTTTTTATTC	* ITCATGCTG	540 AACA	:	540
LpCSa	a	: CGAAATGA	* ACTGCTCA	560 ACAGCTGCTGT	* TAGGCACC	580 TTGCTTCAAGTG	* GTGTCGATG	600 TCTT	:	600
LpCS	a	: CACTGCTC	* TTTCTGGT	620 GCTGTTGGAGC	* TCTATATG	640 GTCCACTGCATG	* GTGGCGCA!	660 ATGA		660
T.nCS	2	· GGCGGTAC	* !TTAAAATC	680 TTAAATGAGAT	* TGGAAGTG	700 TAGAGAATATTC	* CGGAATTC	720 ATTGA		720

FIGURE 1

2/241

		*	740	*	760	*	780		
LpCSa	:	GGGAGTGAAGA	ACAGGAAGCGGA	AAATGTCTGGT'	TTTGGGCAC	CGTGTGTATAAG	ATTA	:	780
		*	800	*	820	*	840		
LpCSa	:	TGATCCTCGTG	CTAAAGTCATCC	GGAAGTTAGCG	GAGGAGGTT	TTCACGATTGTG	GGACG	:	840
		*	860	*	880	*	900		
LpCSa	:	GGATCCTCTTA	TCGAGGTAGCTG	TTGCTTTGGAG	AAGGCAGCA	CTGTCAGACGAG	TATTT	:	900
		*	920	*	940	*	960		0.50
LpCSa	:	TATCAAGAGGA	AGCTGTATCCAA	ATGTGGATT'I'I	TATTCTGGC	CTAATATATAGG	GCAAT	:	960
LpCSa	:	* GGGATTCCCTA	980 CAGAGTTTTTCC	* CTGTTCTGTTT	1000 GCAGTTCCT	* CGCATGGCTGGT	1020 TGGTT	:	1020
-									
Tadea		*	1040	* >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	1060 ***********************************	* ATGAGGCCCCAA	1080		1080
ьрсѕа	:	AGCACATTGGA	AGGAGICACIIG	AIGACCCGAC	MAIMMAAII	AIGAGGCCCAA	CAGGI	•	1000
T GO -		*	1100	*	1120	* .CGGGTGCCATCA	1140		1140
ьрсѕа	:	ATACACCGGTA	CTTGGCTAAGGC	ATTACACCCCA	GIGAGAGAA	AJIAJJBIBBBJ.	AGCGA	•	1140
		*	1160	*	1180	*	1200		1200
ьрсѕа	:	CAGTGAGCAGC	TTGGGCAGATCG	CTACATCAAAC	GCGACGAGG	CGTCGGCGTGCT	GGCIC	•	1200
		*	1220	*	1240	*	1260		1260
Lpcsa	:	TGCCCTGTAGA	ACAGTCTGCATG	ATACAGCATAC	AGTCCACAC	AATAAACCAAGC	TGCCA	:	1260
		*	1280	*	1300	*	1320		
LpCSa	:	AGGGCCACGGC	TGCTTAAATCTG	GGAGCTGCTA1	'ACT'I'G1'G1'I	'ATCACGTATATA	TAGGC	:	1320
		*	1340	*	1360	*	1380		
LpCSa	:	AATAAACTAAT	PAATGCCGCCAGG	ACACTTCACTG	GTGGTCATG	TGAAGTTGGTAG	TAGAA	:	1380
		*	1400	*	1420	*	1440		
LpCSa	:	TGCACTTGTA	ACGTGTTGTTAA'I	TTGTTATCCTG	CAATGTAC	CTCTATAAACTC	FITCAG	:	1440
		*	1460	*	1480	*	1500		
LpCSa	:	TATCTTGAAA	STCTTAATCATG1	rggaccaatgar	AGACATAGAT	CAAGTTCTTTGC	ATGGG	:	1500
		*	1520	*	1540	*			
Taces		רממרממריים <i>יי</i> י		י א א היהיהיהיה א היכ		''''''''''''''''''''''''''''''''''''	550		

FIGURE 1 (cont.)

		* 20 * 40 * 60		
LpCSa	:	YIDGDEGILRYRGYPIEEVAESSSFVEVAYLLMYGNLPTQSQLAGWEFAISQHSAVPQGL	:	60
ĽрСSа	:	* 80 * 100 * 120 LDIIQSMPHDAHPMGVLASAMSTLSVFHPDANPALRGQDLYKSKQVRDKQIVRVLGKAPV	:	120
LрСSа	:	* 140 * 160 * 180 IAAAAYLRLAGRPFVLPSNNLSYSENFLYMLDSMGDKDYKPNPRLARVLDVLFILHAEHE .	:	180
LpCSa	:	* 200 * 220 * 240 MNCSTAAVRHLASSGVDVFTALSGAVGALYGPLHGGANEAVLKMLNEIGSVENIPEFIEG	:	240
LpCSa	:	* 260 * 280 * 300 VKNRKRKMSGFGHRVYKNYDPRAKVIRKLAEEVFTIVGRDPLIEVAVALEKAALSDEYFI	:	300
LpCSa	:	* 320 * 340 * 360 KRKLYPNVDFYSGLIYRAMGFPTEFFPVLFAVPRMAGWLAHWKESLDDPDNKIMRPQQVY	:	360
LpCSa	:	* 380 * 400 TGTWLRHYTPVRERVPSSDSEQLGQIATSNATRRRRAGSAL: 401		

		*	20	*	40	*	60		
LpCSa1.	:	GNNTTATATTGACGG	GGATGAGGG.	AATTCTTCGC	CTACAGAGGCTA	TCCAATTGAG	GAGGT	:	60
LpCSa2	:							:	-
LpCSa3	:							:	-
LpCSa4	:							:	_
LpCSa5	:							:	-
LpCSa6	:						-	:	-
LpCSa7	:				,			:	-
LpCSa8	:							:	-
		*	80	*	100	*	120		
LpCSa1	:	GGCTGAAAGCAGCTC	GTTTGTTGA	GGTCGCCTA	CCTCTTAATGT	TGGGAATTTC	SCCCAC	:	120
LpCSa2	:							:	_
LpCSa3	:							:	-
LpCSa4	:							:	
LpCSa5	:							:	-
LpCSa6	:							:	-
LpCSa7	:							:	-
LpCSa8	:							:	-
		*	140	*	160	*	180		
LpCSa1	:	CCAGAGTCAACTGG	CAGGCTGGGA	GTTTGCAAT	TTCGCAGCACT	CTGCTGTTCC'	rcaagg	:	180
LpCSa2	:		CAGGCTGGGA	GTTTGCAAT	TTCGCA-CACT	CTGCTGTTCC'	rcangn	:	46
LpCSa3	:							:	-
LpCSa4	:			-				:	-
LpCSa5	:			- -				:	_
LpCSa6	:			.				:	-
LpCSa7	:							:	-
LpCSa8	:			- -				:	-
_									
		*	200	*	220	*	240		
LpCSa1	:	ACTCTTGGATATAA'	TACAATCAAT	TGCCTCATGA	TGCCCACCCCA	TGGGTGTCCT	TGCCAG	:	240
LpCSa2	:	ACTCTTGGATATAA'	TACAATCAAT	rgcctcatga	TGCCCACCCCA	TGGGTGTCCT	TGCCAG	:	106
LpCSa3	:							:	-
LpCSa4	:							:	-
LpCSa5	:							:	-
LpCSa6	:							:	_
LpCSa7	:							:	-
LpCSa8	:							:	-
							2.00		
		*	260	*	280	* - CIT CITITITE TO SEE	300		200
LpCSa1	:	TGCAATGAGCACAC	TTTCAGTCT	rccarccaga	TGCAAACCCTG	CTCTTAGAGG	TCAAGA	:	300
LpCSa2	:	TGCAATGAGCACAC	HITTCAGT CT	ICCATCCAGA	NIGCAAACCCIG	CICITAGAGG	ICAAGA	:	166
LpCSa3	:							:	-
LpCSa4								:	-
LpCSa5								:	_
LpCSa6	:							:	-
LpCSa7	:							:	_

		*	320	*	340	*.	360		
LpCSa1	: 1	TCTATACAAGTCGA	AGCAGGTTA	GGGATAAGCAA	ATTGTACGAG	TTCTTGGGAAG	GCACC :	: :	360
LpCSa2	.	TCTATACAAGTCGA <i>I</i>	AGCAGGTTA	GGGATAAGCA	ATTGTACGAG	TTCTTGGGAAG	GCACC	: :	226
LpCSa3	:						,	:	_
LpCSa4	•							:	_
LpCSa5	:							:	-
LpCSa6	:							:	_
LpCSa7	:							:	_
	•							•	_
LpCSa8	•							•	
		*	380	*	400	*	420		
LpCSa1	:	AGTAATAGCAGCTG	CAGCCTATC	TGAGATTAGC	AGGAAGGCC <mark>T</mark> T	TTGTCCTTCCT	TCAAA	:	420
LpCSa2	:	AGTAATAGCAGCTG	CAGCCTATC	TGAGATTAGC	aggaaggcc c t	TTGTCCTTCCT	TCAAA	:	286
LpCSa3	:							:	-
LpCSa4	:							:	_
LpCSa5	:					. .		:	-
LpCSa6	:							:	_
LpCSa7	:							:	_
	:							:	_
LpCSa8	•							-	
		*	440	*	460	*	480		
LpCSa1	:	TAATCTCTCTTATT	CAGAAAATT	TCTTGTATAT	GCTGGACTCTA	ATGGGTGACAA	AGATTA	:	480
LpCSa2	:	TAATCTCTCTTATT	CAGAAAAT'I	TCTTGTATAT	GCTGGACTCT	ATGGGTGACAA	AGATTA	:	346
LpCSa3	:							:	-
LpCSa4	:							:	_
LpCSa5	:							:	-
LpCSa6	:							:	_
LpCSa7	:							:	_
	:							:	_
LpCSa8	٠							-	
						·			
		*	500	*	520	*	540		
LpCSa1	:	TAAGCCAAATCCCA	GACTTGCC	CGGGTTCTGGA	TGTCCTTTTT	ATTCTTCATGC	TGAACA	:	540
LpCSa2	:	TAAGCCAAATCCCA	GACTTGCC	CGGGTTCTGGA	TGTCCTTTTT	ATTCTTCATGC	TGAACA	:	406
LpCSa3	:					NTTNTGC	rg-aca	:	12
LpCSa4	:							:	-
LpCSa5	:							:	-
LpCSa6	:							:	-
LpCSa7	:							:	-
LpCSa8	:							:	_
		*	560	*	580	*	600		
LpCSa1	:	CGAAATGAACTGCT	CAACAGCT	GCTGTTAGGCA	ACCTTGCTTCA	AGTGGTGTCGA	TGTCTT	:	600
LpCSa2	:	CGAAATGAACTGCT	CAACAGCT	GCTGTTAGG <i>CA</i>	ACCTTGCTTCA	AGTGGTGTCGA	TGTCTT	:	466
LpCSa3	:	CGAAATGA <mark>N</mark> CTGCT	CAACAGCT	GCTGTTAGGC	ACCTTGCTTCA	AGTGGTGTCGA	TGTCTT	:	72
LpCSa4	:							:	-
LpCSa5	:							:	-
LpCSa6	:							:	-
LpCSa7	:							:	-
Lnceae								:	-

	*	620	*	640	*	660	
LpCSal :	CACTCCTCTTT	TGGTGCTGTTG	CACCTCTATAT		ATGGNGGCGC		660
LpCSa2 :	CACTGCTCTTT	CTGGTGCTGTTG	GAGCTCTATAT	GGTCCACTGC	ATGGTGGCGC	AAATGA :	526
LpCSa3 :	CACTGCTCTTT	TGGTGCTGTTG	GAGCTCTATA	rGGTCCACTGC	ATGGTGGCGC	AAATGA	132
LpCSa4:	CACICCICI	rosiscione				~	_
LpCSa5 :						:	_
LpCSa6 :							-
LpCSa7 :							-
LpCSa8 :						:	-
превас .							
	*	680	*	700	*	720	
LpCSa1 :	NGCGGTACTT-	AAATGTTAAATO	AGATTGGAAG'	IGTAGAGAATA	TTCCGGAATT	CATTGA	: 719
LpCSa2 :	GGCGGTACTTA	AAATGTTAAATO	AGATTGGAAG'	TGTAGAGAAT <i>A</i>	ATTCCGGAATT	CATTGA	: 586
LpCSa3 :	GGCGGTACTTA	AAATGTTAAATO	AGATTGGAAG'	IGTAGAGAATA	TTCCGGAATT	CATTGA	: 192
LpCSa4 :							: -
LpCSa5 :							: -
LpCSa6:							: -
LpCSa7 :							: -
LpCSa8 :							: -
-							
	•						
	*	740	<u>*</u>	760	*	780	
LpCSa1 :	GGGAGTGAAGA	ACAGGAAGCGG	AAATGTCTGG	NTTTGGGCAC	<u> </u>		: 763
LpCSa2 :	GGGAGTGAAGA	ACAGGAAGCGG?	AAATGTCTGG	T'ITTGGGCAC(CGTGTGTATAA	GAATTA	: 646
LpCSa3 :	GGGAGTGAAGA	ACAGGAAGCGG	AAAATGTCTGG	CTTTGGGCAC	CGTGTGTATAA	GAATTA	: 252
LpCSa4 :						G <u>A</u>	: 2
LpCSa5 :							: -
LpCSa6 :							: -
LpCSa7 :							: -
LpCSa8 :							: -
	*	800.	*	820	*	840	
LpCSa1 :							: -
LpCSa2 :	TCATCCTCGTC	CTAAAGTCATC	CGGAAGTTAGC	GGN			: 682
LpCSa3 :	TGATCCTCGTC	CTAAAGTCATC	CGGAAGTTAGC	GGAGGAGGTT'	TTCACGATTGT	rgggacg	: 312
LpCSa4 :	TTATCCTCCC	CTAAAGTCAT-	CCCCAGTTAGC	GGAGGAGGTT'	TTCACGATTGT	rgggacg	: 61
LpCSa5			-GGAAGTTAGC	GGAGGAGGTT"	TTCACGATTGT	rgggacg	: 37
LpCSa6							: -
LpCSa7							: -
LpCSa8							: -
_ <u>_</u>							
	*	860	*	880	*	900	
LpCSa1							: -
LpCSa2							: -
LpCSa3	GGATCCTCTT	TCGAGGTAGCT	GTTGCTTTGGA	AGAAGG <mark>T</mark> AGCA	CTGTCAGACG	AGTATTT	: 372
LpCSa4		TCGAGGTAGCT					: 121
LpCSa5	GGNTCCTCTT	ATCGAGGTAGCT			CTGTCAGACG	AGTATTT	: 97
LpCSa6					-TNNCAGACG		: 16
LpCSa7					GTCAGACG	ACTATTT	: 15
LpCSa8							: -

		*	920	*	940	*	960	
LpCSa1 :							:	-
LpCSa2 :							· :	-
LpCSa3 :			GTATCCAAATGTG					432
LpCSa4 :	TATCAAG	AGGAAGCTO	TATCCAAATGTG	GATTTTT	ATTCTGGCCTAAT	ATATAGGC	CAAT :	181
LpCSa5 :			STATCCAAATGTG					157
LpCSa6 :			STATCCAAATGTG					76
LpCSa7 :	TATCAAG	AGGAAGCTG	TATCCAAATGTG	GATTTTT	ATTCTGGCCTAAT	ATATAGGO	GCAAT :	75
LpCSa8 :							:	-
		*	980	*	1000	*	1020	
LpCSa1 :							:	_
LpCSa2:								_
LpCSa3 :	CCCATTC	CCTACAGAC	STTTTTCCCTGTT	CTGTTTG	CAGTTCCTCGCAI	GGCTGGT	regit :	492
LpCSa4 :	GGGATTC	CCTCCAGAC	GTTTTTCCCTGTT	CTGTTTG	CAGTTCCTCGCAT	GGCTGGT	rggtt :	241
LpCSa5 :	GGGATTC	CCTACAGAC	GTTTTTCCCTGTT	CTGTTTG	CAGTTCCTCGCAI	GGCTGGT	rggtt :	217
LpCSa6 :			GTTTTTCCCTGTT					136
LpCSa7 :			STTTTTCCCTGTT					135
LpCSa8 :							:	-
- L								
						_		
		*	1040	*	1060	*	1080	
LpCSa1 :							:	-
LpCSa2 :					2 m 2 2 2 2 m 2 m c 2 (acccca a	:	552
LpCSa3 :	AGCACAT	"TGGAAGGA	GTCACTTGATGAC	CCCGACA	ATAAAATTATGAC	IGCCCCAA	CAGGI:	301
LpCSa4:	AGCACA'I	"I'GGAAGGA	GTCACTTGATGA	CCCGACA	ATAAAATTATGAC	CCCCAA	CAGGI	277
LpCSa5:	AGCACA'I	TGGAAGGA	GTCACTTGATGAC GTCACTTGATGAC	CCCGACA	AIAAAAIIAIGAC	CCCCCA	CAGGI:	
LpCSa6 :	AGCACAT	TGGAAGGA	GTCACTTGATGAC GTCACTTGATGAC	CCCGACA	AIAAAAIIAIGAC	GCCCCAA	CACCE:	195
LpCSa7 :	AGCACAT	TGGAAGGA	GICACIIGAIGAC	CCCGACA	AIAAAAIIAIGA			-
LpCSa8 :							•	
		*	1100	*	1120	*	1140	
LpCSa1 :							:	-
LpCSa2 :							<u></u> :	-
LpCSa3 :	ATACACO	CGGTACTTG	GCTAAGGCATTA	CACCCCAG	TGAGAGAACGGG'	IGCCATCA	AGCGA :	612
LpCSa4 :	ATACACO	CGGTACTTG	GCTAAGGCATTA	CACCCCAG	TGAGAGAACGGG'	TGCCATCA	AGCGA :	361
LpCSa5 :	ATACACO	CGGTACTTG	GCTAAGGCATTA(CACCCCAG	TGAGAGAACGGG'	IGCCATCA	AGCGA :	337
LpCSa6 :	ATACACO	CGGTACTTG	GCTAAGGCATTAG	CACCCCAC	TGAGAGAACGGG'	IGCCATCA	AGCGA:	256
LpCSa7 :	ATACAC	CGGTACTTG	GCTAAGGCATTA	CACCCCAG	TGAGAGAACGGG'	IGCCATCA	AGCGA	255
LpCSa8 :	:						:	-
			1160	*	1180	*	1200	
LpCSal :							;	-
LpCSa2								: -
LpCSa3	CAGTGA	GCAGCTTGG	GCAGATC <mark>A</mark> CTAC	ATCAAACC	CGACGAGGCGTC	GGCGTGC1	GG <mark>T</mark> TC	672
LpCSa4	CAGTGA	GCAGCTTGG	GCAGATCGCTAC	ATCAAACC	CGACGAGGCGTC	GGCGTGCT	GGCTC	: 421
LpCSa5	CAGTGA	GCAGCTTGG	GCAGATCGCTAC	ATCAAACO	CGACGAGGCGTC	GGCGTGCT	GGCTC	: 397
LpCSa6	CAGTGA	GCAGCTTGG	GCAGATCGCTAC.	ATCAAACC	CGACGAGGCGTC	GGCGTGC1	GGCTC	: 316
LpCSa7	CAGTGA	GCAGCTTGG	GCAGATCGCTAC.	ATCAAACO	CGACGAGGCGTC	GGCGTGCT	GGCTC	: 315
LpCSa8	:		GCAGATCGCT <mark>-</mark> C	ATCAAACC	GCG <mark>T</mark> CGAGGCGTC	GGCGTGCT	GGCTC	: 45

			*	1220	*	1240	*	1260	
LpCSa1	:							:	: -
LpCSa2	•							- :	; –
LpCSa3	. 1	тессстет	AGAACA	GTCTGCATGATACA	GCATACA	GTCCACACAATAA	ACCAAGC'	rgcca :	732
LpCSa4	:	TGCCCTGT	AGAACA	GTCTGCATGATACA	GCATACA	GTCCACACAATA?	ACCAAGC	rgcca :	: 481
LpCSa5	:	TGCCCTGT	TAGA ACA	GTCTGCATGATACA	GCATACA	GTCCACACAATAA	ACCAAGC'	FGCCA :	: 457
LpCSa6	:	TGCCCTGT	TAGAACA	GTCTGCATGATACA	GCATACA	GTCCACACAATAA	ACCAAGC'	rgcca :	: 376
LpCSa7	•	TGCCCTGT	TACAACA	GTCTGCATGATACA	GCATACA	GTCCACACAATAA	ACCAAGC	rgcca :	: 375
LpCSa7	:	TCCCCTGI	TAGAACA	GTCTGCATGATACA	GCATACA	GTCCACACAATAA	ACCAAGC	rgcca :	: 105
презав	•	IGCCCIGI	ACARCA	<u> </u>		<u> </u>			
			*	1280	*	1300	*	1320	
LpCSa1									: -
LpCSa1	:						- -		: -
LpCSa2	:	ACCCCCA(CCCTCC	TTAAATN					: 753
	:	AGGGCCAC		TTAAATCTGGGAGC	тсстата	CTTGTGTTATCA	CGTATATE	TAGGC	: 541
LpCSa4	:	AGGGCCAC		CTTAAATCTGGGAGC	TTGCTATA	CTTGTGTTATCA	GTATATA	TAGGC	: 517
LpCSa5	:	AGGGCCA	ZEGCTGC	TTAAATCTGGGAG(TTCCTATA	CTTGTGTTATCA	CTATATA	TAGGC	: 436
LpCSa6	:	AGGGCCA		TTAAATCTGGGAG(CTTCTCTTATCA	СТАТАТА	TAGGC	: 435
LpCSa7	:	AGGGCCAG	CGGCTGC	TTAAATCTGGGAG(CTTAAATCTGGGAG(CTATATA	TAGGC	: 165
LpCSa8	:	AGGGCCAG	CGGCTGC	TTAAATCIGGGAGG	LIGCIALE	CITGIGITATCA	COLATALA	INCCC	
				1340	*	1360	*	i380	
			~	1340		1300			
LpCSa1	:								: _
LpCSa2	:								: -
LpCSa3	:			rgccgccaggacac'			CTTCCTAC	TACAA	: 601
LpCSa4	:	AATAAAC'	TAATAAT	rgccgccaggacac' rgccgccaggacac'	TTCACTG(TIGGICAIGIGAA	CTTCCTAC	TACAA	: 577
LpCSa5	:	AA'TAAAC'	TAATAAT	rgccgccaggacac	TICACIGO	AMOURAL TOUTON	GIIGGIAG	TAGAA	: 496
LpCSa6	:	AATAAAC	TAATAA:	rgccgccaggacac'	THEACTE	TOGICAIGIGAA	GIIGGIAC		: 495
LpCSa7	:	AATAAAC	TAATAAT	rgccgccaggacac'	TTCACTG	TGGTCATGIGAA	GIIGGIAG	TAGAA	: 225
LpCSa8	:	AATAAAC	TAATAA'	rgccgccaggacac'	TTCACTG	FIGGICAIGIGAA	GIIGGIAG	IAGAA	. 223
		•	*	1400	•	1420	*	1440	
			•	1400					
LpCSa1	:								
LpCSa2	:								: -
LpCSa3	:		22222	TGTTGTTAATTTGT	TATCCTC	CA A TOTA COOTOT	ATAAACTC	TTCAG	: 661
LpCSa4	:	TGCACTT	GTAACG	TGTTGTTAATTTGT TGTTGTTAATTTGT	TATCCIG	CAAIGIACGCICI	PATABACTO	TTCAG	: 637
LpCSa5	:	TGCACTT	GTAACG	TGTTGTTAATTTGT TGTTGTTAATTTGT	TATCCIG	CAAIGIACGCICI	NTANACTO	TTTCAG	: 556
LpCSa6	:	TGCACTT	'GTAACG'	TGTTGTTAATTTGT TGTTGTTAATTTGT	TAICCIG	CAAIGIACGCICI	ATAAACTC	TTTCAC	: 555
LpCSa7		TGCACTT	'GTAACG	TGTTGTTAATTTGT	TAICCIG	CAAIGIACGCICI	AIMAACIC	TTTCAC	: 285
LpCSa8	:	TGCACTI	'GTAACG'	TGTTGTTAATTTGT	TATCCIG	CAAIGIACGCICI	ATAAACIO	BIICAG	. 205
			*	1460	*	1480	*	1500	
			*	1460		1400			
LpCSa1									• -
LpCSa2									
LpCSa3					2077 077	CACATACATCAA		CATCCC	: 720
LpCSa4		TGTCTTC	AAAGTC	TTAATCATGTGGAC	CAA GAA	GACATAGATCAAC	LICILIG		: 666
LpCSa5		TATCTT	SAAAGTC	TTANTCCNNNNAAA	AAA		TOTAL CONTROL	CATCCC	: 615
LpCSa6		TATCTTC	BAAAGTC	TTAATCATGTGGAC	CAA-GAA	GACATAGATCAA(TICILIE	CAIGGG	
LpCSa7		TATCTTC	GAAAGTC	TTAATCATGTGGAC	CAATCAA				: 597
LpCSa8	:	TATCTTC	SAAAGTC	AAAAA <mark>A</mark> AA <mark>AATT</mark>					: 310

		*	1520	*	1540	*		
LpCSa1	:						:	-
LpCSa2	:						:	•
LpCSa3	:						:	-
LpCSa4	:	CGGCGGCTGTTT	CTTTGG <mark>N</mark> AAAAAA				:	74!
LpCSa5	:						:	•
LpCSa6	:	CGGCGGCTGTT	CTTTCTCTTTTCCT	CTTTTTAT	GGGAGTCTTT	TTTACC	:	665
LpCSa7	:						:	•
LnCGaR							:	

LpCSb :	CTTCT	* CCCTGTNAC	20 IGCTCTCCAA	* IGACACAGTTT	40 ACCACTGGA	* GTGATGGCACTC	60 CAAG :		60
LpCSb :	TTGAG	* AGTGAATTT	80 GCAAAGGCTT	* ATGAGAAGGG	100 ATTCATAAA	* TCAAAGTTCTGG	120 GAGC :		120
LpCSb :	CTACA	* TATGAAGAT	140 AGCTTAAATT	* TGATTGCTCG(160 GCTTCCACAA	* GTGGCTTCATAT	180 GTTT :		180
LpCSb :	ACCGG	* BAGAATTTTC	200 AAGGACGGGA	* AAACTATTGC.	220 AGCTGATAA1	* ACACTGGACTAC	240 GCAG :		240
LpCSb :	CTAA	* TTTTTCACAC	260 CATGCTTGGTT	* TTGATGACCC	280 CAAAATGCTO	* GGAGTTGATGCGC	300 CCTAT	:	300
LpCSb :	: ACAT	* AACAATTCA	320 CACTGATCACO	* GAAGGAGGGAA	340 TGTTAGTGC	* CATGCTGGGCA	360 CTGG	:	360
LpCSb	: TTGG	* AAGTGCTCT(380 GTCAGATCCT	* TATCTTTCTTT	400 TGCAGCGGC	* ACTGAACGGTTT	420 AGCTG	:	420
LpCSb	: GACC	* ACTGCACGG	440 CTTGGCTAAT	* CAGGAAGTGTT	460 TGTNATGGAT	* CAAATCTGTGAT	480 GGAAG	:	480
LpCSb	: AAAC	* :CGGGAGTAA	500 CATTACAACT	* GATCAGCTTA	520 AAGAATATGT	* TTGGAAGACACT	540 GAAGA	:	540
LpCSb	: GTG	* FDTTDDAAAG	560 TCCTGGCTAT	* 'GGTCATGGAG'	580 TTCTACGTA	* TACAGATCCACG	600 ATACT	:	600
LpCSb	: CGT	* GCCAAAGGG	620 AGTTTGCACTO	* BAAGTATTTAC	640 CCGAAGACCC	* CACTTTTCCAACT	660 GGTCT	:	660
LpCSb	: CCA	* AGTTGTACG!	680 AGTTGTGCCT	* CCTATCCTCA	700 CCGAGTTAGO	* GCAAGGTAAAAA	720 ACCCAT	:	720
LpCSb	: GGC	* CTAATGTTG	740 ATGCTCACAG	* TGGAGTTTTGC	760 TCAACCACT	* rcggattagttg	780 AAGCAC	:	780
I week	. ccm	* 'አርጥአርትር	800 TCTTGTTCGG	* CGTCTCAAGG!	820 AGCATGGGAA	* TTGGATCTCAGC	840 TCATTT		840

			*	860	*	880	*	900		
LpCSb	:	GGGACCGTC	CCCTCGG	CCTGCCACTTGA	AAGACCGA	AGAGTGTCACC	ATGGAGTGG	CTGG	:	900
- •										
			*	920	*	940	*	960		
LpCSb		AAAACCAC	 IGCAAGAA	GGCTGCGGCCTG	AAGCTAC	ACCAATGCTTCG	TTTTACAAA	ATCAG	:	960
прессъ	•									
			*	980	*	1000	*	1020		1020
LpCSb	:	GCCGTCTT'	IGATGTTA	ATAATGACTGAG	CATAAGT	raggcatggtta	GCCTTGTT.	TACC	•	1020
			*	1040	*	1060	*	1080		
		자 때 어때 때 어디다!	 ההההככהפפ	CCAATAACTGGA	GCAAGAG	GCTCACAGACGG	TAGAATTT'	TGTAA	:	1080
LpCSb	:	AICIICGI	11100100	COLUMNICACIO						
			*	1100	*	1120	*	1140		1140
LpCSb	:	CCACCGNT	ACTTGAAC	ACCGAATCANTT	AAATGTC	ATTTGGCATAAA	GAGATTAG	GACAT	:	1140
-										
				1160						
_			*	1160	: 1167					
しゃくらり		GACACATA	AGTTTTAT	TGTGTCGCTCGG	: 170/					

LpCSb	:	* SPCXCSPMTC	, QFTTGVMAL	20 QVESEFAKAYE	* KGIHKSKF	40 WEPTYEDSLNI	* :IARLPQVAS	60 YVY	:	60
LpCSb	:	*RRIFKDGKT	* IAADNTLD\	80 (AANFSHMLGFI	* DPKMLELM	100 IRLYITIHTDHE	* :GGNVSAHAC	120 SHLV	:	120
LpCSb	:	GSALSDPYLS	* SFAAALNGI	l40 LAGPLHGLANQI	* *	160 MEETGSNITTI	OOTKEAAMK.	180 TLKS	:	180
LpCSb	:	GKVVPGYGH	* GVLRNTDP	200 RYSCQREFALK	* YLPEDPLF(220 QLVSKLYEVVP	* PILTELGKV	240 KNPW	:	240
LpCSb	:	PNVDAHSGV	* 'LLNHFGLV	260 EARYYTVLFGV	* SRSMGIGS	280 QLIWDRALGLP	* LERPKSVTM	300. EWLE	:	300
LpCSb		NHCKKAAA	: 308							

			*	20	*	40	*	60	
LpCSb1	: (CTTCTCC	CCTGTNAC	TGCTCTCCAAT	GACACAGTT	TACCACTGGAC	STGATGGCAC	TCCAAG :	60
LpCSb2								:	- '
LpCSb3								:	-
LpCSb4								:	-
пресъг	•								
			*	80	*	100	*	120	
LpCSb1		TTGAGA	GTGAATT	TGCAAAGGCTT	ATGAGAAGGG	BAATTCATAAA	TCAAAGTTC1	GGGAGC :	120
LpCSb2	:								-
LpCSb3	:								-
LpCSb4	:								: -
_ <u>r</u>									
			*	140	*	160	*	180	100
LpCSb1	:	CTACAT.	ATGAAGA	TAGCTTAAATT	TGATTGCTC	GCTTCCACAA	GTGGC'I'TCA'	ATGITI	: 180
LpCSb2	:								: - -
LpCSb3	:								
LpCSb4	:								
						220	•	240	
			*	200	* * * * * * * * * * * * * * * * * * *		A CA CTCCA C		: 240
LpCSb1	:	ACCGGA	GAATTTT	CAAGGACGGGA	AAACTATTG	CAGCIGATAAI	ACACIGGAC	ACCCAC	. 240
LpCSb2	:								
LpCSb3	:								
LpCSb4	:								
			*	260	*	280	*	300	
LpCSb1		CTAATT	TTTCAC	ACATGCTTGGTT	TTGATGACC	CCAAAATGCTC	GAGTTGATG	CGCCTAT	: 300
LpCSb2	•								: -
LpCSb3	:				-				:
LpCSb4	:								: -
								260	
			*	320	*	340	*	360	. 260
LpCSb1	:	ACATA	ACAATTC	ACACTGATCAC	GAAGGAGGGA	ATGTTAGTGC'	PCATGCTGGG	CATCIGG	: 360
LpCSb2	:								
LpCSb3	:								
LpCSb4	:								•
				380	*	400	*	420	
		mm C C 7	* amaama	TGTCAGATCCT	TATOTTO TO		ACTGAACGGT		: 420
LpCSb1	:	TIGGA	AGIGCIC	IGICAGAICCI	IAICITICI				: -
LpCSb2	:								: -
LpCSb3									: -
LpCSb4	•		_						
			*	440	*	460	*	480	
LpCSb1	,	GACCA	CTGCACG	GCTTGGCTAAT	'CAGGAAGTG'	ITGT <mark>T</mark> ATGGAT	CAAATCTGT	SATGGAAG	: 480
LpCSb2						TNATGGAT	-NAATCTGT	GATGGAAG	: 24
LpCSb3									: -
ccbs	Ī								: -

			*	500	*	520	*	540	
LpCSb1	:	AAACCGGG	AGTAACATT	CACAACTGATCA	GCTTAAAGI	AATATGTTTGGA	AGACACTGA	AAGA:	540
LpCSb2	:	-AACCGGG	AGTAACATI	ACAACTGATCA	GCTTAAAG	AATATGTTTGGA		AAGA :	83 7
LpCSb3 LpCSb4	:								_
-F	•								
- 00% 1			*	560	*	580	*	600	600
LpCSb1 LpCSb2	:	GTGGAAAG	GTTGTTCC.	rggctatggtca rggctatggtca	TGGAGTTC'	TACGTAATACAG TACGTAATACAG	ATCCACGA: ATCCACGA:	IACT :	143
LpCSb3	:	GTGGAAAG	GTTGTTCC	rggctatggtca	TGGAGTTC'	TACGTAATACAG	ATCCACGA	ract :	67
LpCSb4	:							:	-
		_	*	620	*	640	*	660	
LpCSb1	:	CGTGCCAA	AGGGAGTT	rgcactgaagta	TTTACC <mark>T</mark> G.	AAGACCCACTTT	TCCAACTG(STCT :	: 660 : 203
LpCSb2 LpCSb3	:	CGTGCCAA	AGGGAGT"I" AGGGAGTM	rgcactgaagta egnactgaagta	TTTACCCG.	AAGACCCACTTT AAGACCCACTTT	TCCAACTG(GTCT :	: 203
LpCSb4	:							;	: -
			*	680	*	700	*	720	
LpCSb1	:	CCAAGTTG	TA <mark>T</mark> GAAGT	TGTGCCTCCTAT	CCTCACTG	AGTTAGGCAAGG	TAAAAAAC	CCAT :	: 720
LpCSb2	:	CCAAGTTG	TACGAAGT	TGTGCCTCCTAT	CCTCACCG	AGTTAGGCAAGG AGTTAGGCAAGG	TAAAAAAAC	CCAT	: 263 : 187
LpCSb3 LpCSb4	:	CCAAGIIG	TACGAAGI	IGIGCCICCIAI	CCICACCO	AGITAGGCAAGC			: -
- <u>F</u>									
			*	740	*	760	*	780	
LpCSb1	:	GGCCTAAT	* CGTTGATGC	740 TCACAG <mark>N</mark> GGAGT	* FTTTGCTCA	760 ACCACTTCGGAT	* TAGTTGAA	780 -CAC	: 779
LpCSb1	:	G C CCTAAT	GTTGATGC	TCACAG <mark>N</mark> GGAGT TCACAGTGGAGT	TTTTGCTCA	ACCACTTCGGAT ACCACTTCGGAT	'TAGT'TGAA	-CAC GCAC	: 323
LpCSb2 LpCSb3	:	G C CCTAAT	GTTGATGC	TCACAG <mark>N</mark> GGAGT TCACAGTGGAGT	TTTTGCTCA	ACCACTTCGGAT	'TAGT'TGAA	-CAC GCAC	
LpCSb2	:	G C CCTAAT	GTTGATGC	TCACAG <mark>N</mark> GGAGT TCACAGTGGAGT	TTTTGCTCA	ACCACTTCGGAT ACCACTTCGGAT	'TAGT'TGAA	-CAC GCAC	: 323
LpCSb2 LpCSb3	:	G C CCTAAT	GTTGATGC	TCACAG <mark>N</mark> GGAGT TCACAGTGGAGT TCACAGTGGAGT	TTTTGCTCA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT	'TAGT'TGAA	-CAC GCAC GCAC	: 323
LpCSb2 LpCSb3 LpCSb4	: : :	G <mark>C</mark> CCTAAT GGCCTAAT	GTTGATGC GTTGATGC	TCACAG <mark>N</mark> GGAGT TCACAGTGGAGT TCACAGTGGAGT	TTTTGCTCA	ACCACTTCGGAT ACCACTTCGGAT	'TAGT'TGAA	-CAC GCAC	: 323
LpCSb2 LpCSb3		GCCTAAT GGCCTAAT GGNACTAG GGNACTAG	TGTTGATGC TGTTGATGC * CACTGNCTT CACTGTCTT	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 GNTCGGN GTTCGGCGTCT	TTTTGCTCA TTTTGCTCA * CAAGGAGCA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820	TAGTTGAA TAGTTGAA *	-CAC GCAC GCAC 840 	: 323 : 247 : - : 802 : 383
LpCSb2 LpCSb4 LpCSb1 LpCSb1 LpCSb2 LpCSb3	:	GCCTAAT GGCCTAAT GGNACTAG GGNACTAG	TGTTGATGC TGTTGATGC * CACTGNCTT CACTGTCTT	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 GNTCGGN GTTCGGCGTCT	TTTTGCTCA TTTTGCTCA * CAAGGAGCA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820 ATGGGAATTGGAT	TAGTTGAA TAGTTGAA * * CTCAGCC	GCAC GCAC 840 ATTT	: 323 : 247 : - : 802 : 383 : 307
LpCSb2 LpCSb4 LpCSb1 LpCSb1 LpCSb2	:	GCCTAAT GGCCTAAT GGNACTAG GGNACTAG	TGTTGATGC TGTTGATGC * CACTGNCTT CACTGTCTT	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 GNTCGGN GTTCGGCGTCT	TTTTGCTCA TTTTGCTCA * CAAGGAGCA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820	TAGTTGAA TAGTTGAA * * CTCAGCC	GCAC GCAC 840 ATTT	: 323 : 247 : - : 802 : 383
LpCSb2 LpCSb4 LpCSb1 LpCSb1 LpCSb2 LpCSb3	:	GCCTAAT GGCCTAAT GGNACTAG GGNACTAG	TGTTGATGC TGTTGATGC * CACTGNCTT CACTGTCTT	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 GNTCGGN GTTCGGCGTCTC	TTTTGCTCA * CAAGGAGCA CAAGGAGCA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820 ATGGGAATTGGAT ATGGGAATTGGAT	TAGTTGAA TAGTTGAA * CCTCAGCCC CCTCAGCTC	CAC GCAC GCAC 840 ATTT ATTT	: 323 : 247 : - : 802 : 383 : 307
LpCSb2 LpCSb4 LpCSb1 LpCSb2 LpCSb3 LpCSb3 LpCSb4	:	GCCTAAT GGCCTAAT GGNACTAG GGNACTAG	TGTTGATGC TGTTGATGC * CACTGNCTT CACTGTCTT	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 GNTCGGN GTTCGGCGTCT	TTTTGCTCA TTTTGCTCA * CAAGGAGCA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820 ATGGGAATTGGAT	TAGTTGAA TAGTTGAA * * CTCAGCC	GCAC GCAC 840 ATTT	: 323 : 247 : - : 802 : 383 : 307
LpCSb2 LpCSb4 LpCSb1 LpCSb1 LpCSb2 LpCSb3	:	GGCTAAT GGCCTAAT GGNACTAC GGTACTAC GGTACTAC	TGTTGATGC TGTTGATGC * CACTGNCTT CACTGTCTT CACTGTCTT *	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 GNTCGGN GTTCGGCGTCTC GTTCGGCGTCTC	TTTTGCTCA * CAAGGAGCA CAAGGAGCA *	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820 TGGGAATTGGAT TGGGATTTGGAT TGGGAATTGGAT AGAGTGTCACC	TAGTTGAA TAGTTGAA * TCTCAGCCC TCTCAGCTC TCTCAGCTC	GCAC GCAC GCAC 840 ATTT ATTT ATTT 900 CTGG	: 323 : 247 : - : 802 : 383 : 307
LpCsb1 LpCsb3 LpCsb4 LpCsb1 LpCsb4 LpCsb4 LpCsb4 LpCsb1 LpCsb1 LpCsb2 LpCsb3	: : :	GGACCG'GGGACCG'GGGACCG'	TGTTGATGC TGTTGATGC * CACTGNCTT CACTGTCTT CACTGTCTT * TGCCCTCGG	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 GNTCGGN GTTCGGCGTCTC GTTCGGCGTCTC 860 CCTGCCACTTGA	TTTTGCTCA * CAAGGAGCA CAAGGAGCA * AAAGACCGA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820 ATGGGAATTGGAT ATGGGAATTGGAT GTTTTTTGGAT 880 AAGAGTGTCACCA	* * * * * * * * * * * * * * * * * * *	ECAC 840 ATTT ATTT 900 CTGG	: 323 : 247 : - : 802 : 383 : 307 : 22 : - : 443 : 367
LpCsb1 LpCsb1 LpCsb3 LpCsb4 LpCsb4 LpCsb4 LpCsb4	: : :	GGACCG'GGGACCG'GGGACCG'	TGTTGATGC TGTTGATGC * CACTGNCTT CACTGTCTT CACTGTCTT * TGCCCTCGG	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 GNTCGGN GTTCGGCGTCTC GTTCGGCGTCTC 860 CCTGCCACTTGA	TTTTGCTCA * CAAGGAGCA CAAGGAGCA * AAAGACCGA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820 TGGGAATTGGAT TGGGATTTGGAT TGGGAATTGGAT AGAGTGTCACC	* * * * * * * * * * * * * * * * * * *	ECAC 840 ATTT ATTT 900 CTGG	: 323 : 247 : - : 802 : 383 : 307 : 22
LpCsb1 LpCsb3 LpCsb4 LpCsb1 LpCsb4 LpCsb4 LpCsb4 LpCsb1 LpCsb1 LpCsb2 LpCsb3	: : :	GGACCG'GGGACCG'GGGACCG'	TGTTGATGC TGTTGATGC * CACTGNCTT CACTGTCTT CACTGTCTT * TGCCCTCGG	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT ROO 800 GNTCGGN GTTCGGCGTCTC GTTCGGCGTCTC 860 CCTGCCACTTGA CCTGCCACTTGA	TTTTGCTCA * CAAGGAGCA CAAGGAGCA * AAAGACCGA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820 ATGGGAATTGGAT ATGGGAATTGGAT ATGGGAATTGGAT AGAGTGTCACCAAGAGTGTCACCAAGAGTGTCACCA	* * * * * * * * * * * * * * * * * * *	GCAC GCAC GCAC 840 ATTT ATTT ATTT 900 CTGG CTGG	: 323 : 247 : - : 802 : 383 : 307 : 22 : - : 443 : 367
LpCsb2 LpCsb4 LpCsb1 LpCsb3 LpCsb4 LpCsb4 LpCsb1 LpCsb2 LpCsb3 LpCsb4	: : : : : : : : : : : : : : : : : : : :	GGACCG'GGGACCG'GGGACCG'	TGTTGATGC TGTTGATGC * CACTGNCTT CACTGTCTT CACTGTCTT * TGCCCTCGG	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 GNTCGGN GTTCGGCGTCTC GTTCGGCGTCTC 860 CCTGCCACTTGA	TTTTGCTCA * CAAGGAGCA CAAGGAGCA * AAAGACCGA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820 ATGGGAATTGGAT ATGGGAATTGGAT GTTTTTTGGAT 880 AAGAGTGTCACCA	* * * * * * * * * * * * * * * * * * *	ECAC 840 ATTT ATTT 900 CTGG	: 323 : 247 : - : 802 : 383 : 307 : 22 : - : 443 : 367
LpCsb2 LpCsb4 LpCsb1 LpCsb2 LpCsb3 LpCsb4 LpCsb1 LpCsb2 LpCsb3 LpCsb4		GGNACTAGGTACTAGGTACTAGGTACTAGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGAAAACCA	* PACTGNICTT CACTGTCTT CACTGTCTT * IGCCCTCGG IGCCCTCGG	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 6NTCGGN GTTCGGCGTCTC 860 6CCTGCCACTTGA CCTGCCACTTGA CCTGCCACTTGA CCTGCCACTTGA 920	* CAAGGAGCA * CAAGGAGCA * AAAGACCGA AAAGACCGA AAAGACCGA AAAGACCGA AAAGACCGA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820 ATGGGAATTGGAT ATGGGAATTGGAT 880 AAGAGTGTCACCA AAGAGTGTCACCA 940 ACCAATGCTTCG	* TAGTTGAA TAGTTGAA * CTCAGCCC CTCAGCTC * ATGGAGTGC ATGGAGTGC ATGGAGTGC * TTTTACAAA	ATTT ATTT 900 CTGG CTGG CTGG	: 323 : 247 : - : 802 : 383 : 307 : 22 : - : 443 : 367
LpCsb2 LpCsb4 LpCsb1 LpCsb3 LpCsb4 LpCsb4 LpCsb1 LpCsb2 LpCsb3 LpCsb4		GGNACTAGGTACTAGGTACTAGGTACTAGGTACTAGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGGACCGGGACCGGGACCGGGACCAAAAACCA	* CTGCAAGA	TCACAGNGGAGT TCACAGTGGAGT TCACAGTGGAGT TCACAGTGGAGT 800 6NTCGGN GTTCGGCGTCTC 860 6CCTGCCACTTGA CCTGCCACTTGA CCTGCCACTTGA CCTGCCACTTGA CCTGCCACTTGA 920 AGGCTGCGGCCT	* CAAGGAGCA * CAAGGAGCA * AAAGACCGA AAAGACCGA AAAGACCGA AAAGACCGA AAAGACCGA	ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT ACCACTTCGGAT 820 ATGGGAATTGGAT ATGGGAATTGGAT ATGGGAATTGGAT AGAGTGTCACCAAGAGTGTCACCAAGAGTGTCACCA	TAGTTGAA TAGTTGAA * * * * * * * * * * * * * * * * * *	ECAC GCAC GCAC 840 ATTT ATTT ATTT 900 CTGG CTGG CTGG CTGG	: 323 : 247 : - : 802 : 383 : 307 : 22 : - : 443 : 367 : 82

			*	980	*	1000	*	1020		_
LpCSb1 LpCSb2 LpCSb3 LpCSb4		CCCCTCTT	GTTGTTA	ATAATGACTGAG	CATAAGTT	PAGGCATGGTTAG PAGGCATGG <mark>G</mark> TAG PAGGCATGGTTAG	$\mathtt{CCTTGTT}'$	TTACC	:	563 487 202
			*	1040	*	1060	*	1080		_
LpCSb1	:	a mounted con		CCAATAACTCCA	CAAGAG	GCT <mark>T</mark> ACAGACGGT	AGAATTT	TGTAA	:	623
LpCSb2	:	ATCTTCGT	PTTCCTGG	CCAATAACIGAA	GCAAGAG	GCTCACAGACGGT	AGAATTT	TGTAA	:	547
LpCSb3 LpCSb4		ATCTTCGT	TTTCCTGG	CCAATAACTGGA	GCAAGAG	GCTCACAGACGGT	AGAATTT	TGTAA	:	262
LpCSb1	:		*	1100	*	1120	*	1140	:	-
LpCSb2	:	CCACCGNT	ACTTGAAC	ACCGAATCANTT	AAATGTC	ATTTGGCATAAAG	AGATTAG	GACAT	:	683 606
LpCSb3	:	CCACCGGT	ACTTG-AC	CACCGAATMANNT	AAATG <mark>GN</mark>	ATTTGGCATAAAG ATTTGGCATAAAG	AGALIAG	GACAT	•	322
LpCSb4	:	CCACCGTT	*	1160	: -	ATTIGGCATARAC	AOAT THE		-	
LpCSb2	:	GACACATA	AGTTTTA:	rgtg <mark>ncgn</mark> tcgg	: 710					
LpCSb3	:	GACACATA	AGTTTTA	rgrgrcgcrcgg	: 633					
Tacch4		CACACATA	ACTTTTA	TETTETTEETTEEA	: 349					

LpCSc :	TCNCCGTG	* GCCANAATN	20 CCCCANCATTC	* AAATACCG(40 CCCGTCAGCCAC	* CAATCCTCC	60 IAC :		60
LpCSc :	CTTCTTAT	* TTCCACCCC	80 AACCGCCCAAC	* ATGTGTCC	100 ICCCACCGAANA	* AACACCTGC	120 TAC :	1	20
LpCSc :	CAACGGCC	* 'ATAGCAACG	140 GCACCAACGGC	* GCCAATGG	160 CTCCAAGGAAGG	* GCTTCACAGG	180 CGT :	: 1	.80
LpCSc :	CACGACCA	* AGACAGAACO	200 CCTCACCCTACA	* \CACAAGAG	220 CCCATATGCAC	* CTGTTGGCG#	240 CTT	: 2	240
LpCSc :	TTTGTCA	* AATGTCGGC	260 CGCTTCAAGATI	* TATCGAGAG	280 GCACATTAAGAG	* AGGGCGAGC!	008 TTA	: :	300
LpCSc :	: CGCCAAC	* GCCTACTTC	320 GACCTTGAGGC	* TAAAATCA?	340 AGATCGCCAGAG	* CTCTCGACA	360 ACTT	:	360
LpCSc	: TGGTGTT	* GACTACATT	380 GAAGTTACCAG	* CCCTGCTG	400 CCTCTGAGCAGI	* CAAGAAGGG	420 ACTG	:	420
LpCSc	: CGAAGCC	* CTCTGCAAG	440 CTCGGATTGAA	* .AGCCAAGA	460 TCCTTACCCAC	* GTACGATGCC	480 ACAT	:	480
LpCSc	: GGACGAT	* CGCCAGAATC	500 CGCTGTCGAGAC	* CTGGTGTTG	520 ACGGCCTCGAT	* GTCGTCATTC	540 GAAC	:	540
LpCSc	: CTCTGCC	* GTACCTCCG(560 CGAGCACAGCCA	* ATGGCAAGG	580 BACATGACATAC	* ATCAAAAAC!	600 ACAGC	:	600
LpCSc	: GCTGGA	* GGTGATTGA	620 GTTTGTCAAGA	* GCAAGGGAI	N : 635				

ĽрСSc	:	* XRGXNXPXFKYRPSATI	20 IPPTFLFPPQPPI	* NMCPPT	40 EXTPATNGHSNG	* TNGANGSKE	60 FTGV	:	60
LpCSc	:	* TTRQNPHPTHKSPYAP	80 VGDFLSNVGRFK	* IIESTL	100 REGEQFANAYFI	* OLEAKIKIAR/	120 ALDNF	:	120
LpCSc	:	* GVDYIEVTSPAASEQS	140 RRDCEALCKLGL	* KAKILT	160 THVRCHMDDARI	* AVETGVDGLD	180 VVIGT	:	180
T ₁ DCSc		* SAYLREHSHGKDMTYI	200 KNTALEVIEFVK	* SKG :	211				

18/241

LpCSd :	GTGNTATGG	* GCNCANCCA	20 ENANTCCTNCGT	* PNCTGGCTN	40 CCANANNAGNA	* ANAAGCTAT	60 CGG :	ŧ	60
LpCSd :	CAACGACCI	* CCAGCGATC	80 AGGCCATCAAG	* GACTACCTG	100 TGGTCCACCCI	* 'CAAGGCTGG	120 CCA	: :	120
LpCSd :	AGTCGTTC	* CCGGTTACG	140 GACACGCCGTT	* CTCCGCAAG	160 ACCGACCCCC	* GCTACGTCTC	180 CCA	:	180
LpCSd :	GCGCGAGT"	* TCGCCCAGA	200 AGCACCTTCCC	* GACGACCCI	220 AATGTTCAAGC	* FCGTCAGTC#	240 AGGT	:	240
LpCSd :	: CTACAAGA	* TCGCCCCTC	260 GTGTTCTCACC	* :GAGCACGG	280 CAAGACCAAGA	* ACCCTACC	300 CCAA	:	300
LpCSd	: CGTCGACG	* CCCACTCC	320 GTGTCCTCCTC	* CCAGTACTA	340 CGGCCTCACTG	* AGCAGAACT	360 ACTA	:	360
LpCSd	: CACCGTTC	* CTCTTCGGT	380 GTATCCCGTGC	* GCTCGGTGT	400 CCTTCCCCAGC	* TTATCATTG	420 ACCG	:	420
LpCSd	: TGCCGTCC	* EGTGCCCC	440 ATTGAGAGGCC	* CAAGTCTTT	460 CAGCACTGAGG	* CTTACGCCA	480 AGTT	:	480
LpCSd	: GGTTGGT	* GCTAAGTTG	500 TAAGCGCGTTA	* CTGCAACG1	520 GCTCTACAGCO	* CAGGAGAATO	540 ETGGA	:	540
LpCSd	: GGAATTT	* GTTTAACAI	560 TCAGAGATACC	* TTGTCCTG	580 CTAGAATTGC	* AATGTAAGG!	600 ATAGG	:	600
LpCSd	: GAATGGG	* AGCGTTACO	620 GCGCTACATCA	* ACTACATTT	N : 636				

FIGURE 9

LpCSd	:	XYGXXXXPX	* XWXPXXXXA	20 LIGNDLSDQAIR	* CDYLWSTLK	40 AGQVVPGYGHA	* VLRKTDPRY	60 VSQ	:	60
LpCSd	:	REFAQKHLE	* PDDPMFKLVS	SQVYKIAPGVLT	* FEHGKTKNI	100 PYPNVDAHSGVL	* LQYYGLTE(120 20 120	:	120
I DCSd	:	TVLFGVSRA	* :	140 IDRAVGAPIER	* PKSFSTEA!	160 YAKLVGAKL :	165			

20/241

LpMDHa	:	GGTTGGT	* TGCTGGTAT	20 CACCATTCTGC	* CCTGTTCT	40 CACAGGCAACTO	* CTTCGACTA	60 ATGC :	:	60
LpMDHa	:	ATTGTCT	* 'AGTGAAGAC	80 ATCAAGGCTCT	* CACCAAGA	100 GGACACAGGAGG	* GTGGGACAG	120 AAGT	:	120
LpMDHa	:	TGTTGAG	* GCAAAGGCI	140 GGAAAGGGATC	* TGCAACCT	160 TGTCCATGGCG	* PATGCTGGC	180 CAGT	:	180
T.pMDHa	:	TTTTGGT	* rgatgcatg(200 CTTGAAGGGTCT	* GAACGGAG	220 TTCCTGACATT	* GTTGAATGCT	240 FCCTA	:	240
LpMDHa	:	CGTGCA	* ATCAACTAT	260 CACAGAACTGCC	* ATTCTTTC	280 GCCTCCAAGGTG	* AGGCTCGGG	300 AAGAA	:	300
LpMDHa	:	TGGAGT	* CGAGGAAGT	320 GCTTGGTTTGG(* TGAGCTG	340 ICGGCCTTTGAG	* 'AAGGAAGGT'	360 TTGGA	:	360
LpMDHa	. :	AAGTCT	* CAAGGGTGA	380 .GCTCAAGTCTT(* CAATTGAC	400 AAGGGCATCGCG	* STTCGCCAAT	420 GCGAG	:	420
LpMDHa	ι :	TTAATT	* 'AATTTTGCA	440 GATTATAGCAA	* ACCAGGTC	460 TAGTTAAGGGG	* CTGTTTTTG	480. ACTTT	:	480
LpMDHa	a.	: TTGTTC	* CAGTGCTTT	500 TTCTGCCCATCA	* CGTGGGCA	520 TGGAAGATTTGA	* AGCTTCACA!	540 ATAAAA	. :	540
LpMDHa	a	: ATCCG	* GCGGCGTAA	560 IGCCACAGAACA	* TTACTTG1	580 ACAAGAGGGAA	* CTAGTTCGT	600 ETCAAG	} :	600
LpMDH	a	· TTTTG	* AACTGGTAC	620 ATTAAACGAAC	* \ATTGCTG!	640 ATGCACTTTGAG	* 'AAAAAAA	660 ITGGGG	;	: 660
LpMDH	a	: GTGAN	* TCCATTGGC	680 CTCAAGCCAAA	* \AAAAAA	AAA : 696				

FIGURE 11

LpMDHa	:	* VGCWYHHSALFSQATPS	20 STNALSSEDIK	* ALTKRTQE(40 GTEVVEAKAGE	* GSATLSMA?	60 YAGAV	:	60
LpMDHa	:	* FGDACLKGLNGVPDIV	80 ECSYVQSTITE	* LPFFASKVI	100 RLGKNGVEEVLO	* HGELSAFE	120 KEGLE	:	120
r ~MDU ~		* st.kget.ksstDkgtaf	140 ANAS : 140						

		*	320	*	340	*	360	
LpMDHa1	:	TGGAGTCGAGGAAG	TGCTTGGTT	TGGGTGAGCT	GTCGGCCTTT	GAGAAGGAAGG	TTTGGA	:360
LpMDHa2	•	TGGAGTCGAGGAAG	TGCTTGGTT	TGGGTGAGCT	GTCGGCCTTT	GAGAAGGAAGG	TTTGGA	:359
LpMDHa3	:	TGGAGTCGAGGAAG	TGCTTGGTT	IGGGTGAGCT	GTCGGCCTTT	GAGAAGGAAGG	TTTGGA	:359
LpMDHa4		TGGAGTCGAGGAAC	TGCTTGGTT	rgggtgagct	GTCGGCCTTT	GAGAAGGAAGG	TTTGGA	:356
LpMDHa5	•	TGGAGTCGAGGAAG	TGCTTGGTT	rgggtgagct	GTCGGCCTTT	GANAAGGAAGG	TTTGGA	:257
LpMDHa6	:	TGGAGTCGAGGAAC	TGCTTGGTT	${ t rGGGTGAGCT}$	GTCGGCCTTT	GAGAAGGAAGG	TTTGGA	: 77
LpMDHa7	:	TGGAGTCGAGGAAG	TGCTTGGTT	IGGGTGAGCT	GTCGGCCTTT	GAGAAGGAAGG	TTTGGA	: 62
-								
				400		420		
		* 380 AAGTCTCAAGGGTC	7 A COMO A A COM	400	CAACCCCATC		TGCGAG	:420
LpMDHa1	:	AAGTCTCAAGGGTC AAGTCTCAAGGGTC	JAGCTCAAGT	CTTCAATIGA CTTCAATIGA	CAAGGGCAIC	CCCTTCCCCA	TGCGAG	:419
LpMDHa2	:	AAGTCTCAAGGGT(AAGTCTCAAGGGT(JAGCICAAGI	CTICAATIGA	CAAGGGCATC	GCGTTCGCCAI	TGCGAG	:419
LpMDHa3	:	AAGTCTCAAGGGT(AAGTCTCAAGGGT(CAGCICAAGI	CTICAMIIGA	CAAGGGCATC	GCGTTCGCCAI	TGCGAG	:416
LpMDHa4 LpMDHa5	:	AAGTCTCAAGGGTC AAGTCTCAAGGGTC	ZAGCTCAAGT	CTTCAATICE CTTCAATTCE	CAAGGGCATC	GCGTTCGCCA	TGCGAG	:317
	:	AAGTCTCAAGGGT(AAGTCTCAAGGGT(ZAGCTCAAGT ZAGCTCAAGT	CTTCAATIGE CTTCAATTGE	CAAGGGCATC	GCGTTCGCCA	ATGCGAG	:137
LpMDHa6 LpMDHa7	:	AAGTCTCAAGGGT	TAGETCAAGT TAGEÄTCAAGT	CTTCAATTGE	CAAGGGCATC	GCGTTCGCCA	ATGCGAG	:122
Thimua i	•	AGICICOBAAGIOIO	JAGE I CAACI	CIICIMII	10, 110 0 0 0 112 0			
		•						
		*	440	*	460	*	480	
LpMDHal	:	TTAATTAATTTTG	CAGATTATAG	CAAACCAGGT	CTAGTTAAGO	GGTCTGT	rg – – Trr	:475
LpMDHa2	:	TTAATTAATTTTG	CAGATTATAG	CAAACCAGGT	CTAGTTAAGO	GGTCTGT	IGTIT	:474
LpMDHa3	:	TTAATTAATTTG	CAGATTATAG	CAAACCAGG:	CTAGTTAAGO	eggtete ti	rgTtt	:474
LpMDHa4	:	TTAATTAATTTTG	CAGATTATAG	CAAACCAGG:	CTAGTTAAGO	eggtete T	IGNTI	:471
LpMDHa5	:	TTGATTAAATTTTG	CAGATTATAG	CAATCCAGG	rctagtt@ago	GGTCTGTTTT'	IGACTTT	:377
LpMDHa6	:	TTGATTAAÄTTTG	CAGATTATAG	CAATCCAGG	rctagttgag(GGTCTGTTTT	TGACTT	:197
LpMDHa7	:	TTGATTAAATTTG	CAGATTATAC	CAATCCAGG'	rctagtt <u>g</u> ag(GGTCTGTTT"	TGACTT1	:182
		*	500	*	520	*	540	
LpMDHa1		TTGTTCAGTGCTT	TTTCTGCCC	TCACGTGGG		TTGAGCTTCAC.		:535
LpMDHa2	•	TTGTTCAGTGCTT	TTTCTGCCC	TCACGTGGG	CATGGAAGAT	TTGAGCTTCAC	AATAAA	:534
LpMDHa3	:	TTGTTCAGTGCTT	TTTCTGCCCZ	TCACGTGGG	CATGGAAGAT	TTGAGCTTCAC.	AATAAA	:534
LpMDHa4	•	TTGÑTCAÑÑGCTT	TTTCTGCCC	ATCACGTGNG	CATGÑAAGAT'	TTGAGCTTÑAC	ANTANNT	:531
LpMDHa5	:	TTGTTCAGNGCTT	TTTCTGCCC	ATCACGTGGG	CATGGAAGAT'	TTGAGCTTCAC	AATAAA	:437
LpMDHa6	:	TTGTTCAGTGCTT	TTTCTGCCC	ATCACGTGGG	CATGGAAGAT'	TTGAGCTTCAC	AAAATAA	:257
LpMDHa7	:	TTGTTCAGTGCTT	TTTCTGCCC	ATCACGTGGG	CATGGAAGAT'	TTGAGCTTCAC	AATAAAA	:242
-								
					500		600	
		* ATCCGGCGGCGTA	560	*	580	CAACTACTTCC		:595
LpMDHa1	:	ATCCGGCGGCGTA ATCCGGCGGCGTA	ATGCCACAGA	ACATTACTT	GTACAAGAGG CTACAAGAGG	GAACTAGIICG GAACTACTTCC	TGTCAAG	:594
LpMDHa2	:	ATCCGGCGGCGTA ATCCGGCGGCGTA	ATCCCACACAC	AACAIIACII AACAIIACII	GTACAAGAGG GTACAAGAGG	GAACTAGTICG GAACTAGTTCG	TGTCAAG	:594
LpMDHa3	:	ATCCGGCGGCGTA ATNCCNGCGCGNN		LCALIACII				:544
LpMDHa4	:	ATRICENGEGEGIN	ATCCCACAN	AACATTACTT	GGACAAGAGG	GAACTAGTTCG	GGTNAAG	:497
LpMDHa5	:	ATCCGGCGGCGTA ATCCGGCGGCGTA	ATGCCACALL	ACATTACTI	GTACAAGAGG	GAACTAGTTCG	TGTCAAG	
LpMDHa6	:	ATCCGGCGGCGTA	ATGCCACAG	A A C A T T A C T T	GTACAAGAGG	GAACTAGTTCG	TGTCAAG	:302
LpMDHa7	:	AICCGGCGGCGIF	AT OCCACAO.	TICHLINGII	C.L. C.M. TOMOCO	00 1.10 1 1 0 0		

		•	20	*	40	*	60	
MDU-1	. 1	GTTGGTTGCTGGT	PATICACCATTI	THECCCTETT	CTCACAGGCA	ACTCCTTCGAC	TAATGC :	60
LpMDHa1 LpMDHa2	٠ ١	- <mark>GGTGGTTGCTGG1</mark>	ATCACCATT	TECCCTETT	CTCACAGGCA	ACTCCTTCGAC	TAATGC :	59
	•	-GTGGTGTGCTGGT	RATCACCATT RATCACCATT	CTGCCCTGTT	CTCACAGGC	ACTCCTTCGAC	TAATGC :	59
LpMDHa3 LpMDHa4	•	CCTTCCTCCT	TATCACCATT	СТЕСССТЕТТ	CTCACAGGCA	ACTCCTTCGAC	TAATGC :	56
LpMDHa5	•	GOTTGGTGGT	AICACCAIL				:	-
црирназ црмрна6	•						:	-
цришнао LpMDHa7	•						:	-
י אוימיולת	•							
		*	80	*	100	*	120	•
LpMDHa1		ATTGTCTAGTGAAG	TACATCAAGG	CTCTCACCA	AGAGGACACA	GGAGGGTGGGAC	AGAAGT	120
LpMDHa2	:	ATTGTCTAGTGAA	FACATCAAGG	CTCTCACCA	AGAGGACACAG	GGAGGGTGGGAC	AGAAGT	:119
ърмоназ	:	ATTCTCTACTCAAC	GACATCAAGG	CTCTCACCA	AGAGGACACA	GGAGGGTGGGAC	'AGAAGT	:119
LpMDHa4	:	ATTGTCTAGTGAA	GACATCAAGG	CTCTCACCA	AGAGGACACA	GGAGGGTGGGAC	AGAAGT	:116
LpMDHa5	:					GAGGGTGGGAC	CAGAAGT	: 17
LpMDHa6	:							: -
ьрмона7	:							: -
привиа /	•						•	
							4	
		*	140	*	160	*	180	
LpMDHa1	:	TGTTGAGGCAAAG	GCTGGAAAGC	GATCTGCAA	CCTTGTCCAT	GGCGTATGCTGC	SCGCAGT	:180
LpMDHa2	:	TGTTGAGGCAAAG	GCTGGAAAGG	GATCTGCAA	CCTTGTCCAT	GGCGTATGCTGC	3CGCAG'I	:179
LpMDHa3	:	TGTTGAGGCAAAG	GCTGGAAAGG	GATCTGCAA	CCTTGTCCAT	GGCGTATGCTG(3CGCAGT	:179
LpMDHa4	:	TGTTGAGGCAAAG	GCTGGAAAGG	GATCTGCAA	CCTTGTCCAT	GGCGTATGCTG	GCGCAGT	:176
LpMDHa5	:	TGTTGAGGCAAAG	GCTGGAAAGG	GATCTGCAA	CCTTGTCCAT	GGCGTATGCTG(GCGCAGT	: 77
LpMDHa6	:							: -
LpMDHa7	:							: -
						•		
		*	200	*	220	*	240	
LpMDHa1	:	TTTTGGTGATGCA	TGCTTGAAGO	GTCTGAACG	GAGTTCCTGA	CATTGTTGAAT	GCTCCTA	:240
LpMDHa2	:	TTTTGGTGATGCA	TGCTTGAAG	GTCTGAACG	GAGTTCCTGA	CATTGTTGAAT	GCTCCTA	:239
LpMDHa3	:	TTTTGGTGATGCA	TGCTTGAAG	GGTCTGAACG	GAGTTCCTGA	CATTGTTGAAT	GCTCCTA	:239
LpMDHa4	:	TTTTGGTGATGCA	TGCTTGAAG	GGTCTGAACG	GAGTTCCTGA	CATTGTTGAAT	GCTCCTA	:236
LpMDHa5	:	TTTTGGTGATGCA	TGCTTGAAG	GTCTGAACG	GAGTTCCTGA	CATTGTTGAAT	GCTCCTA	:137
LpMDHa6	:						~	: -
LpMDHa7	:							: -
							300	
		*	260	*	280	· COMON COCHEC		:300
LpMDHa1	:	CGTGCAATCAACT	TATCACAGAA	CTGCCATTCT	"TTGCCTCCAA	AGGTGAGGCTCG	CCAAGAA	:299
LpMDHa2	:	CGTGCAATCAACT	PATCACAGAA	CTGCCATTCT	"TTGCCTCCAA	AGG TGAGGC TCG	CCAAGAA	:299
LpMDHa3	:	CGTGCAATCAAC	PATCACAGAA	CII GCCAIIII CI	TIGCCTCCA	AGGTGAGGCTCG	CCAAGAA	:299
LpMDHa4	:	CGTGCAATCAAC	TATCACAGAA	CTGCCATTCT	TTGCCTCCA	AGGIGAGGCICG	CCAACAA	:197
LpMDHa5	:	TGTGCAATCAAC	ratcacagaa	CIT.GCCATITICI	TIGCCICCA	aggtgaggcteg gtñañgcteg	CATATACAA	: 17
LpMDHa6	:					GTIMETINGCTCG		: 2
LpMDHa7	:							. 4

			*	620	*	640	*	660	
LpMDHa1	:	TTTTGAA	CTGGTAC	CATTAAACGA	ACAATTGCT	BATGCACTTTGAG	AAAAAAA	AN	:650
LpMDHa2	:	TTTTGAA	CTGGTAC	CATTAAACGA	ACAATTGCT	GATGCACTTTGAG	EAAAAAAA	A/A	:649
LpMDHa3	:	TTTTGAA	CTGGTAC	CATTAAACGA	ACAATTGCT	GATGCACTTTGAG	AAAAAAA	AA	:649
LpMDHa4	:								: -
LpMDHa5	:	TTTTGAA	CTGGMAC	CATTAAACAA	CCAATTGTT	en <mark>gc</mark> egettte <mark>n</mark>	JAACEGE'CE	TTTGGGG	:557
LpMDHa6	:	TTTTGAA	CTGGTAC	CATTAAACGA	ACAATTGIT	GATGCACTTTGIC	3AACÇGTC0	T.I.I.GCITIC	:377
LpMDHa7	:	TTTTGAA	CTGGTAC	CATTAAACGA	ACAATTGIJT	GAAAAAAA-			:345
			*	680	*				
LpMDHa1	:		- -			: -			
LpMDHa2	:					: -			
LpMDHa3	:					: -			
LpMDHa4	:					:			
LpMDHa5	:	GTGANTO	CATTGGI	ŢĊŢŊAAGĊĊ <u>Ĩ</u>	AAAAAAAA	: 589			
LpMDHa6	:	TTGATTT	CATTGT	CITTCAAGIT'I	ĬĄĊĠĄĄÑĄĄÑ	AAAA : 413			
LoMDHa7	:					7: -			

25/241

LpMDHb :	:	TTTGGTNCT	* FTTTGCCGA	20 GCGAGAAAGCT	* GTTCGGTG7	40 rcaccaccctto	* NGTTGTTCG	60 TGC	:	60
LpMDHb :	•	TAAAACTT	* ICTACGCTG	80 GGAAGGCAAAC	* !GTGCCAGT(100 CACTGGGGTGAA	* ATGTTCCTGI	120 TGT	:	120
DPMDHb	:	TGGTGGCC	* ATGCTGGTG	140 TTACTATCCTG	* GCCACAGTT	160 CTCACAGGCTA	* CTCCTGCAA(180 ETAA	:	180
LpMDHb	:	TGCATTGT	* CCCATGAGG	200 BACCTTAAGGCO	* CCTCACCAA	220 GAGGACACAAG	* ATGGTGGGA	240 CGGA	:	240
LpMDHb	:	AGTTGTTG	* AAGCAAAGO	260 GCTGGAAAGGG	* CTCAGCAAC	280 ATTGTCAATGG	* CATATGCTG	300 GTGC	:	300
LpMDHb	:	AGTATTTG	* GAGATGCA	320 IGCTTGAAGGG	* GCTCAATGG	340 BAGTTCCTGACA	* TTGTAGAGT	.360 GCTC	:	360
LpMDHb	:	CTTTGTG	* CAATCAACC	380 GTAACAGAGCT	* GCCATTCTI	400 TTGCCTCCAAGG	* TAAGGCTCG	420 GCAA	:	420
LpMDHb	:	GAACGGA	* GTGGAGGAA	440 GTGATTGGGCT	* 'GGGCGAGC'	460 rgtctgccttcc	* BAGAAGGAGG	480 GTCT	:	480
LpMDHb	:	GGAGAGC	* CTCAAGGGC	500 GAGCTGNTGNC	* CTCCATCG	520 AGAAGGGTATCA	* \AGTTCGCG(540 CAGGA		540
LpMDHb	;	GAGCTAG	* TCAACCTGC	560 TCAGATTCTAF	* ACACTCCGC.	580 ACATGAACTCG	* GTGGGATCT(600 ATGA		600
LpMDHb	:	: ATTTTTG	* GTACGACTO	620 CCTTTCACTGC	* CCCTTCTC	640 CTGGGGACATT	* GAGGCGTCG	660 NGCTC		660
LpMDHb)	: CACAATA	* \AAATGGCG	680 TGNCTTGTTGC	* CATACTGAA	700 CTGAACTTGTA	* ATACCAGAA	720 AGAGT		: 720
LpMDHb)	: GAAACCC	* CTGTGCCTT	740 ATGTACCACAG	* TACGGTGAF	760 ACCCGAAAATCA	* .TGAAGGTAG	780 CAGA		: 780
LpMDHb	•	: GATTCTC	* GTGGAAGCT	800 TTTTTCTTTTA	N : 807					

FIGURE 14

LpMDHb	:	* LXLLPSEKAVRCHHPXV	20 VRAKTFYAGKAN	* VPVTGVNV	40 PVVGGHAGVTI	* LPQFSQATP	60 ASN	:	60
ГБМДНР	:	* ALSHEDLKALTKRTQDG	80 GTEVVEAKAGKG	* SSATLSMAY	100 YAGAVFGDACLK		120 ECS	:	120
LpMDHb	:	_	140 LGKNGVEEVIGI	* LGELSAFEI	160 KEGLESLKGELX		180 AQE	:	180
LpMDHb	:	S : 181							

		*	20		ж	40	_	80_		
LpMDHb1 LpMDHb2	:	TTTGGTNCTTT	TGCCGAG-N	AWIAAIICTO AGAGAGCTO	GTTCGGTGTC GTT[[GGTGTC	CACCACCC CACCACCCC	TTGNGTTG TTGÏGTTG	TTCGTGCT TTCGTGCT	:	60 44
LpMDHb1 LpMDHb2	:	* AAAACTTTCTA AAAACTTTCTA	80 CGCTGGGAA	.GGCAAACG'	* 10 TGCCAGTCAC TGCC GTCAC	CTGGGGTG	* AATGTTCC	120 TGTTGTTG TGTTGTTG	:	121 105
LpMDHb1 LpMDHb2		* GTGGCCATGCT GTGGCCATGCT	140 GGTGTTACT GGTGTTACT	* ATCCTGCC ATCCTGCC	160 ACEGTTCTC ACAGTTCTC	ACAGGCTA	* CTCCTGC# CTCCTGC#	180 AGTAATGC AGTAATGC	:	182 166
LpMDHb1 LpMDHb2		* ATTGTCCCATC	200 SAGGAICTTA SAGGACCTTA	* AAGGCCCTC AAGGCCCTC	220 ACCAAGAGG ACCAAGAGG	ACACAAGA ACACAAGA	* TGGTGGG! TGGTGGG!	240 ACGGAAGTT ACGGAAGTT	:	243 227
LpMDHb1 LpMDHb2	:	* GTTGAAGCAA GTTGAAGCAA	260 AGGCTGGAA <i>I</i> AGGCTGGAA <i>I</i>	* AGGGCTCAG AGGGCTCAG	280 CAACATTGT CAACATTGT	CAATGGCA CËATGGCA	* TATGCTGC	300 ETGCAGTAT ETGCAGT¶T	:	304 288
LpMDHb1 LpMDHb2		* TTGGAGATGC	320 ATGCTTGAA(ATGCTTGAA(* GGGCTCAA	340 TGGAGTTCC	* TGACATTG TGACATTG	TAGAGTG	360 CTCCTTTGT CTCCTTTGT		365 349
LpMDHb1 LpMDHb2		* GCAATCAACÉ GCAATCAACC	380 GTAACAGAG GTAACAGAG	* CTGCCATTC CTGCCATTC	400 TTTGCCTCC	* AAGGTAAC	GCTCGGC	2 0 AAGAACGGA AAGAACGGA	:	426 410
LpMDHb1 LpMDHb2		* GTGGAGGAAG GTGGAGGAAG	440 TGATTGGGC TGATTGGGC	* TGGGCGAGC	460 CTGTCTGCCT CTGTCTGCCT	* TCGAGAAC	48 GAGGGTC GAGGGTC	TGGAGAGCC	:	487 471
LpMDHb1 LpMDHb2		TCAAGGGCGA	00 GCTGNTGNC GCTG∏TG∏C	* CTCCATCGA CTCCAT頂GA	520 AGAAGGGTAT AGAAGGGTAT	* CAAGTTCC	540 CGCAGGA CÜCAGGA	GAGCTAGTC GAGCTAGTC	:	548 532
LpMDHb1 LpMDHb2		* 56 AACCTGCTCA AACCTGCTCA	GATTCTGAC	* ACTCCGTA(ACTCCGCA(580 CATGAACTCO	* GTGGGAT GGTGGGAT	600 CTGATGAA CTGATGAA	* TTTTTGGTA TTTTTGGTÄ	:	609 593
LpMDHb1	:	620 CGACTCCTTT CGACTCCTTT	CICTGCCC	TTTTTCGT	640 GGGGACATTO	* BAGGCGTIG	660 ENGCTICA ETGCTCCA	CATTAAAAT CAATAAAAT	:	670 654

		680	*	700	*	720	*		
LpMDHb1	:	GGCGTGNNTTGTT	G-CATACT	FGANCTGACCTT	INTATTON			-	708
LpMDHb2	:	GGCGTGTCTTGTTC	GCCATAC:	rgaactgaact	rgtaatacc <i>i</i>	AGAAAGAGTGA.	AACCCTGTGC	:	715
-									
		740	*	760	*	780	*		
LpMDHb1	:							:	-
LpMDHb2	:	CTTATGTACCACA	GTACGGT	GAACCCGAAAA'	rcatgaagg:	<u> PAGCAGAAGAT</u>	TCTGTGGAAG	:	776
		800							
LpMDHb1	:		<u>-</u> : -						
LpMDHb2	:	CTTTTTTTTTTA	N : 790						

		,	k	20	*	40	*	60		
LpMDHc	:	GNNGGTNTA	CCGAGCGC	NCATACTTINGT	GGGTGAGG	TTCTTGGACT	NGACCCAAG	AGAT	:	60
LpMDHc	:	GTCAATGTT	* CCTGTNGN	80 TGGCGGGCATGC	* CCGGAGTT	100 ACNATATTGCC	* ACTCCTTTC	120 GCAG	:	120
LpMDHc	:	GTTAATCCT	* CCCTGCTC	140 ATTCACCATGAG	* GAAATTA	160 GTATCTCACCT	* TCACAGCAT	180 ACAG	:	180
LpMDHc	:	AATGGTGGG	* ACAGAAGT	200 MGTCGAGGCGA	* AAGCTGGA	220 GCAGGATCGGN	* INACTNTTTC	240 TATG	٠:	240
LpMDHc	:	GCGNATGCG	* GCAGCTA	260 AATTTGCAGATG	* CTTGCTNG	280 AGAGGATTGC	* TGGTGATGC	300 TGGG	:	300
LpMDHc	•	ATAGNGGAN	* TGCTCTT	320 ATGTGGATTCTC	* AGGTGACG	340 GANCTNTCTT	* FNTTTGCATC	360 CAAA		360
T.mMDHc		GTTCGCCT	* rggttgtt	380 CTGGCGTCNAGG	* AGATCTTC	400 CCACTTGGTC	* CACTCAACG!	AGTN	:	419

LpMDHc	:	* XGXPSXHTXVGEVLGXDE	20 PRDVNVPXXGGI	* HAGVXILPL	40 LSQVNPPCSF1	* CMRKLVSHL	60 HSIQ	:	60
LрMDНс	:	* NGGTEXVEAKAGAGSXTX	80 KSMAXAAAKFA	* DACXRGLHG	100 EDAGIXXCSYVI	* DSQVTXXSX	120 FASK	:	120
T.SMDHC		* VPI.GCSGVXETI.PI.GPI.I	NE : 139						

31/241

: pHCMc	(* ODOTTRODE	CCAACACAA	20 CACCACCGCTC	* CCCCGTCC	40 GCATCTCTCC	* TTTCGCCTC	60 CAT	:	60
								120		
LpMDHd :	: (GGATCCAGA	rcccacaca	80 .CCGCCGCAGCC	* CAGCAACGA	100 TGAGGCCGTC			:	120
LpMDHd :	:	GCCGCGCAG	*] CTCCTCCG(.40 CCGCCGCAGCTA	* ACTCGTCCG	160 CGTCCGGCCA	* GCCGGAGCGG	180 AAG	:	180
LpMDHd	:	GTGGCCATC	* 2 CTCGGCGC	200 GGCCGGCGGGA'	* TCGGGCAGO	220 CCGCTGGCGCT	* CCTCATGAAG	240 ECTG	:	240
LpMDHd	:	AACCCGCTC	* GTCTCCTC	260 CCTCTCCCTCT	* ACGACATCO	280 GCCGCCACCC	* CGGCGTCGC	300 CGCC	:	300
LpMDHd	:	GACGTCTCC	* CACATCAA	320 CTCCCCGGCCC	* TGGTGAAG(340 GGTTCATGGG	* CGACGATCA(360 GCTC	:	360
LpMDHd	:	GCGGAGGCG	* STTGGAGGG	380 GGCCGACCTCG	* TCATCATC	400 CCGGCCGGCGT	* TCCGAGGAA	420 GCCC	:	420
LpMDHd	:	GGCATGAC	* CAGGGACGA	440 TCTCTTCAACA	* \TCAACGCC	460 GGCATCGTTAF	* \GAACCTCTG	480 CACC	:	480
LpMDHd	:	GCCATCGC	* CAAGTACTG	500 CCCCAACGCTC	* CTTATCAAC	520 ATGATCAGCA	* ACCCTGTGAA	540 CTCA		540
LpMDHd	:	ACTGTTCC	* AATTGCTG(560 CTGAAGTTTTC	* AAGAAGGCT	580 GGAACCTATG	* ATGAGAAGAA	600 GTTG		600
LpMDHd	:	TTTGGTGT	* GACCACTC	620 TTGATGTTGTT	* CGTGCCAGO	640 BACTTTCTATG	* CTGGGAAGG(660 TAAT		: 660
LpMDHd	:	GTACCTGT	* 'TACTGGTG'	680 TGAACGTTCCT	* GTTGTTGG:	700 FGGTCATGCTG	* GTATCACCA	720 FT C T0		: 720
LpMDHd	. :	: CCACTGTT	* CTCACAGG	740 CAACTCCTTCG	* ACTAATGC	760 ATTGTCTAGTG	* AAGACATN	: 774	4	

FIGURE 19

DHCMq	:	* XXPPTQHHRSPVRISPFF	20 RLHRSRSHTPPQ	* PATMRPSA	40 MRSAAQLLRRR	* Syssasgqp	60 ERK	:	60
грмрнд	:	* VAILGAAGGIGQPLALLI	80 MKLNPLVSSLSI	* YDIAATPO	100 EVAADVSHINSP	* ALVKGFMGI	120 DQL	:	120
LpMDHd	:	* AEALEGADLVIIPAGVP	140 RKPGMTRDDLF1	* VINAGIVKI	160 NLCTAIAKYCPN	* ALINMISNI	180 PVNS	:	180
LpMDHd	:	* TVPIAAEVFKKAGTYDE	200 KKLFGVTTLDV	* VRARTFYA	220 GKANVPVTGVNV	* PVVGGHAG:	240 ITIL	:	240
LpMDHd	:	* PLFSQATPSTNALSSED	X : 258						

33/241

LpMDHe	:	TCCGTACNA	* TTGCTGCT	20 GAAGTATTTAAA	* .AAAGCTGG	40 GACATACAATC	* CTAAGAGAT	60 TGT	:	60
-										
LpMDHe	:	TGGGGGTGA	* CAACACTT	80 GATGTAGTGAGA	* GCCAATAC	100 TTTTGTGGGTG	* BAGGTTCTTG	120 GAC	:	120
LpMDHe	:	TTGACCCCA	* \GAGATGTC	140 AATGTTCCTGTI	* TGTTGGCGG	160 GCATGCCGGAG	* TTACGATAT	180 TAC	:	180
LpMDHe	:	CACTCCTT	* CGCAGGTT	200 AGTCCTCCCTGO	* CTCGTTCAC	220 CCCTGAGGAA	* ATTAGTTATO	240 CTCA	:	240
<u>.</u>				260	*	280	*	300		
LpMDHe	:	CCTCACGC	, ATACAGAAT	GGTGGGACAGA!	 AGTTGTGG#		GAGCAGGAT		:	300
LpMDHe	:	CAACTCTT	* ICTATGGC	320 TATGCGGCAGC	* FAAATTTG(340 CAGATGCTTGC	* L'TGAGAGGA'	360 FTGC	:	360
LpMDHe	:	ATGGTGAT	* GCTGGGAT	380 AGTGGAGTGCTC	* FTATGTGG!	400 ATTCTCAGGTG	* ACCGGAACT(420 GCCT	:	420
LpMDHe	:	TCTTTGCA'	* TCCAAAGTT	440 CCGCCTAGGTCG	* TTCTGGCG:	460 rcgaggagatc	* TTGCAACTT	480 GGGT	:	480
LpMDHe	:	CCACTGAA	* CCAGGTTT:	500 rgaaaganctgg	* ACTGGAAN	520 AAGGCGAAANA	* ANGAGCTAT	540 CCCG	:	540
LpMDHe	:	AGAGCCTT	* CCAGAAAG	560 ENTGTGTCATTT	* CGTNCAAC	580 AAAGTGAGTTA	* CATGCCATC	600 ATCT	:	600
LpMDHe	:	TTGTTGGA	* TGTGCTTC	620 CCCAAAGTTCCA	* ACACACCG	640 TCGNAATTGGC	* ATATANATA	660 TTGC	:	660
LpMDHe	: :	TGGTTTGG	* GGCCTTTT	680 GCNTTNATGCAA	* ACAGGCTA	700 CCTTNTGGGTG	* GGGGGGGTC	720 CGTT	:	720
LpMDHe	: :	: NTGAAAAA	* CTCTTAAC	740 ATTTTTTTTAC	* :GGTTGGNA	760 ACAAAATNTNT	* 'GAAAAGCCT	780 GAGA	:	780
LpMDHe	: :	: ANTATATG	* SATAANTGA	008 ANATTTDAAANA	* AAAAAAAN	: 816				

FIGURE 21

		*	20	*	40	*	60	
LpMDHe	:	RXIAAEVFKKAG	PYNPKRLLGVTT L	DVVRANTFV	GEVLGLDPRDV	NVPVVGGHA	GVTILP :	60
		*	80	*	100	*	120	
LpMDHe	:	LLSQVSPPCSFT	PEEISYLTSRIQN	IGGTEVVEAR	(AGAGSATLSMA	AYAAAKFADA	CLRGLH :	120
		*	140	*	160	*	180	
LpMDHe	:	GDAGIVECSYVD	SQVTGTAFFASK	/RLGRSGVEI	:ILQLGSTEPG	FERXGLEXGE	XXSYPE :	180
		*	200	*	220	, *	240	
LpMDHe	:	SLPERXCHFXQQ	SELHAIIFVGCAS	SPKFQHTVX	[GIXILLVWGL]	LXXCKQATXW	VGGVRX :	240
		*	260	*				
T.nMnHe			KXXEKPEXYMIXI	EXSXXKK :	271			

35/241

		* 20 * 40 * 60	60
гБигонт	:	GGGATGATTNATNCAACAAAAATGCTGGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC:	60
LpMDHf	:	* 80 * 100 * 120 AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC : 1	120
-			
		* 140 * 160 * 180	
LpMDHf	:	ATTGCGGCAGAAGNTTTCAAGAGGGCTGGAACTTACTGCCCCAAACGTCTCCTTGGAGTG :	180
MDII-		* 200 * 220 * 240 ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGGAGNTGATCCT : 2	240
PDMOHE	:	ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGGAGNTGATCCT : 2	2 4 0
		* 260 * 280 * 300	
LpMDHf	:	AGAGAAGNCAGTGTTCCGGNTGTTGGCGGGCATGCAGGGATCACTATATTGCCCCTCCTG : :	300
-			
		* 320 * 340 * 360	
LpMDHf	:	NCCCAGGTCAGCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC : 3	360
T MDYTE		* 380 * 400 * 420	420
грмонг	:	ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG : .	420
		* 440 * 460 * 480	
LpMDHf	:	TCAATGGCTTTTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT :	480
_			
		* 500 * 520 * 540	
LpMDHf	:	GCTGGCATTGTGGAATGTNCATACGTTGCATCTGAGGTGACAGAGCTGCCGTTCTTTGCA :	540
T MDITE		* 560 * 580 * 600	<i>-</i> 00
тЪмпит	:	ACAAAAGTGAGGTTAGGTCGTGGCGGAGCTGAGGAGATCCTCCCTC	800
		* 620 * 640 * 660	
LpMDHf	:	GACTTTGAGAGAGCTGGCCTGGAGAAGGCGAANAAGGAGCTCAGCGAGAGCATCCAGAAG :	660
		* 680 * 700 * 720	
LpMDHf	:	GGTGTGGCGTTCATGAACAAGTGAGATCATATGAATGGATGG	720
Lowouf		* 740 * 760 * 780 ATAGATGATGCAAAGACTAAAGAAGAGTGTGATATAGTGCTCCTATATACCTGTAAAAT:	780
Thint	•	AINORIONIONCIMMOROMOROTOTOMINIMOTOCIOTATATACCIGIARANI .	, 50
		*	

LpMDHf : CTCTCCTGCCTGTAAGAA : 798

FIGURE 23

LpMDHf	:	* MLGIVRSICEGVAKSC	20 PNAIVNLISNPVI	* NSTVPIAA	40 EXFKRAGTYCPK	* RLLGVTTLD	60 VAR	:	60
LPMDHf	:	* ANTFVAEVLGXDPREX	80 SVPXVGGHAGIT	TTBTTXÖA:	100 SPPCSFTPDEIS		120 GTE	:	120
LpMDHf	:	* VVEAKAGAGSATLSMA	140 FAAAKFADACLR	* GMRGDAGI	160 VECXYVASEVTE	* LPFFATKVR	180 LGR	:	180
T.DMDHf		* GGAEETLPLGPLNDFE	200 RAGLEKAXKELS	* ESIOKGVA	220 FMNK : 220				

			*	20	*	. 40	*	60		
LpMDHf1 LpMDHf2	:	GNNHTGAT -GGATGAT	TNATNCAA(TIJATIJCAA(CAAAAATGCTGG CAAAAATGCTGG	GCATTGTC G <mark>-</mark> ATTGTC	CGATCAATCTGT CGATCAATCTGT	GAGGGCGT GAGGGCGT	TGCC TGCC	:	60 58
LpMDHf1 LpMDHf2						100 AACCCTGTGAAC AACCCTGTGAAC			:	120 118
LpMDHf1 LpMDHf2						160 TGCCCCAAACGT TGCCCCAAACGT			:	180 178
LpMDHf1 LpMDHf2		ACAACTCT ACAACTCT	* TGATGTAG	200 CGAGGGCTAACA CGAGGGCTAACA	* \CCTTTGTG \CCTTTGTG	220 GCTGAAGTGCTT GCTGAAGTGCTT	* GMAGNTGA GGAGTTGA	240 TCCT TCCT	:	240 238
LpMDHf1 LpMDHf2		AGAGAAGÑ AGAGAAGÑ	* ICAGTGTTC ICAGTGTTC	260 CGGNTGTTGGCG CGG¶TGTTGGCG	* GGCATGCN GGCATGCA	280 GGGATCACTATA GGGATCACTATA	* ATTGCCCCT ATTGCCCCT	300 CCTG	. :	300 298
LpMDHf1 LpMDHf2	:					340 GAAATCAGCTAT GAAATCAGCTAT			:	360 358
LpMDHf1 LpMDHf2						400 GCTGGAGCAGGG GCTGGAGCAGGG			:	420 418
LpMDHf1 LpMDHf2		TCAATGG(TCAATGG(* CTTTTGCTG CTTTTGCTG	440 CTGCAAAATTCO CTGCAAAATTCO	*. ECCGATGCA ECCGATGCA	460 ATGCTTGCGTGGA ATGCTTGCGTGGA	* AATGCGTGC AATGCGTGC	480 TGAT TGAT	:	480 478
LpMDHf1 LpMDHf2			* TTGTGGAAT TTGTGGAAT		* GCATCTGAC	520 EGTGACAGAGCTO	* GCCGTTCT1	540 TGCA	:	540 497
LpMDHf1 LpMDHf2		ACAAAAG'	* TGAGGTTAG	560 GTCGTGGCGGA	* GCTGAGGAC	580 SATCCTCCCTCT	* TGGGCCACT	600 GAAT	:	600 -
LpMDHf1 LpMDHf2	:	GACTTTG	* AGAGAGCTO	620 GCCTGGAGAAG	* GCGAANAA(640 EGAGCTCAGCGA	* GAGCATCC	660 AGAAC		660 -

			*	680	*	700	*	720	
LpMDHf1	:	GGTGTGGC	GTTCATGA	ACAAGTGAGATC	ATATGAAT	GGATGGATACCC	CGCAACCT	ATAC :	720
LpMDHf2	:							:	-
			*	740	*	760	*	780	
LpMDHf1	:	ATAGATGA	TGCAAAGA	CTAAAGAAAGAG	TGTGATAT	AGTGCTCCTATA	TACCTGTA	: TAAA	780
LpMDHf2	:							:	-
		•							
			*						
LpMDHf1	:	CTCTCCTC	CCTGTAAG	AA : 798					
T.DMDHf2	:			: -					

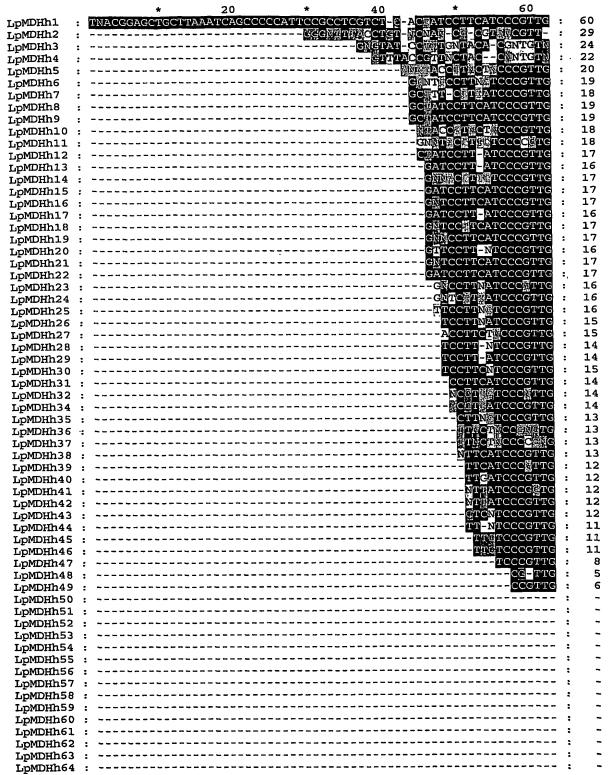
LpMDHg	:	CAATTGCAC	GTTCTTGC	20 FCACTTCAGCAT	* CACCCTCA	40 ACGCTTCTCCTAC	* CACAACCCC	60 TCC	:	60
LpMDHg	:	CAACCGTCA	* CTATGGTC	80 AAGGCTGTCGTC	* GCAGGTGC	100 TGCTGGTGGTA	* CCGGCCAGC	120 CCC	:	120
LpMDHg	:	TCTCTCTTC		140 ACGAGCCCCCTC	* :ATCGATGA	160 AGCTTGCCCTCT	* ACGATGTTG	180 TCA	:	180
LpMDHg	:	ACACTCCCG		200 GCTGATCTTTCC	* CACATCTO	220 CATCCCGCGCTC	* \AATCGCCG	240 GCT	:	240
грмрна	:			260 GGCGCAAAGGC1	* :GCATTCA!	280 \AGATGCCGACA'	* FTATCGTCA	300 ATCC	:	300
LpMDHg	:		* TTCCTCGC	320 AAGCCTGGCATO	* BACCCGTG	340 ATGACCTCTTCA	* ACATCAACG	360 3CCG	:	360
LpMDHg	:	GAATTGTCA		380 ATTGAGGTTGC	* CGCCGAAG	400 FTGCCCCCAAGG	* CCTTCATTC	420 CTGG	:	420
LpMDHg	:	TCATCTCCA	* ACCCTGTC	440 AACTCTACCGT	* CCTATCT	460 CTGCCGAGGTCC	* TCAAGGCC!	480 AAGG	:	480
LpMDHg	:	GCGTCTTCA	* ACCCTCAG	500 CGTCTTTTCGG	* IGTCACCA	520 CCCTCGACATCG	* TCCGTGCC	540 BAGA	:	540
LpMDHg	:	CTTTCGTCG	* CCAGCATO	560 ACCGGCGAGAA	* GCAGCCCC	580 AGAACTTGACCG	* TCCCCGTC!	600 ATTG	:	600
LpMDHg	:	GCGGCCACT	* CCGGCGAG	620 ACCATCGTCCC	* GCTTTTCA	640 GCAAGGNTCAGC	* CCTCTGCT	660 INCA	:	660
		TTCCCGC :								

		*	20	*	40	*	60		
LpMDHg	:	IARSCSLQHHPHASPT	QPLPTVTMVKAV	VAGAAGGI	GOBPRTFFF	LIDELALYD	VVN	:	60
					·				
		*	80	*	100	*	120		
LpMDHg	:	TPGVAADLSHISSRAQ	IAGYLPKDDGAK	AAFKDADI	IVIPAGIPRKPG	MTRDDLFNI	NAG	:	120
_									
						at.	100		
		*	140	*	160	*	180		
LpMDHg	:	IVKGLIEVAAEVAPKA	FILVISNPVNST	VPISAEVL	KAKGVFNPQRLF	GVTTLDIVE	LAET	:	180
		*	200	*	220				
LpMDHq	:	FVASITGEKOPONLTV	BATGGH2GELTA	PTERKYOP	SAXIP : 221				

		*	20	*	40	*	60		
LpMDHh	:	TNACGGAGCTGCTTA	AATCAGCCC(CCATTCCGCCT	CGTCTATAG	CGATCCTTCAT	CCCGT	:	60
		*	80	*	100	*	120		
Грипни	:	TGTCGTCGCCTCCTC	CCGAACCAC	rerecedated	CCCGAACTCC	AGAACCGGC1'C	CAATG	:	120
			- 10		7.50		100		
MDHh	•	GCGGCGAAGGAACCG	140 מיינכרכרכייננ	* ግጥርሩጥር ልርርርረ	160 30600366	፟ አሮፚፚፚጥጥሮሮልባ	180 מדקריד		180
пририи	•	CCCCCARACOPACCC	AIGCCCCIC					•	
		*	200	*	220	*	240		
LpMDHh	:	CTTGTTCCGATGATT		ATTATGCTTG		GCCTGTTATT		:	240
-									
		*	260	*	280	*	300		
LpMDHh	:	ATGCTGGATATTCCA		GAAGCTCTTA	ATGGTGTTAA	GATGGAGTTG	STTGAT	:	300
		*	320	*	340	*	360		
LpMDHh	:	GCCGCATTTCCACTT	CTCAAGGGA	GTTGTTGCAA	CAACTGATGT	TGTTGAGGCT	rgcact	:	360
		*	380	*	400	*	420		
LpMDHh	*:	GGTGTGAATGTTGCG	GTTATGGTT	GGTGGATTCC	CCAGGAAGGA	.GGGAATGGAA	AGGAAG	:	420
		*	440	*	460	*	480		
LpMDHh	:	GATGTTATGTCTAAG	BAATGTTTCA	ATCTACAAAT	CTCAAGCATC	TGCCCTTGAA	GCCCAT	:	480
		*	500	*	520	*	540		
LpMDHh	:	GCAGCCCGAATTGC	CAAGGTTCTG	GTTGTTGCCA	ATCCAGCAAA	CACCAATGCT	CTTATC	:	540
T MDITE		*	560	* ~~~~~~~~~	580	* יחיחייתית א מממממיי	600		600
тЪмони	:	TTAAAGGAGTTTGCT	CCATCIAIT	CCIGAGAAGA	ACAICAGIIG	IIIIGACCCGC	CIAGAC	٠	000
					510		660		
THUMOTI		CATAACAGGGCACTT	620 rggtcagatc	* ТСТGАGAGAС	640 TTGATGTCCA	AGTTAGTGAT	060 GTGAAG	:	660
-p	•								
		*	680	*	700	*	720		
LpMDHh	:	AATGTTATCATCTG	GGCAATCAC	TCTTCCAGTC	AGTACCCTG#	TGTGAACCAC	GCCACC	:	720
_									
		*	740	*	760	*	780		
LpMDHh	:	GTGAAGACTTCCAG		CCTGTTCGCG	AACTTGTTA	\AGACGATGAA	TGGCTA	:	780
		*	800	*	820	*	840		
T.~MDWh		ልልጥ ርሮልርርርርር ውስ	<u> </u>	יראמראמרמיזמי <i>י</i>	стсстссаа	CATCAAAGCG	DAGGAAG		840

LpMDHh	:	* CTCTCCAGTGCT	860 CTCTCTGCTGCCA	* GCTCTGCTT	880 GTGACCACAT	* CCGTGATTG	900 GTTCTC	: 900
LpMDHh	:	* GGAACCCCTGAG	920 GGAACATTTGTTT	* CCATGGGTG	940 FTGTATTCTG	* \TGGTTCATA(960 GGTGTG	: 960
LpMDHh	:	* CCTGCTGGGCTT	980 COTTOOTOATOTA	* CAGTAACTI	1000 GCTGCGGTG	* TGAATGGAC	1020 ATTGTT	:1020
LpMDHh	:	* CAAGGGCTCCCC	1040 BATCGACGAGTTCT	* CAAGAAAG?	1060 AAGATGGATG	* CCACAGCCCA(1080 GAGCTC	:1080
LpMDHh	:	* TCGGAGGAGAA	1100 GCTCTCGCCTACT	* CCGTGCCTCC	1120 SAGTAACTGC	* ATACCAGGGA	1140 SCAGCTG	:1140
LpMDHh	:	* CCGCTCTGATG	1160 TTTTGAATAAAGG	* FAACATTTTC	1180 GCTCCATGA	* AACTCATCTC	1200 CACTCAG	:1200
LpMDHh	:	* AACAGTTGCAC	1220 ATCGCGGTGCCTTI	* TAGCTGGTT	1240 FTTCCAGTGT	* GTATGAATGA	1260 GCTTTT	:1260
LpMDHh	:	* GTAGCTCTATT	1280 TTCGCCTGATGATT	* TTACAGGAC	1300 AGGATATTGG	* CAGGAAGATT	1320 GGAACAA	:1320
LpMDHh	:	* TTTGACGTCTG	1340 ATTAAAACCAACC	* PCTTATTAT	1360 TCCTGTGTGT.	* ATGAATGAGG	1380 CTTTTGT	:1380
LpMDHh	:	* AGCTCTATTTT	1400 CGCCTGATGATTI	* ACAGGCCAT	1420 GATATTGGCA	* GGAGGATTGG	1440 AACAATT	:1440
TabMDHh		* TGACGCCTGAT	1460 TAAAACCAACCTC	* ITATTACTA	1480 AAAAAAAAAA	A : 1484		

		* 20 * 40 *	60		
LpMDHh	:	MAAKEPMRVLVTGAAGQIGYALVPMIARGIMLGADQPVILHMLDIPPAAEALNGVKM	ELV :	:	60
LpMDHh	:		120 LEA	:	120
LpMDHh	:		180 SDV	:	180
LpMDHh	:		240 KAR	:	240
LpMDHh	:		300 WTI	:	300
LpMDHh	:	* 320 * VQGLPIDEFSRKKMDATAQELSEEKALAYSCLE : 333			



		*	80	*	100	*	12	0
LpMDHh1	:					GGCTCCAATGGCGG		122
LpMDHh2	:					GGCTCCAATGGCGC		88
LpMDHh3	:					GGCTCCAATGGCGG		86
LpMDHh4	:					GGCTCCAATGGCGG		83
LpMDHh5	:					GGCTCCAATGGCGG		82
LpMDHh6	:					GGCTCCAATGGCG		80
LpMDHh7	:					GGCTCCAATGGCG		78
LpMDHh8	:					GGCTCCAATGGCGC		81
LpMDHh9	:					GGCTCCAATGGCGC		81
LpMDHh10	:					CGGCTCCAATGGCGC		79
LpMDHh11	፡					GGCTCCAATGGCGC		80
LpMDHh12	:					CGGCTCCAATGGCGC		78
LpMDHh13	:	TCGTCGCCTCCTC				CGGCTCCAATGGCGC		77 78
LpMDHh14	:					EGGCTCCAATGGCG(EGGCTCCAATGGCG(78
LpMDHh15	:	TCGTCGCCTCCTC TCGTCGCCTCCTC				:GGCTCCAATGGCGC :GGCTCCAATGGCGC		78
LpMDHh16 LpMDHh17	:	TCGTCGCCTCCTC				GGCTCCAATGGCG(77
LpMDHh18	:	TCGTCGCCTCCTC				GGCTCCAATGGCG(78
LpMDHh19	:	TCGTCGCCTCCTC				CGGCTCCAATGGCG(78
LpMDHh20	:	TCGTCGCCTCCTC				CGGCTCCAATGGCG		77
LpMDHh21	:	TCGTCGCCTCCTC				CGGCTCCAATGGCG		78
LpMDHh22	:	TCGTCGCCTCCTC				CGGCTCCAATGGCG		78
LpMDHh23	:	TCGTCGCCTCCTC				CGGCTCCAATGGCG		77
LpMDHh24	:					CGGCTCCAATGGCG		77
LpMDHh25	:					CGGCTCCAATGGCG		77
LpMDHh26	:					CGGCTCCAATGGCG		76
LpMDHh27	:	TCGTCGCCTCCTC	CCGAACCACTCTC	CCCATCCCCGA	AACTCCAGAAC	CGGCTCCAATGGCG	3	77
-	.:	TCGTCGCCTCCTC	CCG-ACCACTCTC	CCCATCCCCGA	AACTCCAGAAC	CGGCTCCAATGGCG	3 :	75
LpMDHh29	,:	TCGTCGCCTCCTC	CCG-ACCACTCTC	CCCATCCCCGA	AACTCCAGAAC	CGGCTCCAATGGCG	9 :	75
LpMDHh30	:	TCGTCGCCTCCTC	CCG <mark>-</mark> ACCACTCTC	CCCATCCCCGA	AACTCCAGAAC	CGGCTCCAATGGCG(:	76
LpMDHh31	:	TCGTCGCCTCCTC	CCG <mark>-</mark> ACCACTCTC	CCCATCCCCGA	ACTCCAGAAC	CGGCTCCAATGGÇG	3 :	75
LpMDHh32	:	TCGTCGCCTCCTC	CCGĀACCACTCTC	CCCATCCCCG	AACTCCAGAAC	CGGCTCCAATGGCG	3	76
LpMDHh34	:			and the same of th		CGGCTCCAA∰GGCG(75
LpMDHh35	:	TCGTCGCCTCCTC	CCGAACCACTCTC	406 6 6 6 6 6		CGGCTCCAATGGCG		75
LpMDHh36	:		CCGAACCACTCTC			CGGCTCCAATGGCG		74
LpMDHh37	:	TCGTCGCCTCCTC	CCGAACCACTCTC	CCCMCCCCG	AACTCCAGAAC	CGGCTCCAATGGCG	:	75
LpMDHh38	:					CGGCTCCAATGGCG		74
LpMDHh39	:					CGGCTCCAATGGCG		74
LpMDHh40	:		444			CGGCTCCAATGGCG		73
LpMDHh41	:					CGGCTCCAATGGCG	•	
LpMDHh42	:					CGGCTCCAATGGCG		72 73
LpMDHh43 LpMDHh44	:	TCGTCGCCTCCTC				CGGCTCCAATGGCG CGGCTCCAATGGCG		73 72
LoMDHh45	:					CGGCTCCAATGGCG CGGCTCCAATGGCG		71
LpMDHh46	:					CGGCTCCAATGGCG		72
LoMDHh47	:					CGGCTCCAATGGCG		69
LpMDHh48	:		No. 2 of Contract			CGGCTCCAATGGCG		65
LpMDHh49	:		And the second second			CGGCTCCAATGGCG		68
LpMDHh50	:					CGGCTCCAATGGCG		46
LpMDHh51	:			Necced	NANTCCA-NAC	CGGCTCCAA-GGCG	G:	30
LpMDHh52	:						- :	-
LpMDHh53	:						- :	-
LpMDHh54	:						- :	~
LpMDHh55	:						- ;	-
LpMDHh56	:						- :	-
LpMDHh57	:						- :	-
LpMDHh58	:						- ;	-
LpMDHh59	:						- :	_
LpMDHh60	:						- :	-
LpMDHh61	:						- :	-
LpMDHh62	:					~	- :	-
LpMDHh63	:						- :	-
LpMDHh64	:						- :	-

LpMDHh1	LpMDH113 CAAAGBACCGATTCCGCCTGCTCCCCGCGCCCCGAGCACAAATTCGATATCCTCTTGTT 148 LpMDH15 CAAAGBACCGATTCCGCTGTCTCTCCCGCGCCCCCGAGCACAAATTCGATATCCTCTTGTT 148 LpMDH15 CAAAGBACCGATTCGCGTGCTCTCTCCCGGGCGCCGCAGACAAATTCGATATCCTCTTGTT 148 LpMDH16 CAAAGBACCGATTCGCGTGCTCTCTCCCGGGGCGCCGAGACAAATTCGATATCCTCTTGTT 140 LpMDH17 CAAAGBACCGATTCGCGTGCTCCTCTCCCGGGGCGCCGAGACAAATTCGATATCCTCTTGTT 140 LpMDH16 CAAAGBACCGATTCGCGTGCTCCTCTCCCGGGGGCCGCAGACAAATTCGATATCCTCTTGTT 140 LpMDH110 CAAAGBACCGATTCGCGTGCTCCTCTCCCGGGGGCCGCAGACAAATTCGATATCCTCTTGTT 141 LpMDH111 CAAAGBACCGATTCGCGTGCTCCTCTCCCGGGGCCGCAGACAAATTCGATATCCTCTTGTT 142 LpMDH111 CAAAGBACCGATTCGCGTGCTCCTCTCCCGGGGCCGCAGACAAATTCGATATCCTCTTGTT 143 LpMDH111 CAAAGBACCGATTCGCGTGCTCTCTCCCCGGGGCCCCAGACAAATTCGATATCCTCTTGTT 144 LpMDH111 CAAAGBACCGATTCGCGTGCTCTCTCCCCGGGGCCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH111 CAAAGBACCGATTCGCGTGCTCCTCTCCCCGGGCCCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH111 CAAAGBACCGATTCGCGTGCTCCTCTCCCCCGGCGCCCGAGACAAATTCGATATCCTCTTGTT 140 LpMDH111 CAAAGBACCGATTCGCGTGCTCCTCTCCCCCGGCCCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH112 CAAAGBACCGATTCGCGTGCTCCTCTCCCCCGGCCCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH112 CAAAGBACCGATTCGCGTGCTCCTCTCCCCCGGCCCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH112 CAAAGBACCGATTCGCGTCCTCCTCCCCCCGGCCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH112 CAAAGBACCGATTCGCGTCCTCCTCCCCCCGGCCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH112 CAAAGBACCGATTCGCGTCCTCCTCCCCCCGGCCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH112 CAAAGBACCGATTCGCGTCCTCCTCCCCCCGGCGCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH112 CAAAGBACCGATTCGCTCTCTCCCCCGGCGCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH113 CAAAGBACCGATTCGCTCTCTCCCCCGGCGCCCAGACAAATTCGATATCCTCTTGTT 140 LpMDH113 CAAAGBACCGATTCGCTCTCTCCCCCCGCGCCCCAGACAAATTCGATATCCTCTTTT 140 LPMDH113 CAAAGBACCGATTCGCTCTCTCCCCCCGCGCCCCAGACAAATTCGATATCCTCTTTT 140 LPMDH114 CAAAGBACCGATTCGCTCTCTCCCCCCCCCCCAGGACAAATTCGATATCCTCTTTT 140 LPMDH114 CAAAGBACCGATTCGCTCTCTCCCCCCCCC			*	140	*	160	*	180		
LPMDHHB : GAAGGAACCGATIGGCCGTGCTGTCATCACCGGCCGCGGAGGACAATTGGATTGGTTTGTT : 145 LPMDHHB : GAAGGAACCGATIGGCCGTGCTGTCATCACCGGGCAGGACAATTGGATTATGCTTTGTT : 142 LPMDHB : GAAGGAACCGATIGGCCGTGTTGTCACCGGGCAGGACAATTGGATTATGCTTTGTT : 142 LPMDHB : GAAGGAACCGATIGGCCGTGTTGTCACCGGGCAGGAGACAATTGGATTATGCTTTGTT : 142 LPMDHB : GAAGGAACCGATIGGCCGTGTTGTCACCGGGCAGGAGAAATTGGATTATGCTTTGTT : 142 LPMDHB : GAAGGAACCGATIGGCCGTGTCTGTCACCGGGCAGGACAAATTGGATTATGCTTTGTT : 143 LPMDHB : GAAGGAACCGATIGGCCGTGTCTGTCACCGGCAGGACAAATTGGATTATGCTTTGTT : 141 LPMDHB : GAAGGAACCGATIGGCCGTGCTCTCACCGGCAGGACAAATTGGATTATGCTTTGTT : 141 LPMDHB : GAAGGAACCGATIGGCCGTGCTCTCACCGGCAGGACAAATTGGATTATGCTTTGTT : 141 LPMDHB : GAAGGAACCGATIGGCCGTGCTCTCACCGGCAGGACAAATTGGATTATGCTTTGTT : 142 LPMDHB : GAAGGAACCGATIGGCCGTGCTCTCACCGGCAGGACAAATTGGATTATGCTTTGTT : 142 LPMDHB : GAAGGAACCGATIGGCCGTGCTCTCACCGGGCCGCAAGGACAAATTGGATTATGCTTTGTT : 142 LPMDHB : GAAGGAACCGATIGGCCGTGTCTCACCGGGCCGCAAGGACAAATTGGATTATGCTTTGTT : 144 LPMDHB : GAAGGAACCGATIGCCCGTGCTCTCACCGGGCCGCAAGGACAAATTGGATTATGCTTTTTT : 144 LPMDHB : GAAGGAACCGATIGCCCGTGCTCTCACCGGGCCGCAAGGACAAATTGGATTATGCTTTTTT : 140 LPMDHB : GAAGGAACCGATIGCCCGTGCTCTCACCGGGCCGCAAGGACAAATTGGATTATGCTTTTTT : 140 LPMDHB : GAAGGAACCGATIGCCGTGTCTCACCGGGCCGCAAGGACAAATTGGATTATGCTTTTTT : 140 LPMDHB : GAAGGAACCGATIGCCGTGTCTCACCGGGCCGCAAGGACAAATTGGATTATGCTTTTTT : 140 LPMDHB : GAAGGAACCGATIGCCGTGTCTCACCGGGCCGCAAGGACAAATTGGATTATGCTTTTTT : 140 LPMDHB : GAAGGAACCAATTGCGTGTCTCACCGGGCCGCAAGGACAAATTGGATTATGCTTTTTT : 140 LPMDHB : GAAGGAACCAATTGGATTGCGTGTCTCACCGGGCCGCAAGGACAAATTGGATTATGCTTTTTT : 140 LPMDHB : GAAGGAACCAATTGCGTGTCTCACCGGGCCGCAAGGACAAATTGGATTATGCATTTTTT : 131 LPMDHB : GAAGGAACCAATTGCGTGTCTCTCACCGGGCCGCAAGGACAAATTGGATTATGCATTTTTT : 132 LPMDHB : GAAGGAACCAATTGCGTGT	LphDHhh	LpMDHh1 :	CGA!	AGGAACCGA'	TGCGCGTGCT	CGTCACCGGCG	CCGCAGGACA	AATTGGATATO	CTCTTGTT	:	
LPMDHIS : CRANGARCCANTGCCCTGCTCTCTCACCGCCGCCGCAGGACAATTGCATTGCTTTGTT : 144 LPMDHIS : CRANGARCCANTGCCCTGTCTTCTACCGCGCCGCAGGACAATTGCATTATGCTTTGTT : 144 LPMDHIS : CRANGARCCANTGCCCTGTCTCTCTCCGCGCCGCAGGACAATTGCATTATGCTTTGTT : 144 LPMDHIS : CRANGARCCANTGCCCTGTCTCTCTCCGCGCCGCAGGACAATTGCATTATGCTTTGTT : 143 LPMDHIS : CRANGARCCANTGCCCTGTCTCTCTCTCTCGCGCCGCCGCAGGACAATTGCATTATGCTTTGTT : 143 LPMDHII : CRANGARCCANTGCCCTGTCTCTCTCTCCGCGCCGCCGAGGACAATTGCATTATGCTTTGTT : 143 LPMDHII : CRANGARCCANTGCCCTGTCTCTCTCCGCGCCGCCGCAGGACAATTGCATTATGCTTTGTT : 141 LPMDHII : CRANGARCCANTGCCCTGTCTCTCTCCGCGCCGCCGAGGACAATTGCATTATGCTTTGTT : 142 LPMDHII : CRANGARCCANTGCCCTGTCTCTCTCCGCGCCGCCGAGGACAATTGCATTATGCTTTGTT : 142 LPMDHII : CRANGARCCANTGCCCTGTCTCTCTCCGCGCCGCCGAGGACAATTGCATTATGCTTTGTT : 141 LPMDHII : CRANGARCCANTGCCCTGCTCTCTCACCGGCCGCCGCAGGACAATTGCATTATGCTTTGTT : 140 LPMDHII : CRANGARCCANTGCCCTGCTCTCTCACCGCGCCGCAGGACAAATTGCATTATGCTTTGTT : 140 LPMDHII : CRANGARCCANTGCCCTGCTCTCTCACCGCGCCGCAGGACAAATTGCATTATGCTTTGTT : 140 LPMDHII : CRANGARCCANTGCCCTGCTCTCTCACCGCGCGCCGCAGGACAAATTGCATTATGCTTTGTT : 140 LPMDHII : CRANGARCACANTGCCCTGCTCTCTCACCGCGCGCCGCAGGACAAATTGCATTATGCTTTGTT : 140 LPMDHII : CRANGARCACANTGCCCTGCTCTCACCGCGCGCCGCAGGACAAATTGCATTATGCTTTGTT : 140 LPMDHII : CRANGARCACANTGCCCTGTCTCTCACCGCGCGCCGCAGGACAAATTGCATTATGCTTTGTT : 140 LPMDHII : CRANGARCACANTGCCCTGCTCTCACCGCGCGCCGCAGGACAAATTGCATTATGCTTTGTT : 140 LPMDHII : CRANGARCCANTGCCCTGTCTCACCGCGCGCCAGGACAAATTGCATTATGCTTTTT : 140 LPMDHII : CRANGARCCANTGCCCTGTCTCACCGCGCGCCAGGACAAATTGCATTATGCTTTGTT : 140 LPMDHII : CRANGARCCANTGCCCTGTCTCACCGCGCCGCAGGACAAATTGCATTGC	LpMDHhb CAAAGAACGATTGGGGTGCTCTTCACCGGGCCGCAGACAATTGGATATGCTTTGT 144 LpMDHh7 CAAAGAACGATTGGGGTGCTCTCACCGGGGCCGCAGACAATTGGATATGCTTTTGT 144 LpMDH7 CAAAGAACGATTGGGGTGCTCTCACCGGGGCCGCAGACAAATTGGATATGCTTTTGT 140 LpMDH1 CAAAGAACGATTGGGGTGCTCTCACCGGGGCCGCAGACAAATTGGATATGCTTTTGT 140 LpMDH1 CAAAGAACGATTGGGGTGCTCTCACCGGGGCCGCAGACAAATTGGATATGCTCTTGT 141 LpMDH1 CAAAGAACCGATTGGGGTGCTCTCTCACCGGGGCCGCAGACAAATTGGATATGCTCTTGT 142 LpMDH1 CAAAGAACCGATTGGGGTGCTCTCTCACCGGGGCCGCAGACAAATTGGATATGCTCTTGT 140 LpMDH1 CAAAGAACCGATTGGGGTGCTCTCTCACCGGGGCCGAGACAAATTGGATATGCTCTTGT 140 LpMDH1 CAAAGAACCGATTGGGGTGCTCTCTCACCGGGGCCAGACAAATTGGATATGCTCTTGT 140 LpMDH1 CAAAGAACCGATTGGGGTGCTCTCTCTCTCTCTCTCTCTC	LpMDHh2 :	CGA	AGGAACCGA'	TGCGCGTGCT	CGTCACCGGCG	CCGTAGGACA	AATTGGATATO	CTCTTGTT	:	
LPMDHHS : GAAGGAACCGATGCCCGTGCTCTCACCGCCGCCGCAGGACAATTGCATTGCTTTTT : 142 LPMDHHB : GAAGGAACCGATGCCCGTGCTCTCACCGCGCCGCAGGACAATTGCATTATGCTTTTTT : 143 LPMDHHB : GAAGGAACCGATGCCCGTGCTCTCACCGCGCCGCAGGACAATTGCATTGCTTTTTT : 143 LPMDHHB : GAAGGAACCGATGCCCGTGCTCTCACCGGCCGCAGGACAATTGCATTGCTTTTTT : 143 LPMDHHB : GAAGGAACCGATGCCCGTGCTCTCACCGGCCGCAGGACAATTGCATTGCTTTGTT : 143 LPMDHHB : GAAGGAACCGATGCCCGTGCTCTCACCGGCCGCAGGACAAATTGCATTTGCTTTTTT : 141 LPMDHHB : GAAGGAACCGATGCCCGTGCTCTCACCGGCCGCAGGACAAATTGCATTTGCTTTTTT : 141 LPMDHHB : GAAGGAACCGATGCCCGTGCTCTCACCGGCCGCAGGACAAATTGCATTTGCTTTTTT : 142 LPMDHHB : GAAGGAACCAATGCCCGTGCTCTCACCGGCCGCAGGACAAATTGCATTTGCTTTTTT : 142 LPMDHHB : GAAGGAACCCATTGCCCGTGCTCTCACCGGCCCCAAGGACAAATTGCATTTGCTTTTTT : 144 LPMDHHB : GAAGGAACCAATGCCCGTGCTCTCACCGGCCGCAAGGACAAATTGCATTTGCTTTTTT : 144 LPMDHHB : GAAGGAACCCATTGCCCGTGCTCTCACCGGCGCCCAAGGACAAATTGCATATGCTTTTTT : 140 LPMDHHB : GAAGGAACCAATGCCCGTGCTCTCACCGGCGCCCAAGGACAAATTGCATATGCTTTTTT : 140 LPMDHHB : GAAGGAACCAATGCCCGTGCTCTCACCGGCGCCCAAGGACAAATTGCATATGCTTTTTT : 140 LPMDHHB : GAAGGAACCAATGCCGTGCTCTCACCGGCGCCCAAGGACAAATTGCATATGCTTTTTT : 140 LPMDHHB : GAAGGAACCAATGCCGTGCTCTCACCGGCGCCCAAGGACAAATTGCATATGCATTTGTT : 140 LPMDHHB : GAAGGAACCAATGCCGTGCTCTCACCGGCGCCCAAGGACAAATTGCATATGCATTTTTT : 140 LPMDHHB : GAAGGAACCAATGCCGTGCTCTCACCGGGCGCCAAGGACAAATTGCATATGCATTTTTT : 140 LPMDHHB : GAAGGAACCAATGCCGTGCTCTCACCGGGCGCCAAGGACAAATTGCATATGCATTTTTT : 140 LPMDHHB : GAAGGAACCAATGCGCTTGCTCACCGGGCGCCAAGGACAAATTGCATATGCATTTTTT : 140 LPMDHHB : GAAGGAACCAATGCGCTTGCTCACCGGGCCGCAAGGACAAATTGCATATGCATTTTTT : 140 LPMDHHB : GAAGGAACCAATGCGCTTGCTCACCGGGCCGCAAGGACAAATTGCATATGCATTTTTT : 140 LPMDHB : GAAGGAACCAATGCGCTTGCTCACCGGGCCGCAAGGACAAATTGCATTTGCATATGCATTTTT : 140 LPMDHB : GAAGGAACCAATTGCGTTGCTCACCGGGCCGCAAGGACAAATTGCATTGCATTTTT : 140 LPMDHB : GAAGGAACCAATTGCGTTGCTCACCGGGCCGCAAGGACAAATTGCATTTTTT : 140 LPMDHB : GAAGGAACCAATTGCGTTGCTCACCGGGCCGCAAGGACAAATTGCATTTGCATTTTT : 131 LPMDHB : GAAGGAACCAATTGCGTTGCTCACCGGGCCCCAAGGACAAATTGCATTTTTT : 137 LPMDHB : GAAGGAACCAATTGCGTTGCTCACCGGGCCCC	LphOHHBS : CARAGIAACCGATEGGGTCCTCSTCACCGGGCCGGAGACAAATTGGATATGCTTTGT : 144 LphOHHBA : CARAGIAACCGATEGGGGTGCTCTGTACCGGGCCGGAGACAAATTGGATATGCTCTTGT : 144 LphOHHBA : CGARGGAACCGATEGGGGTGCTCTGTACCGGGGCCGGAGACAAATTGGATATGCTCTTGT : 143 LphOHHBA : CGARGGAACCGATEGGGGTGCTCTGTACCGGGGCCGCAGACAAATTGGATATGCTCTTGT : 143 LphOHHBA : CGARGGAACCGATEGGGGTGCTCTGTACCGGGGCCGCAGACAAATTGGATATGCTCTTGT : 144 LphOHHBA : CGARGGAACCGATEGGGTGCTCTGTACCGGGGCCGCAGACAAATTGGATATGCTCTTGT : 141 LphOHHBA : CGARGGAACCGATEGGGTGCTCTGTACCGGGGCCGCAGACAAATTGGATATGCTCTTGT : 141 LphOHHBA : CGARGGAACCGATEGGGTGCTCTGTACCGGGGCCGCAGACAAATTGGATATGCTCTTGT : 141 LphOHHBA : CGARGGAACCGATEGGGTGCTCTGTACCGGGGCCGCAGACAAATTGGATATGCTCTTGT : 140 LphOHHBA : CGARGGAACCGATEGGGTGCTCTGTACCGGGGCCCCAGGACAAATTGGATATGCTCTTGT : 140 LphOHHBA : CGARGGAACCGATEGGGTGCTCTGTACCGGGGCCCCAGGACAAATTGGATATGCTCTTGT : 140 LphOHHBA : CGARGGAACCGATEGGGTGCTCTGTACCGGGGCCCCAGGACAAAATTGGATATGCTCTTGT : 140 LphOHHBA : CGARGGAACCGATEGGGTGCTCTGTACCGGGGCCCCAGGACAAAATTGGATATGCTCTTGT : 140 LphOHHBA : CCARGGAACCGATEGGGTGCTCTGTACCGGGGCCCCAGGACAAAATTGGATATGCTCTTGT : 140 LphOHHBA : CCARGGAACCGATEGGGTGCTCTGTACCGGGGCCCCAGGACAAAATTGGATATGCTCTTGT : 140 LphOHHBA : CCARGGAACCGATEGGGTGCTCTGTACCGGGGCCCCAGGACAAAATTGGATATGCTCTTGT : 140 LphOHHBA : CCARGGAACCGATEGGGTGCTCTGTACCAGGGCCCCAGGACAAAATTGGATATGCTCTTTGT : 140 LphOHHBA : CCARGGAACCGATEGGGTGCTCTGTACACGGGCCCCAGGACAAAATTGGATATGCTCTTTT : 140 LphOHHBA : CCARGGAACCGATTGGCGTGCTCTGTACACGGGCCCCAGGACAAAATTGGATATGCTCTTTT : 140 LphOHHBA : CCARGGAACCGATTGGCGTGCTCTGTACACGGGCCCCAGGACAAAATTGGATATGCTCTTTT : 140 LphOHHBA : CCARGGAACCGATTGGCGTGCTCTGTACACGGCCCCCAGGACAAAATTGGATATGCTCTTTT : 140 LphOHHBA : CCARGGAACCGATTGGCGTGCTCTGTACACGGCCCCCAGGACAAAATTGGATATGCTCTTTT : 140 LphOHHBA : CCARGGAACCGATTGGCCGTGCTCTGTACACGGCCCCCAGGACAAAATTGGATATGCTTTTT : 140 LphOHHBA : CCARGGAACCGATTGGCCGTGCTCTGTACACGGCCCCCAGGACAAAATTGGATATGCTTTTT : 140 LphOHHBA : CCARGGAACCGATTGGCCGTGCTCTCTGTACACGGCCCCCAGGACAAATTGGATATGCTTTTT : 141 LphOHHBA : CCARGGAACCGATTGGCCGTGCTCTGTACACGGCCCCCAGGACAAATTGGATATGCTTTTT : 141 Lp	LpMDHh3 :	CGA/	AGGAACCGA'	TGCGCGTGCT	CGTCACCGGCG	CCGCAGGACA	AATTGGATATO	CTCTTGTT	:	
LPMMH6	ImpMPHH6	-								-	
		_									
LPMDHHB : CAAGGAACCGATGCCCCTCTCTCTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 143 LPMDHHD : CAAGGAACCGATGCCCTGCTCTCTCACCGGCCCCGCAGGACAAATTGGATATGCTCTTGTT : 141 LPMDHHD1 : CGAAGGAACCGATTGCCCTTGCTCCTCTCTCTCTCTT : 141 LPMDHHD1 : CGAAGGAACCGATTGCCCTTGCTCTCTCTCTCTCTCTT : 141 LPMDHHD1 : CGAAGGAACCGATTGCCCTTGCTCACCGGCCCCGCAGGACAAATTGGATATGCTCTTGTT : 142 LPMDHHD1 : CGAAGGAACCGATTGCGCTTGCTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 140 LPMDHHD1 : CGAAGGAACCGATTGCGCTTGCTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 140 LPMDHHD1 : CGAAGGAACCGATTGCGCTTGCTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 140 LPMDHHD1 : CGAAGGAACCGATTGCGCTTGCTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 140 LPMDHHD1 : CGAAGGAACCGATTGCGCTTGCTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 140 LPMDHHD1 : CGAAGGAACCGATTGCGCTTGCTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 140 LPMDHHD2 : CGAAGGAACCGATTGCGCTTGCTCACCGGCCCCCCAGGACAAATTTGGATATCCTCTTGTT : 140 LPMDHHD2 : CGAAGGAACCGATTGCGCTTGCTCACCGGCCCCCCAGGACAAATTTGGATATCCTCTTGTT : 140 LPMDHHD2 : CGAAGGAACCGATTGCGCTTGCTCTCACCGGCCCCCCAGGACAAATTTGGATATCCTCTTGTT : 140 LPMDHHD2 : CGAAGGAACCGATTGCGCTTGCTCTCACCGGCCCCCAGGACAAATTTGGATATCCTCTTGTT : 140 LPMDHHD2 : CGAAGGAACCGATTGCCCTTGCTCTCACCGGCCCCCAGGACAAATTTGGATATCCTCTTGTT : 130 LPMDHHD2 : CGAAGGAACCGATTGCCCTTGCTCTCACCGGCCCCCAGGACAAATTTGGATATCCTCTTGTT : 131 LPMDHHD2 : CGAAGGAACCGATTGCCCTTGCTCTCACCGGCCCCCAGGACAAATTTGGATATCCTCTTGTT : 132 LPMDHHD2 : CGAAGGAACCGATTGCCCTTGCTCTCACCGGCCCCCAGGACAAATTTGGATATCCTCTTGTT : 133 LPMDHHD3 : CGAAGGAACCGATTGCCCTTGCTCTCACCGGCCCCCAGGACAAATTTGGATATCCTCTTGTT : 133 LPMDHHD3 : CGAAGGAACCGATGCCCCTTGCTCTCACCGGCCCCCAGGACAAATTTGGATATCCTCTTGTT : 137 LPMDHD3 : CGAAGGAACCGATGCCCCTTGCTCTCACCGGCCCCCAGGACAAAATTGGATATCCTCTTGTT : 137 LPMDHB3 : CGAAGGAACCGATGCCCCTCTCTCACCGC	Image	-	3								
LPMMH10 : CAAAGAACCGATGCGCTGCTCTCTCACCGGCGCGCAGACAAATTGGATATGCTCTTGTT : 141 LPMMH112 : CAAAGAACCGATGCGCTGCTCTCACCGGGCGCAGGACAAATTTGGATATGCTCTTGTT : 142 LPMMH12 : CAAAGAACCGATGCGCTGCTCACCGGGCCGCAGGACAAATTTGGATATGCTCTTGTT : 142 LPMMH13 : CAAAGAACCGATGCGCTGCTCTCACCGGGCCGCAGGACAAATTTGGATATGCTCTTGTT : 142 LPMMH14 : CAAAGAACCGATGCGCTGCTCTCACCGGGCCGCAGGACAAATTTGGATATCCTCTTGTT : 140 LPMMH15 : CAAAGAACCGATGCGCTGCTCTCACCGGGCCCGCAGGACAAATTTGGATATCCTCTTGTT : 140 LPMMH16 : CAAAGAACCGATGCGCTGCTCTCTCACCGGGCCCGCAGGACAAATTTGGATATCCTCTTGTT : 140 LPMMH17 : CGAAGGAACCGATGCGCTGCTCTCTCACCGGGCCCCAGGACAAATTTGGATATCCTTTGTT : 140 LPMMH19 : CGAAGGAACCGATGCGCTTCATCACCGGCCCCCAGGACAAATTTGGATATCCTTTGTT : 140 LPMMH19 : CGAAGGAACCGATTGCGCTTCATCACCGGCCCCCAGGACAAATTTGGATATCCTTTGTT : 140 LPMMH19 : CGAAGGAACCGATTGCGCTTCATCACCGGCCCCCAGGACAAATTTGGATATCCTTTGTT : 140 LPMMH12 : CGAAGGAACCGATTGCGCTTCATCACCGGCCCCCAGGACAAATTTGGATATCCTTTGTT : 140 LPMMH12 : CGAAGGAACCGATTGCGCTTCATCACCGGCCCCCAGGACAAATTTGGATATCCTTTGTT : 140 LPMMH12 : CGAAGGAACCGATTGCGCTTCATCACCGGCCCCCCAGGACAAATTTGGATATCCTTTGTT : 140 LPMMH19 : CGAAGGAACCGATGCGCCTTCATCACCGGCCCCCCAGGACAAATTTGGATATCCTTTGTT : 139 LPMMH19 : CGAAGGAACCGATGCGCCTTCATCACCGGCCCCCCAGGACAAATTTGGATATCCTTTGTT : 139 LPMMH19 : CGAAGGAACCGATGCGCCTTCATCACCGGCCCCCCAGGACAAATTTGGATATCCTTTGTT : 139 LPMMH19 : CGAAGGAACCGATGCCCCTTCACCGGCCCCCCAGGACAAATTTGGATATCCTTTGTT : 139 LPMMH19 : CGAAGGAACCGATGCCCCTTCACCGGCCCCCCAGGACAAATTTGGATATCCTTTGTT : 139 LPMMH19 : CGAAGGAACCGATGCCCCTTCACCGGCCCCCCCCCAGGACAAATTTGGATATCCTTTGTT : 139 LPMMH19 : CGAAGGAACCGATGCCCCTTCACCGGCCCCCCCCCAGGACAAATTTGGATATCCTTTTTT : 137 LPMMH19 : CGAAGGAACCGATGCCCCTTCACCGGCCCCCCCCCCCAGGACAAATTTGGATATCCTTTTTT : 137 LPMMH19 : CGAAGGAACCGATGCCCCTTCACCGGCCCCCCCCCCAGGACAAATTTG	ImpMinis	-								-	
Lipholith		-									
Image	LPMBHL1 CAAAGAACCGATGCCGTGCTCTCAC CGGGCCGCAGACAAATTGGTATGCTCTTGTT 142 LPMBHL2 CAAAGAACCGATGCGGTGCTCTCCTCCTCTT 139 LPMBHL3 CAAAGAACCGATGCGGTGCTGTCTCCCCGGCCCCAGACAAATTGGTATAGCTCTTGTT 139 LPMBHL3 CAAAGAACCGATGCGGTGCTGTTCACCGGGCCCCAGACAAATTGGTATAGCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCGGTGCTGTTCACCGGGCCCCAGACAAATTGGTATAGCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCGGTGCTGTTCACCGGGCCCCAGACAAATTGGTATAGCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCGGTGCTGTTCACCGGGCCCCAGACAAATTGGATATGCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCGCTGTCTGTTCACCGGGCCCCAGACAAATTGGATATGCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCGCTGTCTGTTCACCGGCCCCCAGACAAATTGCATATGCTCTTGTT 140 LPMBHL3 CAAAGAAACCGATGCGCTGTCTGTTCACCGGCCCCCAGACAAATTGCATATGCTCTTGTT 140 LPMBHL3 CAAAGAAACCGATGCGCTGTCTGTTCACCGGCCCCAGACAAATTGCATATACCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCGCGTGTCTGTCACCGGCCCCAGACAAATTGCATATACCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCGCGTGTCTGTCACCGGCCCCCAGACAAATTGCATATACCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCGCGTGTCTGTCACCGGCCCCCAGACAAATTGCATATACCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCGCGTGTCCTTCACCGGCCCCCAGACAAATTGCATATACCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCCGTTGTCTCACCGGCCCCCAGACAAATTGCATATACCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCCGTTGCTCACCGGCCCCCAGACAAATTGCATATACCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCCGTTGCTCACCGGCCCCCCAGACAAATTGCATATACCTCTTGTT 140 LPMBHL3 CAAAGAACCGATGCGCGTTCTCTCACCGGCCCCCCAGACAAATTGCATATACCTCTTGTT 139 LPMBHL3 CAAAGAACCCATTGCCGTTCACCGGCCCCCAGACAAATTGCAATTGCTCTTGTT 139 LPMBHL3 CAAAGAACCCATTGCGCTTTCACCGGCCCCCCAGACAAATTGCAATTGCTCTTGTT 139 LPMBHL3 CAAAGAACCCATTGCGCTTCACCGGCCCCCAGACAAATTGCAATTGCTCTTGTT 139 LPMBHL3 CAAAGAACCCATTGCGCTTCACCGGCCCCCAGACAAATTGCAATTGCCTTTGTT 139 LPMBHL3 CAAAGAACCCATTGCGCTTCACCGGCCCCCCAGACAAATTGCAATTGCCTTTGTT 139 LPMBHL3 CAAAGAACCCATTGCGCTTCACCGGCCCCCCAGACAAATTGCAATTGCCTTTGTT 139 LPMBHL3 CAAAGAACCCATTGCGCTTCACCGGCCCCCCAGACAAATTGCAATTGCCTTTGTT 139 LPMBHL3 CAAAGAACCCATTGCGCTTCACCGGCCCCCCAGACAAATTGCAATTGCCTTTGTT 130 LPMBHL3 CAAAGAACCCATTGCGCTTCACCGGCCCCCCAGACAAATTGCAATTGCCTT	-									
LPMDHH12: CAAAGAACCATGCGCTGCTCGTCACCGGCGCGGGGACAATTGGATAGCCTTGTT 199. LPMDHH14: CGAAGGAACCATGCGCTGCTCACCGGGCCGCGGGGACAATTGGATATGCTCTTGTT 140. LPMDHH15: CGAAGGAACCGATGCGGTGCTGTCACCGGGGCGCGGAGACAATTGGATATGCTCTTGTT 140. LPMDHH16: CGAAGGAACCGATGCGGTGCTGTCACCGGGGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH17: CGAAGGAACCGATGCGGTGCTGTCACCGGGGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH19: CGAAGGAACCGATGCGGTGCTGTCACCGGGGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH19: CGAAGGAACCGATGCGGTGCTGTCACCGGGGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH19: CGAAGGAACCGATGCGGTGCTGTCACCGGGGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH19: CGAAGGAACCGATGCGGTGCTGTCACCGGGGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH10: CGAAGGAACCGATGCGGTGCTGTCACCGGGGCGCAGACAAATTGGATATGCTCTTGTT 140. LPMDHH10: CGAAGGAACCGATGCGGTGCTGTCACCGGGGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH10: CGAAGGAACCGATGCGGTGTCTGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH12: CGAAGGAACCGATGCGGTGTCTGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH12: CGAAGGAACCGATGCGGTGTCTGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH12: CGAAGGAACCGATGCGGTGTCTGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDHH12: CGAAGGAACCGATGCGGTGTCGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH12: CGAAGGAACCGATGCGGTGCTCGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH12: CGAAGGAACCGATGCGGTGCTCGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH12: CGAAGGAACCGATGCGGTGCTCGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH12: CGAAGGAACCGATGCGGTGCTCGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH13: CGAAGGAACCGATGCGGTGTCTGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH13: CGAAGGAACCGATGCGGTGTCTGTCACCGGGCGCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH13: CGAAGGAACCGATGCGCTGTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH13: CGAAGGAACCGATGCGCTGTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH13: CGAAGGAACCGATGCGCTGTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH13: CGAAGGAACCGATGCGCTGTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH13: CGAAGGAACCGATGCGCTGTCCTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT 140. LPMDH13: CGAAGGAACCG	Image: I	-								-	
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LpMDHh16: LpMDHh17: LpMDHh18: LpMDHh18: CGAAGGAACCGATGCGGTGCTGTCACCGGGCGCGAGGACAAATTGGATATGCTCTTGTT: LpMDHh19: CGAAGGAACCGATGCGGTGCTGTCACCGGGGCGCGAGGACAAATTGGATATGCTCTTGTT: LpMDHh20: LpMDHh21: LpMDHh21: LpMDHh21: LpMDHh21: LpMDHh21: LpMDHh22: CGAAGGAACCGATGCGCGTGCTTGTCACCGGGGCCGAGGACAAATTGGATATGCTCTTGTT: LpMDHh21: LpMDHh22: CGAAGGAACCGATGCGCGTGCTCGTCACCGGGGCCGAGGACAAATTGGATATGCTCTTGTT: LpMDHh22: LpMDHh23: LpMDHh24: LpMDHh24: LpMDHh24: LpMDHh24: LpMDHh24: LpMDHh24: LpMDHh25: LpMDHh24: LpMDHh26: LpMDHh26: LGAAGGAACCGATGCGGTGCTCGTCACCGGGCCCCAGGACAAATTGGATATGCTCTTGTT: LpMDHh26: LpMDHh26: LpMDHh27: LpMDHh26: LGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT: LpMDHh26: LpMDHh27: LpMDHh26: LGAAGGAACCGATGCGGTGCTCGTCACCGGGCCCCCAGGACAAATTGGATATGCTCTTGTT: LpMDHh27: LpMDHh29: CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT: LpMDHh29: CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT: LpMDHh29: CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT: LpMDHh29: CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT: LpMDHh30: CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT: LpMDHh31: LpMDHh32: CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT: LpMDHh31: LpMDHh32: CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT: L137: LpMDHh31: LpMDHh32: CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT: L137: LpMDHh33: CGAAGGAACCCATTCGCGTGCTCTGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT: L137: LpMDHh34: CGAAGGAACCCATTCGCGTGCTCTGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT: L37-LpMDHh34: CGAAGGAACCCATTCGCGTGCTCTGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT: L37-LpMDHh34: CGAAGGAACCCATTCGCGTGCTCTGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT: L37-LpMDHh34: CGAAGGAACCCATTCGCGTGCTCTGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT: L37-LpMDHh34: CGAAGGAACCCATTCGCGTGCTCTGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT: L37-LpMDHh34: CGAAGGAACCCATTCGCGTGCTCTGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT: L37-LpMDH34: CGAAGGAACCCATTCGCGTGCTCTGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT: L37-LpMDH34: CGAAGGAAC	Lpmbilia : camedaaccarrecectercectercectercececeaeaacaantegatatectertett : 139 Lpmbilia : camedaaccarrececetercetercetercececeaeaacaantegatatectertett : 139 Lpmbilia : camedaaccarreceterceterceterceceaeaacaantegatatectertett : 139 Lpmbilia : camedaaccarreceterceterceterceceaeacaattegatatectertett : 140 Lpmbilia : camedaaccarreceterceterceterceceaeacacaaattegatatectertett : 139 Lpmbilia : camedaaccarreceterceterceteaeacacacaaattegatatectertett : 139 Lpmbilia : camedaaccarreceterceterceceaeacacacaaattegatatectertett : 139 Lpmbilia : camedaaccarreceaeacacacacacacacacacacaaattegatatectertett : 139 Lpmbilia : camedaaccarreceaeacacacacacacacacacaaattegatatectertett : 140 Lpmbilia : camedaaccarreceaeacacacacacacacacacacaaattegatatectertett : 140 Lpmbilia : camedaaccarreceaeacacacacacacacacacacacacacac	-								:	-
LpMDHh17 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGAGGACAAATTGGATATGCTCTTCTT 139 LpMDHh18 CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh121 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh221 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh221 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh221 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh222 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh245 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 139 LpMDHh252 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 139 LpMDHh264 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 139 LpMDHh275 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 139 LpMDHh276 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 139 LpMDHh276 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh39 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh39 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh39 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh39 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh39 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh39 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh49 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh49 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGAGGACAAATTGGATATGCT	LpMDH11: canadancoarrececteroctcaccaeacacaeacacaeacaeacaeacaeacaeacae	-								•	
LpMDHh18 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140 LpMDHh19: CGAAGGAACCGATGCGCTGTCTCGTCACCGGCGCCCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh21: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh22: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140 LpMDHh23: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 140 LpMDHh24: NGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh25: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCGAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh26: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCGAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh27: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh28: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh28: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh29: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh29: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh30: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh31: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh31: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh31: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh31: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh32: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh33: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh31: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh33: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh34: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh34: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh34: CGAAGGAACCGATGCGCGTGCTCGTCCCGCCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh34: CGAAGGAACCGATGCGCGTGCTCGTCCCCGCCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh35: C	LpMDHh18 : GAAGGAACCATTCGGCTGCTCATCACCGGCGCGCAGGACAAATTGGATATGCTTTCTT : 140 LpMDHh19 : GAAGGAACCATTCGGCTGCTCTTCATCAGGGCGCCAGGACAATTGGATATGCTTTTTT : 140 LpMDHh20 : GGAAGGAACCATTCGGGTGCTCTTCACCGGCGCCGCAGGACAATTGGATATGCTTTTTT : 139 LpMDHh21 : GGAAGGAACCATTCGGGTGCTCTTCACCGGCGCCGCAGGACAATTGGATATGCTTTTTT : 140 LpMDHh21 : GGAAGGAACCATTCGGGTGCTCTTCACCGGCGCCGCAGGACAAATTGGATATGCTTTTTT : 140 LpMDHh22 : GGAAGGAACCATTCGGGTGCTCTTCACCGGCGCCGCAGGACAAATTGGATATGCTTTTTT : 140 LpMDHh24 : MGAAGGAACCATTCGGGTTGCTCTTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTTT : 139 LpMDHh25 : GGAAGGAACCATTCGGCTTGCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTTT : 139 LpMDHh26 : GGAAGGAACCATTCGGCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTTT : 139 LpMDHh27 : GAAGGAACCATTCGGCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTTT : 139 LpMDHh28 : GGAAGGAACCATTCGGCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTTT : 139 LpMDHh28 : GGAAGGAACCATTCGGCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTTT : 139 LpMDHh29 : CGAAGGAACCATTCGCCTTGCTCACCGGCGCCCAGGACAAATTGGATATGCTCTTTTT : 139 LpMDHh32 : CGAAGGAACCATTCGCCTTGCTCACCGGCGCCCAGGACAAATTGGATATGCTCTTTTT : 137 LpMDHh33 : CGAAGGAACCATTCGCCTTGCTCACCGGCGCCCAGGACAAATTGGATATGCTCTTTTT : 137 LpMDHh34 : CGAAGGAACCCATTCGCCTTGCTCACCGGCGCCCAGGACAAATTGGATATGCTCTTTTT : 138 LpMDHh35 : CGAAGGAACCCATTCGCCTTGCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTTTT : 138 LpMDHh36 : CGAAGGAACCCATTCGCCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTTT : 138 LpMDHh37 : CGAAGGAACCCATTCGCCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTTT : 137 LpMDHh37 : CGAAGGAACCCATTCGCCTTGCTCACCGGCGCCCAGGACAAATTGGATATGCTCTTTTT : 137 LpMDHh37 : CGAAGGAACCCATTCGCCTTGCTCACCGGCGCCAGGACAAATTGGATATTCCTCTTTTT : 134 LpMDHh47 : CGAAGGAACCCATTCGCCTTGCTC	_								•	
CQMAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140	LpmDHh19 : CGAAGGAACCCATTGCGCTGCTCCTCATCAGGGGCGCAGGACAATTGGATATGCTCTTCTT : 140 LpmDHh21 : CGAAGGAACCGATGCGGTGCTCTCTTCACCGGGGGCGCAGGACAATTGGATATGCTCTTGTT : 140 LpmDHh22 : CGAAGGAACCGATGCGGTGCTCTTCACCGGGGGCGCAGGACAATTGGATATGCTCTTGTT : 140 LpmDHh23 : CGAAGGAACCGATGCGGTGCTCTCTCACCGGGGGCGCAGGACAATTGGATATGCTCTTGTT : 140 LpmDHh24 : MGAAGGAACCGATGCGGTGCTCTCTCACCGGGGGCGCAGGACAAATTGGATATGCTCTTGTT : 140 LpmDHh24 : MGAAGGAACCGATGCGGTGCTCTCTCACCGGGGCGCGAGGACAAATTGGATATGCTCTTGTT : 139 LpmDHh26 : GGAAGGAACCGATGGGCTGCTCTCTCACCGGGGCGCGAGGACAAATTGGATATGCTCTTGTT : 139 LpmDHh26 : GGAAGGAACCAATGGGCTGTCTCTCTCACCGGGGCGCGAGCACAAATTGGATATGCTCTTGTT : 138 LpmDHh27 : CGAAGGAACCAATGGCCTTGCTCACCGGGGCGCGAGGACAAATTGGATATGCTCTTGTT : 138 LpmDHh28 : CGAAGGAACCAATGGCCTTGCTCACCGGGGCGCGAGGACAAATTGGATATGCTCTTGTT : 137 LpmDHh39 : CGAAGGAACCAATGGCGTGCTCTCACCACGGGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpmDHh39 : CGAAGGAACCAATGGCGTTCTCACCACGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpmDHh39 : CGAAGGAACCAATGCGCTTGCTCACCACGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpmDHh39 : CGAAGGAACCAATGCGCTTGCTCACCACGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpmDHh39 : CGAAGGAACCAATGCGCTTGCTCACCACGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpmDHh39 : CGAAGGAACCAATGCGCTTGCTCCTCACCACGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpmDHh39 : CGAAGGAACCAATGCGCCTTGCTCCTCACCACGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpmDHh39 : CGAAGGAACCAATGCGCCTTCCTCACCACGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpmDHh39 : CGAAGGAACCAATGCGCCTTCCTCACCACGCCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpmDHh39 : CGAAGGAACCAATGCGCCTTCCTCACCACGCCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpmDHh39 : CGAAGGAACCAATGCGCCTTCCTCACCACGCCCCCAGGACAAATTGGATATGCTCTTTGTT : 136 LpmDHh40 : CGAAGGAACCAATGCGCCTTCCTCACCACGCCCCCAGGACAAAATTGGATATGCTCTTTGTT : 136 LpmDHh40 : CGAAGGAACCAATGCGCCTTCCTCACCACGCCCCCCAGGACAAATTGGATATGCTCTTTGTT : 136 LpmDHh40 : CGAAGGAACCAATGCGCCTTCCTCCACCACGCCCCCAGGACAAATTGGATATGCTCTTTGTT : 136 LpmDHh40 : CGAAGGAACCAATGCGCCTTCCTCCACCACGCCCCCAGGACAAATTGGATATGCTCTTTGTT : 137 LpmDHh41 : CGAAGGAACCAATGCGCCTTCTCCACCACGCCCCCAGGACAAATTGGATATG	_								•	
LpMDHh20 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh21 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 140 LpMDHh22 : CGAAGGAACCGATGCGCTGGTCGTCACCGGCGCCCCCAGGACAAATTGGATATGCTCTTGTT : 140 LpMDHh23 : NGAAGGAACCGATGCGCTGTCGTCACCGGCGCCCCCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh24 : NGAAGGAACCGATGCGCTGTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh25 : CGAAGGAACCGATGCGCTGTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh26 : CGAAGGAACCGATGCGCTGTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh27 : CGAAGGAACCGATGCGCTGTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh28 : CGAAGGAACCGATGCGCTGTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh29 : CGAAGGAACCGATGCGCTGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh30 : CGAAGGAACCGATGCGCTGTCCTCCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh31 : CGAAGGAACCGATGCGCTGTCCTCCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh32 : CGAAGGAACCGATGCGCTGTCCTCCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh35 : CGAAGGAACCGATGCGCTGTCCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh35 : CGAAGGAACCGATGCGCTGTCCTCGTCACCGGCGCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh35 : CGAAGGAACCGATGCGCTGTCCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh36 : CGAAGGAACCGATGCGCTGTCCTCGTCACCGGCGCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh39 : CGAAGGAACCGATGCGCTGTCCTCGTCACCGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh39 : CGAAGGAACCGATGCGCTGTCTCTCTCTCTCTCTCTCTCT	LpMDHh20: LpMDHh21: LpMDHh22: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGAGGACAAATTGGATATGCTCTTGTT: LpMDHh22: LpMDHh23: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT: LpMDHh24: LpMDHh24: LpMDHh25: LpMDHh25: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT: LpMDHh26: LpMDHh26: CGAAGGAACCATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT: LpMDHh27: LpMDHh27: LpMDHh27: LpMDHh28: CGAAGGAACCATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT: LpMDHh29: LpMDHh29: CGAAGGAACCATGCGCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT: LpMDHh29: CGAAGGAACCATGCGCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT: LpMDHh30: CGAAGGAACCATGCGCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT: LpMDHh31: LpMDHh32: CGAAGGAACCATGCGCTTGCTCACCGGCGCCGAGGACAAATTGGATATGCTCTTGTT: LpMDHh32: CGAAGGAACCATGCGCTTGCTCACCGGCGCCGAGGACAAATTGGATATGCTCTTGTT: LpMDHh31: CGAAGGAACCATGCGCTTGCTCACCGGCGCCGAGGACAAATTGGATATGCTCTTGTT: LpMDHh32: CGAAGGAACCATGCGCTTGCTCACCGGCGCCGAGGACAAATTGGATATGCTCTTGTT: LpMDHh34: CGAAGGAACCATGCGCTTGCTCCTCACCGGCGCCGAGGACAAATTGGATATGCTCTTTGTT: LpMDHh35: LpMDHh36: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh36: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh37: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh38: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh39: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh39: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh39: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh39: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh39: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh41: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh41: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh41: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh41: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT: LpMDHh42: CGAAG	_								:	
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LpMDHh23 : CGAAGGAACCGATGCGGTGTCCTCACCGGCGCGCAGGACAATTGGATATCTCTTGTT : 139 LpMDHh25 : CGAAGGAACCGATGCGGTGTCCTCACCGGCCGCAGGACAAATTGGATATCTCTTGTT : 139 LpMDHh25 : CGAAGGAACCGATGCGGTGTCTCACCGGCGCCGCAGGACAAATTGGATATCTCTTGTT : 139 LpMDHh27 : CGAAGGAACCGATGCGGTGTCTCACCGGCGCGCAGGACAAATTGGATATCTCTTGTT : 139 LpMDHh28 : CGAAGGAACCGATGCGGTGTCTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh28 : CGAAGGAACCGATGCGGTGTCTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh29 : CGAAGGAACCGATGCGGTGTCATCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh30 : CGAAGGAACCGATGCGCTGTCACCACCGGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh31 : CGAAGGAACCGATGCGCTGTCACCACCGGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh32 : CGAAGGAACCGATGCGCTGTCACCACCGGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh34 : CÄAAGGAACCGATGCGCTGTCACCACGGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh35 : CGAAGGAACCGATGCGCTGTCACCACGGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh36 : CGAAGGAACCGATGCGCTGTCTCACCACGGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh37 : CGAAGGAACCGATGCGCTGTCTCACCACGGCCCGCAGGACAAATTGGATATCCTCTTGTT : 137 LpMDHh36 : CGAAGGAACCGATGCGCTGTCTCACCAGGCCCCCAGGACAAATTGGATATCCTCTTGTT : 137 LpMDHh38 : CGAAGGAACCGATGCGCTGTCTCACCAGGCCCCCAGGACAAATTGGATATCCTCTTGTT : 137 LpMDHh38 : CGAAGGAACCGATGCGCTGTCTCACCAGGCCCCCAGGACAAATTGGATATCCTCTTGTT : 136 LpMDHh41 : CGAAGGAACCGATGCGCTGTCTCACCAGGCCCCCAGGACAAATTGGATATCCTCTTGTT : 135 LpMDHh42 : CGAAGGAACCGATGCGCTGTCTCTCACCAGGCCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCCGTTCTCTCACCAGGCCCCCAAGACAAATTGGATATGCTCTTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCCGTTCCTCTCACCAGGCCCCCAAGACAAATTGGATATTGCTCTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCCGTTCTCTCACCAGGCCCCCAAGACAAATTGGATATTGCTCTTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCCCTTCTCTCACCAGCCCCCCAAGACAAATTGGATATTGCTCTTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCCCTTCTCTCACCAGCCCCCCAAGACAAATTGGATATTGCTCTTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCCCTTCTCTCACCAGCCCCCCAAGACAAATTGGATATTGCTCTTTGTT : 134 LpMDHh50 : CGAAGGAACCGATGCCCTTCTCTCACCAGCCCCCCAAGACAAATTGGATATTGCTCTTTGTT : 131 LpMDHh51 : CGAAGGAACCGATGCCCTTCTCTCA	LpmDHh23									-	
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LpMDHh25 : GAAAGAACCATGCGCTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh26 : GAAAGAACCATGCGCGTGCTCGTCACCGGGCCGCAGGACAAATTGGATATGCTCTTGTT : 139 LpMDHh27 : CAAAGAACCATGCGGTGCTCGTCACCGGGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh28 : CGAAGGAACCATGCGGTGCTCGTCACCGGGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh30 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh31 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh32 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh34 : CAAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh35 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh36 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh37 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh37 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh39 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh40 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh41 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh42 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh45 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh46 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh47 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh46 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 : CGAAGGAACCGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh51 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGT	LpMDHh25 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh27 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh28 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh29 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh30 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh31 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh32 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh32 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh34 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh35 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh36 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh40 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh46 : CGAAGGAACCGATGCCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh46 : CGAAGGAACCGATGCCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 : CGAAGGAACCGATGCCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh51 : CGAAGGAACCGATGCCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh51 : CGAAGGAACCGATGCCGTGCTCTCTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh56 : LpMDHh57 : LpMDHh58 : LpMDHh58 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDH	•									
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LpMDHh29 : CGAAGGAACCGATGCGCGTGCTCGTCACCGCGCGCGCAGGACAAATTGGATATGCTCTTGTT 138 LpMDHh31 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 138 LpMDHh32 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCAGGACAAATTGGATATGCTCTTGTT 138 LpMDHh34 : CMAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh35 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh36 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh36 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh39 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh39 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh39 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh39 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh40 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTTGTT 134 LpMDHh56 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTTGTT 134 LpMDHh56 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh56 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh56 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh56 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh56 : CG	LpMDHh29 : CGAAGGAACCGATGCGCTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : LpMDHh31 : CGAAGGAACCGATGCGCGTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh32 : CGAAGGAACCGATGCGCTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh34 : CGAAGGAACCGATGCGCGTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138 LpMDHh35 : CGAAGGAACCGATGCGCGTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh36 : CGAAGGAACCGATGCGCTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh36 : CGAAGGAACCGATGCGCTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh37 : CGAAGGAACCGATGCGCTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh38 : CGAAGGAACCGATGCGCTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh39 : CGAAGGAACCGATGCGCTGCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh40 : CGAAGGAACCGATGCGCTGCTCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh41 : CGAAGGAACCGATGCGCTGCTCTTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh42 : CGAAGGAACCGATGCGCTGCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh42 : CGAAGGAACCGATGCGCTGCTCTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCGCTGCTCTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCGCTGCTCTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCGCTGCTCGTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCCGTGCTCTCTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh49 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh49 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh49 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCCCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh49 : CGAAGGAACCGATGCCGCTGCTCGTCACCGGCCCCCAAGACAAATTGGATATGCTCTTGTT : 134 LpMDHh50 : CGAAGGAACCGATGCCGCTGCTCGTCACCGGCCCCCAAGACAAATTGGATATGCTCTTGTT : 134 LpMDHh51 : CGAAGGAACCGATGCCGCTGCTCGTCACCGGCCCCCAAGACAAATTGGATATGCTCTTGTT : 134 LpMDHh55 : LpMDH56 :									:	
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LpMDHh31: CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAATTGGATATGCTCTTGTT 137 LpMDHh32: CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAATTGGATATGCTCTTGTT 137 LpMDHh35: CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh36: CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh37: CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh39: CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh39: CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh39: CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh41: CGAAGGAACCGATGCGCTGCTCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh42: CGAAGGAACCGATGCGCTGCTCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh44: CGAAGGAACCGATGCGCTGCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh45: CGAAGGAACCGATGCGCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46: CGAAGGAACCGATGCGCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46: CGAAGGAACCGATGCGCTTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 134 LpMDHh46: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 134 LpMDHh50: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh51: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh54: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh55: CGAAGGAACCGATGCGCTTGCTCCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh54: CGAAGGAACCGATGCGCTTGCTCCTCCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh54: CGAAGGAACCGATGCGCTTGCTCCTCCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 150 LpMDHh55: CGAAGGAACCGATGCGCTTGCTCACCGGCCCCCAGGACAAATTGGA	LpMDHh31: CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGAGGACAAATTGGATATGCTCTTGTT LpMDHh34: CGAAGGAACCGATGCGCTGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 138 LpMDHh35: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh35: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh37: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh38: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh38: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh39: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh39: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh40: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh41: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh42: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh55: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh55: CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh56: CGAAGGAACCGATGCGCTGCTCGTCACCGGCCCCAGGACAAATTGGATATGCTCTTGTT 157 LpMDHh56: CGAAGGAACCGATGCCGTGCTCGTCACCGGCCCCAGGACAAATTGGATATGCTCTTGTT 157 LpMDHh56: CGAAGGAACCGATGCCGTGCTCGTCACCGGCCCCAGGACAAATTGGATATGCTCTTGTT 157 LpMDHh56: CGAAGGAACCGATGCCCGTGCTCGTCACCGGCCCCAGGACAAATTGGATATGCTCTTGTT 157 LpMDHh56: CGAAGGAACCGATGCCCGTGCTCGTCACCGGCCCCAGGACAAATTGGATATGCTCTTGT	-								:	138
LpMDHh34 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAÄATTGGATATGCTCTTGTT : 137 LpMDHh36 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh37 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh37 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh39 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh40 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh52 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh54 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh55 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh55 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 157 LpMDHh55 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCG	LpMDHh32 : GAAGGAACGATGCGGTGCTCGTCACCGGCGCGCAGGACAATTGCATATGCTCTTGTT : 134 LpMDHh35 : CGAAGGAACGATGCGGTGCTCGTCACCGGCGCCGCAGGACAAATTGCATATGCTCTTGTT : 137 LpMDHh36 : CGAAGGAACGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGCATATGCTCTTGTT : 137 LpMDHh37 : CGAAGGAACCCATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGCATATGCTCTTGTT : 136 LpMDHh39 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGCATATGCTCTTGTT : 136 LpMDHh39 : CGAAGGAACCCATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh40 : CGAAGGAACCCATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh41 : CGAAGGAACCCATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh41 : CGAAGGAACCCATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh43 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh52 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh54 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh55 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh56 : CDAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh56 : CDAAGGAACCGATGCCGTGCTCGTCACCGGCCGCAGGACAAATTG									:	137
LpMDHh34 : CÑAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh36 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh37 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh39 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh40 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh43 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh53 : LpMDHh54 : LpMDHh55 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh57 : LpMDHh57 : LpMDHh58 : LpMDHh59 :	LpMDHh34:	LpMDHh32 :	: CGA	AGGAACCGA	TGCGCGTGCT	CGTCACCGGC	GCCGCAGGAC?	ajį̇̃attggatat	GCTCTTGTT	:	138
LpMDHh35 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAATTGGATATGCTCTTGTT LpMDHh36 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAATTGGATATGCTCTTGTT 136 LpMDHh37 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh40 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 131 LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 127 LpMDHh50 : CGAAGGAACCGATGCGCTTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 127 LpMDHh51 : CGAAGGAACCGATGCGCTTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh51 : CGAAGGAACCGATGCGCTTCGTCACCGGCCCGCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh53 : CGAAGGAACCGATGCGCTTCGTCACCGGCCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh55 : CGAAGGAACCGATGCGCTTCGTCACCGGCCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh53 : CGAAGGAACCGATGCGCTTCGTCACCGGCCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh55 : CGAAGGAACCGATGCGCTTCGTCACCGGCCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh55 : CGAAGGAACCGATGCGCTTCGTCACCGGCCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh55 : CGAAGGAACCGATGCGCTTCGTCACCGGCCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh56 : CGAAGGAACCGATGCGCTTCGTCACCGGCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh56 : CGAAGGAACCGATGCGCTTGTCACCGGCCGCAGGACAAATTGG	LpMDHh35 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAATTGGATATGCTCTTGTT 19MDHh36 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAATTGGATATGCTCTTGTT 136 LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh39 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh40 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh48 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh48 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 135 LpMDHh59 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh59 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh59 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 130 LpMDHh59 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 150 LpMDHh59 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 150 LpMDHh59 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 150 LpMDHh59 : CGAAGGAACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 150 LpMDHh59 : CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 150 LpMDHh59 : CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 150 LpMDHh59 : CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 150 LpMDHh59 : CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 150 LpMDHh59 : CGAAGG	LpMDHh34 :	CÑA	AGGAACCGA	ATGCGCGTGCT	CGTCACCGGC	GCCGCAGGAC	AÄATTGGATAT	GCTCTTGTT	:	137
LpMDHh37 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh40 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh41 : CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh41 : CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh53 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh54 :	LpMDHh37 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh39 : CGAAGGAACCGATGCGCGTCTGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh41 : CGAAGGAACCGATGCGCGTCCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh41 : CGAAGGAACCGATGCGCGTCCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh43 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh53 : LpMDHh54 : LpMDHh55 : LpMDHh55 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh57 : LpMDHh59 : LpMDHh59 : LpMDHh59 : LpMDHh59 : LpMDHh56 : LpMDHh66	LpMDHh35								:	137
LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAATTGGATATGCTCTTGTT LpMDHh39 : CGAAGGAACCGATGCGCTGCTCTTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh40 : CGAAGGAACCGATGCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 131 LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 108 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 108 LpMDHh52 :GGACCGATGCCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 108 LpMDHh53 :GGACCGATGCCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT 57 LpMDHh53 :	LpMDHh38: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh39: CGAAGGAACCGATGCGCGTGCTCTTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh40: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh41: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh42: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh43: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh45: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh46: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh47: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh48: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh49: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh49: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh50: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh52:GGACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh53: LpMDHh54: LpMDHh55:	LpMDHh36	: CGA	AGGAACCGA	ATGCGCGTGCT	CGTCACCGGC	GCCGCAGGAC	AAATTGGATAT	GCTCTTGTT	:	136
LpMDHh40: CGAAGGAACCGATGCGCGTGCTCATCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh41: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh42: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh43: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh45: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh46: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh47: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 131 LpMDHh48: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 131 LpMDHh49: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 131 LpMDHh50: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh52: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh53: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh55: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh54: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh55: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh55: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh55: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh55: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh56: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh56: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh58: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh56: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh58: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 150 LpMDHh56: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGC	LpMDHh49 : CGAAGGAACCGATGCGCTGCTCTTCTCTCTCTCTCTCTCT	LpMDHh37								:	
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LpMDHh42: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh45: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 133 LpMDHh46: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh47: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 134 LpMDHh48: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 127 LpMDHh49: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 127 LpMDHh50: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 130 LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 108 LpMDHh52:GGACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 108 LpMDHh54:	LpMDHh42: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh43: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh45: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh46: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh47: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh48: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh49: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh49: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh40: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh52:GĞACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh54: LpMDHh54: LpMDHh54: LpMDHh55:GĞACCGATGCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT LpMDHh54: LpMDHh56: LpMDHh56:	LpMDHh40	_							:	
LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 133 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 108 LpMDHh52 :GGACCGATGCCGCTGCTCGTCACCGGCGCCCCAGGACAAATTGGATATGCTCTTGTT : 57 LpMDHh54 :	LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh44: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh45: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh46: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh47: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh48: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh49: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh50: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh52:GGACCGATGCCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh54:	LpMDHh41									
LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 133 LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 108 LpMDHh51 : CGAAGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 91 LpMDHh52 :GGACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT : 57 LpMDHh54 :GGACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT : 57 LpMDHh56 :	LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAATTGGATATGCTCTTGTT LpMDHh45 : CGAAGGAACCGATGCGCTTGTCACCGGCGCCGCAGGACAATTGGATATGCTCTTGTT LpMDHh46 : CGAAGGAACCGATGCGCTTGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh47 : CGAAGGAACCGATGCGCTTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh48 : CGAAGGAACCGATGCGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh49 : CGAAGGAACCGATGCGCTTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh50 : CGAAGGAACCGATGCGCTTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51 : CGAAGGAACCGATGCGCTTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51 : CGAAGNAACCGA GCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT LpMDHh52 :GGACCGATGCCGCTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTTGTT LpMDHh53 :	-								-	
LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 108 LpMDHh52 :GGACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 91 LpMDHh53 :	LpMDHh45: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh47: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh48: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh49: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh50: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh52: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh53: CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh54: CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh54: CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh55: CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh56: CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh56: CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh56: CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh56: CGAAGGAACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh66: CGAAGGAACCGATGCCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh66: CGAAGGAACCGATGCCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh66: CGAAGGAACCGATGCCGCTGCTCGTCACCGGCGCGCGCGC										_
LpMDHh46: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh47: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh48: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh49: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh50: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 108 LpMDHh51: CGAAGNAACCGA-GCGCTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 91 LpMDHh52:GGACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 57 LpMDHh54:	LpMDHh46: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT	-	: CGA	AGGAACCG	ATGCGCGTGCT	CGTCACCGGC	GCCGCAGGAC.	AAATTGGATAT	GCTCTTGTT		
LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 108 LpMDHh51 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 91 LpMDHh52 :GGACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 57 LpMDHh53 :	LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT	-								-	-
LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 108 LpMDHh51 : CGAAGNAACCGA—GCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 91 LpMDHh52 :GGACCGATGCCCGTGCTCACCGGCGCCGCAGGNCAAATTGGATATGCTCTTGTT : 57 LpMDHh53 :	LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT	•								:	
LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 108 LpMDHh51 : CGAAGNAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 91 LpMDHh52 :GGACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGNCAAATTGGATATGCTCTTGTT : 57 LpMDHh53 :	LpMDHh49: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh50: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGNAACCGA GCGCTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh52:GĞACCGATGCĞCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh54:	-								:	
LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCACCGGCGCCGAGGACAAATTGGATATGCTCTTGTT : 108 LpMDHh51 : CGAAGÑAACCGA GCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 91 LpMDHh52 :GGACCGATGCCCGTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 57 LpMDHh53 :	LpMDHh50: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51: CGAAGÑAACCGA—GCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT 91 LpMDHh52:	-									
LpMDHh51 : CGAAGÑAACCGA GCGCGTGCTCGTCACCGGCGCGCAGACAAATTGGATATGCTCTTGTT : 91 LpMDHh52 : GGACCGATGCCCGTGCTCACCGGCGCCGCAGGÑCAAATTGGATATGCTCTTGTT : 57 LpMDHh53 :	LpMDHh51 : CGAAGÑAACCGA GCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT 91 LpMDHh52 : GGACCGATGCCCGTGCTCACCGGCGCGCAGGÑCAAATTGGATATGCTCTTGTT 57 LpMDHh53 :	•								:	
LpMDHh53 :	LpMDHh53 : : : : : : : : : : : : : : : : : : :	-	CG	AGGAACCGA A CÑÎA A CCCI	AIGCGCGIGCI	CGTCACCGGC	CCCCCAGGAC	AAAIIGGAIAI NNNTTCCNTNT	CCTCTTGTT		
LpMDHh53 :	LpMDHh53 : : : : : : : : : : : : : : : : : : :		GG/	AGNAACCG	ATCCCCCTCCT	CGTCACCGGC	GCCGCAGGÃC GCCGCAGGÃC	AAAIIGGAIAI AATTGGATAT	COTOTIGIT		
LpMDHh54 :	LpMDHh54 :			- GCACCC				AAMIIGCAIMI	GGEGIIGII	•	<i>-</i>
LpMDHh55 :	LpMDHh55 :	-								•	_
LpMDHh56 :	LpMDHh56 :									:	_
LpMDHh57::: - LpMDHh58::: - LpMDHh59::: -	LpMDHh57 :									;	_
LpMDHh58 : : - LpMDHh59 : : -	LpMDHh58 : : : :		:							:	_
LpMDHh59 : : -	LpMDHh59 :									•	_
•	LpMDHh60::: LpMDHh61::: LpMDHh62:: LpMDHh63::		:						- -	:	_
	LpMDHh61 : : : : : : : : : : : : : : : :	-	:							:	_
<u>-</u>	LpMDHh62 : : LpMDHh63 : : :	-	:							:	_
<u>-</u>	LpMDHh63 :::	-	:							:	-
<u>-</u>	-	-	:							:	-
	LpMDHh64 : :	_	:							:	_

		* 200 * 220 * 240		
LpMDHh1 :	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	246
LpMDHh2:		CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	212
LpMDHh3 :		CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	210
LpMDHh4 :		CCGATGATTGCTAGGCNÃAATTATGCTTGGNGNGSACTAGCCTGTTATTNTGCATATC	:	202
LpMDHh5 :		CCGATGATTGCTAGGGGAATTATGCTTGGTGJGGACCAGCCTGTTATTCTGCATATGCTGGA	:	206
LpMDHh6 :		CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	204
LpMDHh7 :		CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	202 205
LpMDHh8 :		CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	205
LpMDHh10:	• '	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	203
LpMDHh11:	.	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	204
LpMDHh12 :	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	202
LpMDHh13:	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	201
LpMDHh14:	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	202
LpMDHh15 :	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	202
LpMDHh16:	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	202
LpMDHh17:	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	201
LpMDHh18 :	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	202 202
LpMDHh19 : LpMDHh20 :	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	201
	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	202
LpMDHh22	•	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	202
	:	CCGATGATTGCTANGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	201
LpMDHh24	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	201
LpMDHh25	:	${\tt CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA}$:	201
LpMDHh26	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	200
	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	201
LpMDHh28	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	199
	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	199
LpMDHh30	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	200
LpMDHh31 :	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	199 200
LpMDHh34	:	CCGATGATIGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	199
LpMDHh35	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	199
LpMDHh36	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	198
LpMDHh37	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	199
LpMDHh38	:	CCGATGATTGCTAGGGGAATTATGCT@GGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	198
LpMDHh39	:	CCGATGATTGCTANGGGAATTATGCTTGGTGCGGACCANCCTGTTATTCTGCATATGCTGGA	:	198
	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCAGGA	:	197
LpMDHh41	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCGGTTATTCTGCATATGCTGGA	:	197
<u></u>	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	196
LpMDHh43 LpMDHh44	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	197 196
LpMDHh45	:	CCGATGATIGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	195
_ -	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	196
LpMDHh47	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	193
LpMDHh48	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	189
LpMDHh49	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	192
	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	170
	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	_
	:	CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA	:	
LpMDHh53	:	TATGCTTGGTGCGG-CCAGCCTGTTATTCTGCATATGCTGGA	:	41
LpMDHh54 LpMDHh55	:		:	_
LpMDHh56	:		:	_
LpMDHh57	:		•	_
LpMDHh58	:		:	_
LpMDHh59	:		:	_
LpMDHh60	:		:	-
LpMDHh61	:		:	-
LpMDHh62	:		:	-
LpMDHh63	:		:	-
LpMDHh64	:		:	-

	*	260	*	280	* 300	,	*
LpMDHh1 :	TATTCCAC	CAGCTGCTGAAG	CTCTTAATGO	TGTTAAGATGG	SAGTTGGTTGATGCCGCATTTC	:	308
LpMDHh2 :	TATTCCAC	CAGCTGCTGAAG	CTCTTAATGO	TGTTAAGATGG	agttggttgatgccgñatttñ	:	274
LpMDHh3 :	TATTGCAC	CAGCTGCTGAAG	CTCTTAATGG	GGTTAATATGG	BAAGTGNNT-NGGCGGCNTAGN		271
LpMDHh4 :						:	_
LpMDHh5 :	TATTCCAC	CCAGCTGCTGAAG	CTCTTAATGO	TGTTAAGATGO	SAGTTGGTTGATGCCGCATTTC		268
LpMDHh6 :					SAGTTGGTTGATGCCGCATTTC		266
LpMDHh7 :					SAGTTGGTTGATGCCGCATTTC		264
LpMDHh8 :					SAGTTGGTTGATGCCGCATTTC		267
LpMDHh9 :					SAGTTGGTTGATGCCGCATTTC		267
LpMDHh10 :					GAGTTGGTTGATGCCGCATTTC		265
LpMDHh11:					SAGTTGGTTGATGCCGCATTTC		266
LpMDHh12 :					SAGTTGGTTGATGCCGCATTTC		264
LpMDHh13 :					SAGTTGGTTGATGCCGCATTT		263
LpMDHh14:					GAGTTGGTTGATGCCGCATTT	L.	264
LpMDHh15 :					EAGTTGGTTGATGCCGCATTT		264
LpMDHh16:					GAGTTGGTTGATGCCGCATTT		264
LpMDHh17:					GAGTTGGTTGATGCCGCATTT		263
LpMDHh18 :					GAGTTGGTTGATGCCGCATTT		264
LpMDHh19:					GAGTTGGTTGATGCCGCATTT(264
LpMDHh20 :					GAGTTGGTTGATGCCGCATTT		263
LpMDHh21:					GAGTTGGTTGATGCCGCATTT		264
LpMDHh22 :					GAGTTGGTTGATGCCGCATTT		264
LpMDHh23:					GAGTTGGTTGATGCCNCATTT(263
LpMDHh24 :					GAGTTGGTTGATGCCGCATTT		263
LpMDHh25 :					GAGTTGGTTGATGCCGCATTT		263
LpMDHh26 :					GAGTTGGTTGATGCCGCATTT(262
LpMDHh27 :					GAGTTGGTTGATGCCGCATTT		263
LpMDHh28 :					GAGTTGGTTGATGCCGCATTT		261
LpMDHh29 :	TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT		261
LpMDHh30 :					GAGTTGGTTGATGCCGCATTT		262
LpMDHh31 :	TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	:	261
LpMDHh32 :	TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	:	262
LpMDHh34 :					GAGTTGGTTGATGCCGCATTT(261
LpMDHh35 :					GAGTTGGTTGATGCCGCATTT		261
-					GAGTTGGTTGATGCCGCATTT		260
LpMDHh37 :					GAGTTGGTTGATGCCGCATTT		261
LpMDHh38:	TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	:	260
LpMDHh39 :	TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	:	260
LpMDHh40:	TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGNTGATGCCGCATTT	:	259
LpMDHh41 :	TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	9 :	259
LpMDHh42 :	TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	9 :	
LpMDHh43 :	: TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	9 :	259
LpMDHh44 :	: TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	9 :	258
LpMDHh45 :	: TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	9 :	
LpMDHh46 :	: TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	3 :	258
LpMDHh47	: TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT [,]	9 :	
LpMDHh48 :	: TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	9:	251
LpMDHh49 :	: TATTCCA	CCAGCTGCTGAA	GCTCTTAATG	GTGTTAAGATG	GAGTTGGTTGATGCCGCATTT	9 :	
LpMDHh50	· IIII I C CII		0010111110	0 1 0 1 1 1 1 1 1 1 1 1	GAGTTGGTTGATGCCGCATTT		232
LpMDHh51					GAGTTGGTTGATGCCGCATTT		215
					GAGTTGGTTGATGCCGCATTT		181
LpMDHh53	: TATTCCA				GAGTTGGTTGATGCCGCATTT	_	103
LpMDHh54	:					- :	_
LpMDHh55	:					- :	-
LpMDHh56	:					- :	-
LpMDHh57	:					- :	-
LpMDHh58	:					- :	-
LpMDHh59	:					- :	-
LpMDHh60	:					- :	-
LpMDHh61	:					- :	-
LpMDHh62	:					- :	-
LpMDHh63	:					- :	-
LpMDHh64	:					- :	-

LpNDHh1			320	*	340	*	360		*
LPMDHHA : ACTTCTCAAGGASTIGTTGCAACAACTGATGTTGTAGGCTTGCACCTGGTGGATGT 328 LPMDHHA : ACTTCTCAAGGASTIGTTGCAACAACTGATGTTGTAGGCTTGCACCTGGTTGGATGTT 328 LPMDHHA : ACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACCTGGTTGGATGTT 328 LPMDHHA : ACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGGATGTT 328 LPMDHHA : ACTTCTCAAGGAGTTGTTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGGAACTGT 329 LPMDHHA : ACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGGAACTGT 329 LPMDHHA : ACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGGAACTGT 329 LPMDHHA : ACTTCTCAAGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTTGGAATGT 327 LPMDHHA : ACTTCTCAAGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTTGAATGT 327 LPMDHHA : ACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGT 326 LPMDHHA : ACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGGAGTTGTTGCACAACACTGATGTTGTTGAGGCTTGCACTGGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGGAGTTGTTGCACAACACTGATGTTGTTGAGGCTTGCACTGGGTTGAAATGT 326 LPMDHHA : ACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGGTTGAAATGT 326 LPMDHHA : ACTTCTCAA	•								370
LPMDHIBS: LPMDHIBS: CACTTCTCAAAGGGATTGTTGCAACAACTGATGTTGTAAGGCTTGCACTGGTGTAAATGTT 2320 LPMDHIB6: LCACTTCTCAAAGGGATTGTTGCAACAACTGATGTTTGTTCAAGCCTTTGCACTGGTTGTAAATGTT 2321 LPMDHIB7: CACTTCTCAAAGGGATTGTTGCAACAACTGATGTTTGTTCAAGCCTTTGCACTGGTTGTAAATGTT 2326 LPMDHIB9: LCACTTCTCAAAGGGATTGTTGCAACAACTGATGTTTGTTGAGGCTTTGCACTGGTTGGAATGTT 2326 LPMDHIB1: CACTTCTCAAAGGGATTGTTGCAACAACTGATGTTTGTTGAGGCTTTGCACTGGTTGGAATGTT 2327 LPMDHIB1: CACTTCTCAAAGGGATTGTTGCAACAACTGATGTTTGTTGAGGCTTTGCACTGGTTGGAATGTT 2328 LPMDHIB1: CACTTCTCAAAGGGAGTTGTTGCAACAACTGATGTTTGTT	_			IGTTGCAACAA	CTGATGTTGTT	'GAGGCTTGCA	CTGGNGNGAATGT	- :	335
LPMDHIS : CACTTCTCNAGGGGTTGTTGTACANCHARTGAGTTGTTGAGCTTGCACTGGTGTAATGTT : 328 LPMDHIP : CACTTCTCNAGGGGGTTGTTGCAACANCTGAGTTGTTGAGCGTTGCACTGGTGTGAATGTT : 326 LPMDHIB : CACTTCTCNAGGGGGTTGTTGCAACANCTGAGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 329 LPMDHID : CACTTCTCNAGGGGGTTGTTGCAACANCTGAGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 329 LPMDHID : CACTTCTCNAGGGGGTTGTTGCAACANCTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT : 329 LPMDHID : CACTTCTCNAGGGGGTTGTTGCAACANCTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT : 329 LPMDHID : CACTTCTCNAGGGGGTTGTTGCAACANCTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT : 326 LPMDHID : CACTTCTCNAGGGGGTTGTTGCAACANCTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT : 326 LPMDHID : CACTTCTCNAGGGGGTTGTTGCAACANCTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LPMDHID : CACTTCTCNAGGGGGTTGTTGCAACANCTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LPMDHID : CACTTCTCAAGGGAGTTGTTGCAACANCTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LPMDHID : CACTTCTCAAGGGAGTTGTTGCAACANCTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LPMDHID : CACTTCTCAAGGGAGTTGTTGCAACANCTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 3	-	NCTT	TNTCGCN					- :	282
LPMPHHS : CATTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 328 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGAGTGATGTT 329 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTGAGGCTTGCACTGAGTGATGTT 329 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTGAGGCTTGCACTGAGTGAATGTT 329 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTGAGGCTTGCACTGAGTGAATGTT 329 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGAGTGAATGTT 322 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGAGTGAATGTT 322 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGAGTGAATGTT 326 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGAGTGAATGTT 326 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGAGTGAATGTT 326 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGAGTGAATGTT 326 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGAATGTTGTTGAGGCTTGCACTGAGTGAATGTT 3224 LPMPHHS : CATTCTCAAGGGAGTTGTTGCAACAACTGAATGTTGTTGAGGCTTGCACTGAGTGAATGTT 3224 LPMPHHS	-	·						- :	-
LpMDHBH7 CATTETCAAGGAGTTETTGCAACAACTGATGTTTGAGCCTTGCACTGGTTGAATGTT 326 LpMDHBH01 CATTETCAAGGAGTTETTGCAACAACTGATGTTGTTGAGCCTTGCCACTGGTTGAATGTT 327 LpMDHBH10 CATTETCAAGGAGTTETTGCAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 328 LpMDHB11 CATTETCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 328 LpMDHBH11 CATTETCAAGGAGTTGTTGTAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 328 LpMDHBH12 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 328 LpMDHBH13 CACTTGTCAAGGAGTTGTTGTAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 326 LpMDHBH14 CACTTGTCAAGGAGTTGTTGTAACAACTGATGTTGTTGAGCCTTGCACTGCTGGTGAATGTT 326 LpMDHBH15 CACTTGTCAAGGAGTTGTTGTAACAACTGATGTTGTTGAGCCTTGCACTGCTGGTGAATGTT 326 LpMDHBH17 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGCTGAATGTT 326 LpMDHBH19 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGCTGAATGTT 326 LpMDHBH19 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGCTGAATGTT 326 LpMDHBH19 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGCTGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGCTGATGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGCTGGTGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGTCAACAACTGATGTTGTTGAGCCTTGCACTGCTGGTGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGCTGGTGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGCTGGTGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGCTGGTGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMDHBH2 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMDHBH3 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMDHBH3 CACTTGTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGA	_								
LPMDHIBS : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGATTGTT : 329 LPMDHID10 : CACTTCTCAAGGGAGTTGTTGCAACCAACTGATGTTGTTGAGGCTTGCACTGATGTTGTTGAATGTT : 327 LPMDHID11 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LPMDHID12 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LPMDHID14 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LPMDHID14 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LPMDHID14 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LPMDHID16 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LPMDHID16 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LPMDHID16 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LPMDHID18 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTGAGGCTTGCACTGGTGTGAATGTT : 326 LPMDHID18 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LPMDHID18 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACCTGGTGTGAATGTT : 326 LPMDHID18 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTGAGGCTTGCACTGGTGTGAATGTT : 326 LPMDHID18 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LPMDHID18 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAACACTGATGTTGAACACTGATGTTGAACACTGATGTTGTAACACTTGAGGGTTGAATGTT : 322 LPMDHID18 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAACACTGACTG	-								
LpMDH101 : ACTTOTICANGGGATTETTEGAACGACTGATTGTTGAGCCTGCCTGGGTGAATGTT ; 327 LpMDH111 : ACTTOTICANGGGATTGTTGCAACGACTGATTGTTGAGCCTGCCCTGGGTGAATGTT ; 328 LpMDH112 : ACTTOTICANGGGATTGTTGCAACGACTGATTGTTGAGCCTGCCCTGGTGTGATTGTT ; 328 LpMDH113 : ACTTOTICANGGGATTGTTGTCAACGACTGATTGTTGTGAGCCTTGCCCTGGTGTGAATGTT ; 326 LpMDH114 : ACTTOTICANGGGATTGTTGTCAACGACTGATTGTTGAGCCTTGCCCTGCTGGATTGATT	-	CACI	TCTCAAGGGAGT	rgrtgcaacaa	CTGAGGTTGTI	'GAGGCTTGCA	CTGGTGTGAATGT'	:	
LPMPHA10 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGCTTTCAACTGGTGAATGTT : 327 LPMPHA11 : CACTTCTCAAGGGAFTGTTGCAACACTGATGTTGTTGAGGCTTTCAACTGGATGATT : 326 LPMPHA12 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGCTTTCAACTGGAATGTT : 325 LPMPHA14 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGCTTTCAACTGGAATGTT : 325 LPMPHA14 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGCTTGCAACTGGAATGTT : 326 LPMPHA16 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGGTTTGCAACTGGAATGTT : 326 LPMPHA17 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGGTTTCCAACTGGAATGTT : 326 LPMPHA18 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGGTTGCAACTGGTAGAATGTT : 326 LPMPHA18 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGCTTGCAACTGGTAGAATGTT : 326 LPMPHA18 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGCTTGCAACTGGTAGAATGTT : 326 LPMPHA19 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGCTTGCAACTGGTAGAATGTT : 326 LPMPHA19 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGCTTGCAACTGGTAGAATGTT : 326 LPMPHA12 : CACTTCTCAAGGGAFTGTTGCAACAACTGAACTGTTGTTGAGGCTTGCAACTGGTAGAATGTT : 326 LPMPHA12 : CACTTCTCAAGGGAGTTGTTGCAACAACTGAACTGTTGTTGAGGCTTGCAACTGGTAGAATGTT : 326 LPMPHA12 : CACTTCTCAAGGGAGTTGTTGCAACAACTGAACTGTTGTTGAGGCTTGCAACTGGTAGAATGTT : 326 LPMPHA12 : CACTTCTCAAGGGAGTTGTTGCAACAACTGAACTGTTGTTGAGGGCTTGCAACTGGTAGAATGTT : 326 LPMPHA12 : CACTTCTCAAGGGAGTTGTTGCAACAACTGAACTGTTGTTGAGGGCTTGCAACTGGTAGAATGTT : 326 LPMPHA12 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGAACTGTTGTTGAGGGCTTGCAACTGGTAGAATGTT : 325 LPMPHA14 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGAACTGTTGTTGAGGGCTTGCAACTGGTAGAATGTT : 325 LPMPHA14 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGAACTGTTGTTGAGGCTTGCAACTGGTAGAATGTT : 325 LPMPHA14 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGAACTGTTGTTGAGGCTTGCAACTGGTAGAATGTT : 322 LPMPHA14 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGAACTGTTGTTGTAGAGCTTGCAACTGGTAGAATGTT : 323 LPMPHA14 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGAACTGTTTGTT	-	CACI	TCTCAAGGGAGT	rgriggaacaa	CTGATGTTGTT	GAGGCTTGCA	CTGGTGTGAATGT	:	
LPMPHH11	-	CACT	"TCTCAAGGGAGT"	rgrirgcaacaa	CTGATGTTGTT	'GAGGCT'TGCA	CTGGTGTGAATGT'	:	
LPMPHH12 : CACTTCTCAAGGGGTGTTGTTGCAACACTGATGTTGTTGAGGCTTGCACTGGTGAATGTT : 326 LPMPHH14 : CACTTCTCAAGGGATTGTTGCAACACTGATGTTGTTGAGGCTTTGCACTGGTGAATGTT : 326 LPMPHH16 : CACTTCTCAAGGGATTGTTGCAACACTGATGTTGTTGAGGCTTGCACTGGTTGGAATGTT : 326 LPMPHH16 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGGAATGTT : 326 LPMPHH18 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGGAATGTT : 326 LPMPHH18 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGGAATGTT : 326 LPMPHH18 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPHH18 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPHH29 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGAATGTT : 326 LPMPHH29 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPHH21 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPHH22 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPHH23 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPHH24 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCAACTGGTGGAATGTT : 326 LPMPHH25 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCAATGGTGGAATGTT : 326 LPMPHH26 : CACTTCTCAAGGGATTGTTGCAACAACTGAATGTTGTTGAGGCTTGCAATGGTGGAATGTT : 325 LPMPHH26 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCAATGGTGGAATGTT : 326 LPMPHH29 : CACTTCTCAAGGGATTGTTGCAACAACTGAATGTTGTTGAGGCTTGCAATGGTGGAATGTT : 322 LPMPH19 : CACTTCTCAAGGGATTGTTGCAACAACTGAATGTTGTTGAGGCTTGCAATGGTGGAATGTT : 322 LPMPH19 : CACTTCTCAAGGGATTGTTGCAACAACTGAATGTTTGTTGAGGCTTTGCAATGGTGGAATGTT : 322 LPMPH19 : CACTTCTCAAGGGATTGTTGCAACAACTGAATGTTGTTGAGGCTTTGCAATGGTGGAATGTT : 322 LPMPH19 : CACTTCTCAAGGGATTGTTGCAACAACTGAATGTTTGTTGAGGCTTTGCAATGGTGGAATGTT : 322 LPMPH	-	CACT	"TCTCAAGGGAGT".	IGTTGCAACAA	CTGATGTTGTT	'GAGGCTTGCA	CTGGTGTGAATGT"	4 :	
LPMPHH13 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGAATGTT : 325 LPMPHH15 : CACTTCTCAAGGGAFTTGTTGCAACTGATGTTGTTGAGGCTTGCACTGGTGAATGTT : 326 LPMPHH16 : CACTTCTCAAGGGAFTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPHH17 : CACTTCTCAAGGGAFTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPHH18 : CACTTCTCAAGGGAFTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 325 LPMPHH18 : CACTTCTCAAGGGAFTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 325 LPMPHH19 : CACTTCTCAAGGGAFTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 325 LPMPHH19 : CACTTCTCAAGGGAFTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPH19 : CACTTCTCAAGGGAFTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPH19 : CACTTCTCAAGGGAFTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 326 LPMPH19 : CACTTCTCAAGGGAFTTGTTGCAACAACTGATGTTGTTGTAGGCTTGCACTGGTGGAATGTT : 326 LPMPH19 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGTAGGCTTGCACTGGTGGAATGTT : 326 LPMPH19 : CACTTCTCAAGGGAFTGTTGCAACAACTGATGTTGTTGTAGGCTTGCACTGGTGGAATGTT : 326 LPMPH19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTGCACTGGTGGAATGTT : 326 LPMPH19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTGCACTGGTGGAATGTT : 325 LPMPH19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTGCACTGGTGGAATGTT : 325 LPMPH19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 325 LPMPH19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 325 LPMPH19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT : 322 LPMPH19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTGCACTGGTGGAATGTT : 322 LPMPH19 : CACTTCTCAAGGGAGTTGTTCCAACAACTGATGTTGTTGTAGGCTTGCACTGGTGTGAATGTT : 323 LPMPH19 : CACTTCTCAAGGGAGTTGTTCCAACAACTGATGTTGTTGTAGGCTTTGCACTGGTGGAATGTT : 323 LPMPH19 : CACTTCTCAAGGGAGTTGTTCCAACAACTGATGTTGTTGTAGAGCTTTGCACTGGTGGAATGTT : 322 LPMPH19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGAGCTTTGCACTGGTGGAATGTT : 322 LPMPH19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGAGCTTGCACTGGTGGAATGTT : 322 LPMPH19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGAGCTTGCACTGGTGGAATGTT : 3	_	CACI	TCICAAGGGAGI.	TCTTCCAACAA		GAGGCTTGCA	CTGGTGTGAATGT"	:	
LPMPHH14 CACTITCTAAGGGACTIGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LPMPHH15 CACTITCTAAGGGACTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LPMPHH17 CACTITCTAAGGGACTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LPMPHH17 CACTITCTAAGGGACTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LPMPHH18 CACTITCTCAAGGGACTTGTTGCACACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LPMPHH19 CACTITCTCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LPMPHH19 CACTITCTCAAGGGACTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LPMPHH21 CACTITCTCAAGGGACTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LPMPHH22 CACTITCTCAAGGGACTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LPMPHH23 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAAATGTT 325 LPMPHH24 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAAATGTT 325 LPMPHH25 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAAATGTT 325 LPMPHH26 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAAATGTT 325 LPMPH182 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGGAATGTT 324 LPMPH183 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH183 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH183 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCCTTGCACTGGTGTGAATGTT 324 LPMPH183 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCCTTGCACTGGTGTGAATGTT 324 LPMPH183 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH183 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH183 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH183 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 324 LPMPH184 CACTITCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGCCTTGCACTGGTGTGAATGTT 324 LPMPH184 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGCCTTGCACTGGTGTGAATGTT 322 LPMPH184 CACTTCTCAAGGGAGTTGTTTGCAACAACTGATG	-	CACI	TCTCAAGGGAGT.	TCTTCCN NCN N		GAGGCTTGCA	CTGGTGTGAATGT	4 :	_
LpMpHh15 : CACTICTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMpHh18 : CACTICTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMpHh18 : CACTICTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMpHh18 : CACTICTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMpHh20 : CACTICTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMpHh21 : CACTICTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMpHh22 : CACTICTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMpHh23 : CACTICTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMpHh23 : CACTICTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMpHh25 : CACTICTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMpHh26 : CACTICTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMpHh27 : CACTICTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMpHh28 : CACTICTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMpHh29 : CACTICTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMpHh29 : CACTICTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMpHh30 : CACTICTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMpHh30 : CACTICTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMpHh31 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMpHh31 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMpHh31 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMpHh31 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMpHh32 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMpHh33 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMpHh34 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMpHh35 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMpHh34 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMpHh34 : C	-	CACT	TEACHADOCACTY TOTON NOCCEACTY	TGTTGCAACAA TGTTGCAACAA	CIGAIGIIGII CTCNTCTTCTT	GAGGCTTGCA	CTCCTCTCAATGT		-
LPMPHH16 : CACTICTCAAGGGACTIGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT 325 LPMPHH19 : CACTICTCAAGGGACTTGTTGCACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT 325 LPMPHH19 : CACTICTCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT 326 LPMPHH19 : CACTICTCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT 326 LPMPHH121 : CACTICTCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT 326 LPMPHH122 : CACTICTCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT 326 LPMPHH123 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTTTGAGGCTTGCACTGGTTGAATGTT 326 LPMPHH124 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTTTTTAGGCCTTGCACTGGTTGAATGTT 326 LPMPHH125 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTTTTTAGGCCTTGCACTGGTTGAAATGTT 325 LPMPHH126 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTTGAGGCTTGCACTGGTGTGAAATGTT 325 LPMPH127 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTGTGAAATGTT 324 LPMPH128 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTGTGAAATGTT 324 LPMPH129 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTGTGAAATGTT 324 LPMPH129 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH130 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH131 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH132 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH133 : CACTICTCCAAGGGACTTGTTGCACACACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH134 : CACTICTCCAAGGGACTTGTTGCACACCACACTGATTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH135 : CACTICTCCAAGGGACTTGTTGCACACCACACTGATTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH135 : CACTICTCCAAGGGACTTGTTCCAACCACACTGATTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH137 : CACTTCTCCAAGGGACTTGTTCCAACACACTGATTTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH135 : CACTTCTCCAAGGGACTTGTTTCCAACACACTGATTTTTTGAGGCTTGCACTGGTGTGAATGTT 324 LPMPH137 : CACTTCTCCAAGGGACTTGTTTCCAACACACTGATTTTTTTGAGCCTTGCACTGGTGTGAATGTT 324 LPMPH137 : CACTTCTCCAAGGGACTTGTTTCCAACACACTGATTTTTTTT	-	CACT	"TOTOAAGGGAGT"	TGTTGCAACAA	CTGATGTIGTT	CAGGCTTGCA	CTGGTGTGAATGT CTGGTGTGAATGT		
LpMDHih18 : CACTTCTCAAGGGATTGTTGCÄCAACTGATGTTGTTGAGGCTTGCATGGTGTGAATGTT 325 LpMDHib19 : CACTTCTCAAGGGATTGTTGCÄCACAACTGATGTTGTTGAGGCTTGCATGGGTGAATGTT 326 LpMDHib20 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT 326 LpMDHib21 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT 326 LpMDHib22 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT 326 LpMDHib23 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGCTTTGCACTGGTGTGAATGTT 326 LpMDHib24 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMDHib25 : CACTTGTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 325 LpMDHib26 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 325 LpMDHib27 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 325 LpMDHib28 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 325 LpMDHib39 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib30 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib31 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib32 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib33 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib33 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib33 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib34 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib35 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib36 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib37 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHib38 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTTGCACTGGTGTGAATGTT 322 LpMDHib49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCT	-	CACT	TCTCAAGGGAGT'	TGTTGCAACAA	CTGATGTTGTT	CAGGC I I GCA	CTGGTGTGAATGT		
LpMBihl8 : CACTTCTCAAGGGATTGTTGGÄCAACTGATGTTGTTGAGGCTTGCACTGGTGAATGTT 326 LpMBihl20 : CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGTAGGGCTTGCACTGGTGTGAATGTT 325 LpMBihl21 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 326 LpMBihl22 : CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMBihl23 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMBihl24 : CACTTGTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTTGCACTGGTGTGAATGTT 325 LpMBihl25 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTTGCACTGGTGTGAATGTT 322 LpMBihl26 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTTGCACTGGTGTGAATGTT 322 LpMBihl27 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTTGCACTGGTGTGAATGTT 322 LpMBihl28 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTTGCACTGGTGTGAATGTT 322 LpMBihl30 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGCTTTGCACTGGTGTGAATGTT 322 LpMBihl31 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATTGTTGTAGGCTTTGCACTGGTGTGAATGTT 322 LpMBihl32 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATTGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMBihl33 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTGAGGCTTGCACTGGTGTGAATGTT 322 LpMBihl34 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTGAGGCTTGCACTGGTGTGAATGTT 322 LpMBihl34 : <td< td=""><td>-</td><td>CACT</td><td>"TCTCAAGGGAGT"</td><td>TGTTGCAACAA</td><td>CTGATGTTGTT CTGATGTTGTT</td><td>ADDITODDADI CACCUTUCCA</td><td>CTCCTCTCAATCT</td><td></td><td>-</td></td<>	-	CACT	"TCTCAAGGGAGT"	TGTTGCAACAA	CTGATGTTGTT CTGATGTTGTT	ADDITODDADI CACCUTUCCA	CTCCTCTCAATCT		-
LpMDHih19: CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCATGGGTGAATGTT 325 LpMDHib12: CACTTCTCAAGGGATTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMDHib22: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMDHib23: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LpMDHib24: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMDHib25: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 325 LpMDHib26: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 325 LpMDHib27: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 325 LpMDHib28: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 325 LpMDHib29: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 326 LpMDHib30: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 327 LpMDHib31: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT 327 LpMDHib32: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTCACTGGTGTGAATGTT 324 LpMDHib33: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTCACTGGTGTGAATGTT 322 LpMDHib34: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTCACTGGTGTGAATGTT 322 LpMDHib35: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTCACTGGTGTGAATGTT 322 LpMDHib36: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTCACTGGTGTGAATGTT 322 LpMDHib39: CACTTCTCCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTCACTGGTGTGAATGTT 322 LpMDHib40: CACTTGCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTCACTGGTGTGAATGTT 322 LpMDHib41: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTTGAGGCTTTCACTGGTGTGAATGTT 322 LpMDHib41: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTTGAGGCTTTCACTGGTGTGAATGTT 322 LpMDHib41: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTTGAGGCTTTCACTGGTGTGAATGTT 3	-	CACT	TCTCAAGGGAGT	TGTTGCĞACAA	CTGATGTTGTT	GAGGCTTGCA	TOTAGOTOTODIO: CTGGTGTGAATGT'		
DMDHR10	-								
LpmDHh21	_								
LpmDiH122 CACTITCTCAAGGGAGTTGTTGCAACACTGATGTTTGTAGAGGCTTGCACTGGTGTAGATGTT 326 12 12 12 12 12 12 13 15 15 15 15 15 15 15	LpMDHh21 :								-
LpMDH133 : CACTTCTCAAGGGGTTGTTGCAACACTGATGTTGTTGAGGCTTGCACTGGGTGAATGTT : 325 LpMDH125 : CACTTCTCAAGGGGTTGTTGCAACACTGATGTTTGTAGGGCTTGCACTGGTGGAATGTT : 325 LpMDH126 : CACTTCTCAAGGGAGTTGTTGCAACACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325 LpMDH127 : CACTTCTCAAGGGAGTTGTTGCAACACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325 LpMDH128 : CACTTCTCAAGGGAGTTGTTGCAACACTGATGTTTGTTGAGGCTTGCACTGGTGGAATGTT : 325 LpMDH129 : CACTTCTCAAGGGAGTTGTTGCAACACTGATGTTTGTTGAGGCTTGCACTGGTGGAATGTT : 323 LpMDH130 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTGCACTGGTGGAATGTT : 323 LpMDH131 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTGCACTGGTGGAATGTT : 324 LpMDH32 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTGCACTGGTGGAATGTT : 324 LpMDH32 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTGCACTGGTGGAATGTT : 324 LpMDH33 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGAGGCTTGCACTGGTGGAATGTT : 324 LpMDH34 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGAGGCTTGCACTGGTGGAATGTT : 322 LpMDH35 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTAGGCTTGCACTGGTGGAATGTT : 322 LpMDH38 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTAGGCTTGCACTGGTGGAATGTT : 322 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTAGGCTTGCACTGGTGGAATGTT : 322 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTAGGCTTGCACTGGTGGAATGTT : 322 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTAGGCTTGCACTGGTTGAATGTT : 322 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 322 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 322 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTTGAATGTT : 322 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTGCACTGGTTGAATGTT : 322 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTGCACTGGTTGAATGTT : 321 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTGCACTGGTTGAATGTT : 321 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTGCACTGGTTGAATGTT : 321 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTGCACTGGTGTGAATGTT : 321 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDH39 : CACTTCTCAAGGGAGTTGTTGCAA	LpMDHh22:								
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LpMDHh27 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh29 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh30 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh31 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LpMDHh32 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LpMDHh32 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh36 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh37 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh38 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh40 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh59 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh59 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh59 : CACTTCT	-								325
LpMDHh28 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGAATGTT 323 LpMDHh30 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh31 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh32 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh34 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh36 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh37 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh40 : CACTTTTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh40 : CACTTTTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh41 : CACTTTTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh42 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 320 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 320 LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh55 : LpMDHh56 : LpMDHh57 : LpMDHh58 : LpMDHh58 : LpMDHh59 : LpMDH61 : LpMDH61 : LpMDH61 : LpMDH62 : LpMDH63 : LPMDH6	-								324
LpMDHh29 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh31 : CACTTCTCAAGGGAGTTGTTGCAACCAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh32 : CACTTCTCAAGGGAGTTGTTGCAACCAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh34 : CACTTCTCAAGGGAGTTGTTGCAACGACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACGACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh36 : CACTTCTCAAGGGAGTTGTTGCAACGACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh36 : CACTTCTCAAGGGAGTTGTTGCAACACACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT 322 LpMDHh38 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT 322 LpMDHh39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT 322 LpMDHh40 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT 322 LpMDHh40 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGGAATGTT 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 320 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 320 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 320 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 310 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTTGGAATGTT 311 LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTTGGAATGTT 311 LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTTGGAATGTT 311 LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTTGGAATGTT 311 LpMDH	-								325
LpMDHh30 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LpMDHh31 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh34 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh35 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh36 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh37 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh38 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh38 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh39 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh40 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh41 : CACTTCTCAAGGAGTTGTTCCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh42 : CACTTCTCAAGGAGTTGTTCCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 322 LpMDHh44 : CACTTCTCAAGGAGTTGTTCCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh44 : CACTTCTCAAGGGAGTTGTTCCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh44 : CACTTCTCAAGGGAGTTGTTCCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh45 : CACTTCTCAAGGGAGTTGTTCCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh46 : CACTTCTCAAGGGAGTTGTTCCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 321 LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 319 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 319 LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTGTGAATGTT 311 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTTGGAATGTT 311 LpMDHh50 : LpMDH50 : Lp	_								323
LpMDHh31 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh34 : CACTTCTCAAGGGAGTTGTTGCAACGACTGATGTTTTTGAGGCTTTGCACTGGTTGTGAATGTT 323 LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACGACTGATGTTTTTGAGGCTTTGCACTGGTTGGAATGTT 323 LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACACTGATGTTTTTGAGGCTTGCACTGGTTGTGAATGTT 323 LpMDHh37 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTGAGGCTTTGCACTGGTTGTGAATGTT 322 LpMDHh38 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTGAGGCTTTGCACTGGTTGTGAATGTT 322 LpMDHh39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTTGAGGCTTTGCACTGGTTGTGAATGTT 322 LpMDHh40 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTTTGAGGCTTTGCACTGGTTGTAATGTT 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTTTT	-								
LpMDHh32 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 324 LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACGACTGATGTTGTTGAGGCTTTGCACTGGTTGTAATGTT : 323 LpMDHh36 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGTAATGTT : 322 LpMDHh37 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGTAATGTT : 322 LpMDHh38 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGTAATGTT : 322 LpMDHh39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGTAATGTT : 322 LpMDHh40 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTGCACTGGTTGTAATGTT : 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 322 LpMDHh42 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 321 LpMDHh42 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 320 LpMDHh43 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 320 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 320 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 320 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 321 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 321 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 319 LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTAGGCTTTGCACTGGTTGAATGTT : 311 LpMDHh48 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTAGGCCTTGCACTGGTTGAATGTT : 311 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTAGGCCTTGCACTGGTTGAATGTT : 312 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTAGGCCTTGCACTGGTTGAATGTT : 312 LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTAGGCCTTGCACTGGTTGAATGTT : 294 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGAGGCTTGCACTGGTTGAATGTT : 294 LpMDHh54 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTAGGCCTTGCACTGGTTGAATGTT : 294 LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTTAGGCCTTGCACTGGTTGAATGTT : 294 LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTTAGAGCCTTGCACTGGTTGAATGTT : 294 LpMDHh56 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTTAGA									
LpMDHh34 : CACTTCTCAAGGGAGTTGTTGCAACGACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323 LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323 LpMDHh36 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LpMDHh37 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LpMDHh39 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LpMDHh40 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh42 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 312 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 312 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 317 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 317 LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 316 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGGCTTGCACTGGTGTGAATGTT : 294 LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGGCTTGCACTGGTGTGAATGTT : 294 LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTAGGGCTTGCACTGGTGTGAATGTT : 294 LpMDHh56 : CACTTCTCAAGGGAGTTGTTG	-	CACI	"TCTCAAGGGAGT"	TGTTGCAACAA	CTGATGTTGTT	GAGGCTTGCA	CTGGTGTGAATGT	:	
LpMDHh35 : CACTTCTCAAGGAGTTGTTGCAACACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323 LpMDHh36 : CACTTCTCAAGGAGTTGTTGCAACACTGATGTTGTTTGAGGCTTTGCACTGGTGTGAATGTT : 322 LpMDHh38 : CACTTCTCAAGGAGTTGTTGCAACACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT : 322 LpMDHh39 : CACTTCTCAAGGAGTTGTTGCAACACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LpMDHh40 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LpMDHh41 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh41 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh42 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh43 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320 LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320 LpMDHh48 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTCACTGGTGTGAATGTT : 319 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT : 311 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT : 312 LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTGTGAATGTT : 313 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTTGAATGTT : 294 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTTGCACTGGTTGAATGTT : 294 LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT : 294 LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTTGCACTGGTTGAATGTT : 294 LpMDHh56 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTTGAATGTT : 294 LpMDHh56 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTTGAGGCTTTGCACTGGTTGAATGTT : 294 LpMDHh56 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTTTGAGGCTTTGCACTGGTTGAATGTT : 294 LpMDHh56 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTTTT	-	: CACI	"TCTCAAGGGAGT"	TGTTGCAACAA	CTGATGTTGTT	IGAGGCTTGCA	CTGGTGTGAATGT	:	
LpMDHh36 : CACTTCTCAAGGGGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT 12MDHh37 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTAGAGCTTTCCACTGGTTGAATGTT 1323	_								
LpMDHh37 : CACTTCTCAAGGGAGTTGTTGCAACACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT	-								
LpMDHh38 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LpMDHh40 : CACTTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LpMDHh41 : CACTTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh42 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh43 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320 LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 319 LpMDHh48 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 319 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 312 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 313 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 313 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 294 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 294 LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 243 LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 243 LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 243 LpMDHh55 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh57 : LpMDHh58 : LpMDHh59 :	-								
LpMDHh39 : CACTTCTCAAGGGAGÑTGCAACACTGATGTTGÑTGAGGCTMGCACTGGTGAATGTT 1 322 LpMDHh40 : CACTTÑTCAAGGGAGTTGÑTCCAACACTGATGTÑGTTGAÑGCTTGCACTGGÑGTGAATGTT 2 321 LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCACACACTGATGTTÄGTTGAGGCTTGCACTGGTGTGAATGTT 2 321 LpMDHh42 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 321 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 321 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 320 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 320 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 310 LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 310 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 317 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 316 LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 294 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 294 LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 277 LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 243 LpMDHh54 : LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 243 LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 243 LpMDHh56 : LpMDHh57 : LpMDHh58 : LpMDHh58 : LpMDHh59	_								
LpMDHh40 : CACTTNTCAAGGAGTTGNTCAACAACTGATGNGTTGANGCTTGCACTGCNGTGAATGTT LpMDHh41 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTTGAGGCTTGCACTGGTGTAATGTT LpMDHh42 : CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh43 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh48 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh54 : LpMDHh56 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh56 : LpMDHh66 : LpMD	-	CACT	TCTCAAGGGAGT	TGI IGCAACAA TGÑTCCAACAA	CTCATGIIGII	CAGGCTTGCA	CTCCTCTCAATGT	# :	
LpMDHh41: CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh42: CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh43: CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh44: CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh45: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh46: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh47: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh48: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh49: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh50: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh51: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh52: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh52: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh53: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh54: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh54: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh55: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh55: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh66: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh66: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh66: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh66: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGATGTT LpMDHh66: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGATGTT LpMDHh66: CACTTCTAAGGGAGTTGTTGAACAACTGATGTTGTAGGCTTGACTGGTGTGATGTTGAGGAGTGTTGA	-	CACT	MOADDDAACTRT	TGNTGCAACAA TGNTGCAACAA	LATO TO TABLE.	CAGGCINGCA	CTGCÑGTCAATGI		
LpMDHh42: CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh44: CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh45: CACTTCTCAAGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh46: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh47: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh48: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh49: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh49: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh50: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh51: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh52: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh53: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh54: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh55: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh54: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh55: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh57: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTTGT	_	CACT	TOADDDAADTEST TOADDDAADTOTT	AACAACDI MOT A A C A A C O TTTOT	CTGATGTIGTT	rcacecrreca	CTCCTCTCN ATCT		
LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 1 320 LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 320 LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 2 320 LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGCCTTGCACTGGTGTGAATGTT 2 320 LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 317 LpMDHh48 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 3 17 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 3 16 LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 24 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 24 LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 243 LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 243 LpMDHh54 : LpMDHh55 : LpMDHh55 : LpMDHh56 : LpMDHh61 : LpMDHh62 : LpMDHh62 : LpMDHh62 : LpMDHh63 : LpMDHh63 : LpMDHh64 : LpMDHHA4 : LpMDHHA4 : LpMD	_	CACT	TCTCAAGGGAGT	TGTTGCAACAA	CTCATCTTCTT	CAGGCTTGCA	CTGCTCTCAATCT		
LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh48 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh54 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh56 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh66 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh66 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh66 : CACTTCTCAAGGGAGTTGTTGCACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh66 : CACTTCTCAAGGGAGTTGTTGCACTGATGTTGTTGAGGCTTGCACTGGTTGAATGTT LpMDHh66 : CACTTCTCAAGGGAGTTGTTGCACTGATGTTGTTGTTGAGGCTTGCACTGGTTGTAATGTT LpMDHh66 : CACTTCTCAAGGGAGTTGTTGCACTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	-	CACT	TCTCAAGGGAGT	TGTTGCAACAA	CTGATGTTGTT	GAGGCTTGCA	CTGGTGTGAATGT		
LpMDHh45: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 1 320 LpMDHh47: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 317 LpMDHh48: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 3 318 LpMDHh49: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 3 318 LpMDHh50: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 318 LpMDHh51: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 294 LpMDHh51: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 277 LpMDHh52: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 2 243 LpMDHh53: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 1 65 LpMDHh54:	_	: CACI	TCTCAAGGGAGT	TGTTGCAACAA	CTGATGTTGTT	GAGGCTTGCA	CTGGTGTGAATGT		
LpMDHh46: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT	LpMDHh45								
LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 313 LpMDHh48 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 313 LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 316 LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 294 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 277 LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 243 LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 165 LpMDHh54 :	LpMDHh46								
LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 294 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 277 LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 243 LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 243 LpMDHh54 :	LpMDHh47	: CACT	TCTCAAGGGAGT	TGTTGCAACAA	CTGATGTTGTT	rgaggcttgca	CTGGTGTGAATGT		317
LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 294 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 277 LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 243 LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 165 LpMDHh54 :		: CACT	"TCTCAAGGGAGT"	TGTTGCAACAA	CTGATGTTGTT	rgaggcttgca	CTGGTGTGAATGT	ľ:	313
LpMDHh51: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh52: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh54: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh55: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh56: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh57: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh59: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh59: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh69: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGTGT	-	: CACI	TCTCAAGGGAGT	TGTTGCAACAA	CTGATGTTGTT	rgaggcttgca	CTGGTGTGAATGT	ı :	316
LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 243 LpMDHh54 : CACTTCTCAAGGGAGTTGTTGCAACACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 165 LpMDHh55 : CACTTCTCAAGGGAGTTGTTGCAACACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 165 LpMDHh57 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 165 LpMDHh58 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 165 LpMDHh59 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 165 LpMDHh60 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT : 165 LpMDHh61 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 165 LpMDHh61 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 165 LpMDHh61 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 165 LpMDH61 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGAGTTGTTGTTGAGGATGTTGTTGAGGATGTTGT		: CACT	TCTCAAGGGAGT	TGTTGCAACAA	CTGATGTTGT1	rgaggcttgca	CTGGTGTGAATGT	ı :	294
LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTAGGGCTTGCACTGGTGTAATGTT 165 LpMDHh55 :		: CACT	TCTCAAGGGAGT	TGTTGCAACAA	CTGATGTTGTT	rgaggcttgc <i>p</i>	CTGGTGTGAATGT	Ē :	277
LpMDHh54 :		: CACI	TCTCAAGGGAGT	TGTTGCAACAA	CTGATGTTGTT	rgaggcttgca	CTGGTGTGAATGT	Ū :	243
LpMDHh55 :			"TCTCAAGGGAGT					<u> </u>	165
LpMDHh56		:						- :	-
LpMDHh57:		:						- :	-
LpMDHh58 :								- :	-
LpMDHh59 :								- :	-
LpMDHh60 :								- :	_
LpMDHh61:		•						- : -	_
LpMDHh62:		:						- :	_
LpMDHh63 :		:						- : -	- -
		:						- :	<u>-</u>
		:						_ :	-

		380	*	400	*	420	*		
LpMDHh1	:	GCGGTTATGGTTGG	TGGATTCC	CCAGGAAGGA	GGAATGGAAA	AGGAAGGATGT	TATGTCTAA	;	432
LpMDHh2	:							:	-
LpMDHh3	:							:	-
LpMDHh4	:							:	-
LpMDHh5	:	GCGGTTATGGTTGG	TGGATTCC	CCAGGAAGGA	GGAATGGAAA	AGGAAGGATG	TTATGTCTAA		392
LpMDHh6	:	GCGGTTATGGTTGC	TGGATTCC	CCAGGAAGGA	GGAATGGAA	AGGAAGGATG	TTATGTCTAA	:	390
LpMDHh7	:	GCGGTTATGGTTGG						:	388
LpMDHh8	:	GCGGTTATGGTTGC						:	391
LpMDHh9	:	GCGTTTATGGTTG	TGGATTCC	CCAGGAAGGA	GGAATGGAAA	AGGAAGGATG'	TTATGTCTAA	:	391
LpMDHh10	:	GCGGTTATGGTTGC	STGGATTCC	CCAGGAAGGA	GGGAATGGAAA	AGGAAGGATG'	TTATGTCTAA	:	389
LpMDHh11	:	GCGGTTATGGTTG	STGGATTCC	CCAGGAAGGA	GGGAATGGAAA	AGGAAGGATG'	TTATGTCTAA	:	390
LpMDHh12	:	GCGTTTATGGTTGC	STGGATTCC	CCAGGAAGGA	GGGAATGGAA	AGGAAGGATG'	TTATGTCTAA	:	388
LpMDHh13	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA	AGGAAGGATG'	TTATGTCTAA	:	387
LpMDHh14	:	GCGGTTATGGTTGC	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA	AGGAAGGATG'	TTATGTCTAA	:	388
LpMDHh15	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA	AGGAAGGATG'	TTATGTCTAA	:	388
LpMDHh16	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA	AGGAAGGATG'	TTATGTCTAA	:	388
LpMDHh17	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA	AGGAAGGATG'	TTATGTCTAA	:	387
LpMDHh18	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA	AGGAAGGATG	TTATGTCTAA	:	388
LpMDHh19	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA	AGGAAGGATG'	TTATGTCTAA	:	388
LpMDHh20	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA	AGGAAGGATG	TTATGTCTAA	:	3.87
LpMDHh21	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA	AGGAAGGATG	TTATGTCTAA	:	388
LpMDHh22	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA.	AGGAAGGATG	TTATGTCTAA	:	388
LpMDHh23	:							:	-
LpMDHh24	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	GGGAATGGAA.	AGGAAGGATG	TTATGTCTAA	:	387
LpMDHh25	:	GCGGTTATGGTTG						:	387
LpMDHh26	:	GCGGTTATGGTTG						:	386
LpMDHh27	:	GCGGTTATGGTTG	GTGGATTCC	CCCAGGAAGGA	GGGAATGGAA	AGGAAGGATG	TTATGTCTAA	:	387
LpMDHh28	:	GCGGTTATGGTTG						ŧ	385
LpMDHh29	:	GCGGTTATGGTTG	GTGGATTCC	CCAGGAAGGA	.GGGAATGGAA	AGGAAGGA'I'G	TTATGTCTAA	:	385
LpMDHh30	:	GCGGTTATGGTTG						:	386
LpMDHh31	:	GCGGTTATGGTTG						:	385
LpMDHh32	:	GCGGTTATGGNTG						:	386
LpMDHh34	:	GCGGTTATGGTTG	GTGGATTC	CCCAGGAAGGA	GGGAATGGAA	AGGAAGGATG	TTATGTCTAA	:	385
LpMDHh35	:	GCGGTTATGGTTG						:	385
LpMDHh36	:	GCGGTTATGGTTG	GTGGATTCC	CCCAGGAAGGA	GGGAATGGAA	AGGAAGGATG	TTATGTCTAA	:	384
LpMDHh37	:	GCGGTTATGGTTG	GTGGATTC	CCCAGGAAGGA	GGGAATGGAA	AGGAAGGATC	TIAIGICIAA	:	385 384
LpMDHh38	:	GCGGTTATGGTTG	GTGGATTCC	CCCAGGAAGGA	IGGGAATGGAA	AGGAAGGAIG	ITAIGICIAA		341
LpMDHh39	:	GCGGTTATGGÄTG	CIGGAII	AND ONLY				•	349
LpMDHh40	:	GCGGŅŅ <mark>N</mark> TGŅ <mark>C</mark> ŅŅ GCGGTTATGGTTG	GUUGANGI	AANAINN		ACCAACCATO	TTTATCTCTAA	:	383
LpMDHh41	:	GCGGTTATGGTTG	GTGGATTC	CCCAGGAAGGA	AGGGAA I GGAA	ACCAACCATC	TAIGICIAA	:	382
LpMDHh42	:	GCGGTTATGGTTG	GIGGATIC	CCCAGGAAGGA	AGGGAA I GGAA	ACCAACCATO	TIAIGICIAA	:	383
LpMDHh43	:	GCGGTTATGGTTG	GIGGALIC CTCCNTTC	CCCAGGAAGGA	CCCAATGGAA	ACCANCGATO	ATTOTOTICE A TOTO	:	382
LpMDHh44	:	GCGGTTATGGTTG	CTCCATTC	CCCAGGAAGGA	AGGGAA I GGAA	ACCAACCATC	AATOTOTATE	•	381
LpMDHh45	•	GCGGTTATGGTTG						:	382
LpMDHh46		GCGGTTATGGTTG	CTCCATTC	CCCAGGA AGG	AGGGAATGGAA	AGGAAGGATO	TTATGTCTAA	:	379
LpMDHh47 LpMDHh48		GCGGTTATGGTTG	CTCCATTC	CCCAGGAAGG?	AGGGAATGGAA	ACGAAGGATO	TTATGTCTAA	•	375
LpMDHh49		GCGGTTATGGTTC						:	378
LpMDHh50		GCGGTTATGGTTC						:	356
LpMDHh51		GCGGTTATGGTTG	OTTADDTO:	CCCAGGAAGG	AGGGAATGGAA	AGGAAGGAT	TTATGTCTAA	:	339
LpMDHh52			GTGGATTC	CCCAGGAAGG	AGGGAATGGAA	AGGAAGGAT	STTATGTCTAA	:	305
LpMDHh53			GTGGATTC	CCCAGGAAGG	AGGGAĞTGGAZ	AGGAAGGAT	GTTATGTCTAA	:	
LpMDHh54			GTGGATTC	CCCAGGAAGG	AGGGAATGGAA	AGGAAGGAT	GTTATGTCTAA	:	56
LpMDHh55								:	_
LpMDHh56								:	-
LpMDHh57								:	~
LpMDHh58								:	-
LpMDHh59								:	_
LpMDHh60								:	-
LpMDHh61								:	-
LpMDHh62								:	-
LpMDHh63								:	-
LpMDHh64								:	-

= .seperbe		440 * 460 * 480 * GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA		494
LpMDHh1	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA		474
LpMDHh2	:			_
LpMDHh3	:			_
LpMDHh4	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	454
LpMDHh5	:		•	452
LpMDHh6	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCÄAATTGCA	:	450
LpMDHh7	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGCAGCCCCATGCAGCCCCAATTCCA	•	453
LpMDHh8	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA	:	453
LpMDHh9	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA	:	451
LpMDHh10	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA	•	452
LpMDHh11	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA	•	450
LpMDHh12	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA	•	449
LpMDHh13	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	•	450
LpMDHh14	:		:	450
LpMDHh15	:	Old i I Old i I Clust Citici ii i i C I Clusto Citico Co Co C I I Clusto C I I I C I I I C I I C I I C I I C I I C I I C I I C I I C I I C I I C I I I C I I I C I I I C I I I C I I I C I I I C I I I C I I I C I I I C I I I C I I I C I I I C I I C I I C I I C I I C I I C I I C I I C I I C I I C I I I	:	450
LpMDHh16	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	449
LpMDHh17	:	Offild 1 1 Cinii Cilicinnii Cicinnii Ci	•	450
LpMDHh18	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	450
LpMDHh19	:	Craff Cff ff Cff ff Cff ff Cff ff Cff ff Cff ff	•	449
LpMDHh20	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCÄGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	450
LpMDHh21	:	GAATGTTTCAATCTACAAATCTCAAGCATCGGCCCTGAAGCCCCAATTGCA	:	450
LpMDHh22	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	450
LpMDHh23	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	449
LpMDHh24	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA	:	449
LpMDHh25	:		:	448
LpMDHh26	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	•	449
LpMDHh27	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	447
LpMDHh28	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	447
LpMDHh29	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	448
LpMDHh30	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA NAATGTTTCAATCTACAAATCTNAAGCATCTGCCCTTGAAGCCCATGCA-CCCCNAATTGCA	:	446
LpMDHh31	:	NAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA NAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	•	448
LpMDHh32	:	NAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	447.
LpMDHh34	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	447
LpMDHh35	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	446
LpMDHh36	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	•	447
LpMDHh37	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAG-CCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAG-CCATGCAGCCCCGAATTGCA	:	445
LpMDHh38	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAG-CCATGCAGCCCCGAATTGCA	:	773
LpMDHh39	:		•	_
LpMDHh40	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	•	445
LpMDHh41	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	444
LpMDHh42 LpMDHh43	:	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	445
LpMDHh44	•	GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	444
LpMDHh45		GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	443
LpMDHh46		GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	444
LpMDHh47		AATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	;	441
LpMDHh48		GAATGTTTCAATCTACAAATCTCAAGTATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	437
LpMDHh49		GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	440
LpMDHh50		GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	418
LpMDHh51			:	
LpMDHh52			:	
LpMDHh53		GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	
LpMDHh54		GAATGTTTCAATCTACAAATCTCAAG <mark>N</mark> GNNTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA	:	
LpMDHh55		######################################	:	
LpMDHh56		CCATGCAA-CCCCGÑANTGCA	:	
LpMDHh57		TGCAGCCCCG-ATTGCA	:	
LpMDHh58			:	
LpMDHh59			:	_
LpMDHh60			:	_
LpMDHh61			:	-
LpMDHh62			:	_
LpMDHh63			:	_
LpMDHh64			:	-

		500 * 520 * 540 * 5	
LpMDHh1	:		556
LpMDHh2	:	:	-
LpMDHh3	:	:	-
LpMDHh4	:	:	-
LpMDHh5	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA:	516
LpMDHh6	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA:	514
LpMDHh7	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	512
LpMDHh8	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	515
LpMDHh9	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	515
LpMDHh10	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA:	513
LpMDHh11	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	514
LpMDHh12	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	512
LpMDHh13	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	511 512
LpMDHh14	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	512
LpMDHh15	:	AGGTTCTGGTTGTTGCCAATCCAGCAACACCAATGCTCTTATCTTAAAGGAGTTCGCTCCA	512
LpMDHh16	:	AGGTTCTGGTTGTTGCCAATCCAGCAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	511
LpMDHh17	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : AGGTTCTGGTTGTTGCCAATCCAGRAAACACCAATGCTCTTATCGTAAAGGAGTTTGCTCCA :	512
LpMDHh18 LpMDHh19	:	AGGTTCTGGTTGTTGCCAATCCAG@AAACACCAATGCTCTTATCTTA	512
LpMDHh20	:	AGGTTCTGGTTGTTGCCAATCCAGCAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	511
LpMDHh21	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTATTATCTTAAAGGAGTTTGCTCCA	512
LpMDHh22	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	512
LpMDHh23	:		_
LpMDHh24	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATNTTAAAGGAGTTTGCTCCA	511
LpMDHh25	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	511
LpMDHh26	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA:	510
LpMDHh27	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA:	511
LpMDHh28	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	509
LpMDHh29	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	509
LpMDHh30	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA:	510
LpMDHh31	:	AGGGTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTTTTATTTTAAANGAGTTTGCTCCA	508
LpMDHh32	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAMTGCTCTTATCTTA	510
LpMDHh34	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	509
LpMDHh35	:	AGGTTCTGGTTGTCCAATCCA:	470
LpMDHh36	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	508
LpMDHh37	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	509
LpMDHh38	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	507
LpMDHh39	:	:	-
LpMDHh40	:		-
LpMDHh41	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGNTTGCTCCA AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	507 506
LpMDHh42	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA :	507
LpMDHh43	:	AGGITCIGGITGITGCCAATCCAGCAAACACCAATGCTCITATCTTAAAGGAGTITGCTCCA : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA :	
LpMDHh44 LpMDHh45	:	AGGITCIGGIIGIIGCCAATCCAGCAAACACAATGCICIIAICIIA	
LpMDHh46	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	506
LpMDHh47	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCT#TTATCTTAAAGGAGTTTGCTCCA	
LpMDHh48	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA	499
LpMDHh49	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA :	502
LpMDHh50	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA:	480
LpMDHh51	:		463
LpMDHh52	:		429
LpMDHh53	:		351
LpMDHh54	:		180
LpMDHh55	:	AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA:	
LpMDHh56	:		82
LpMDHh57	:		
LpMDHh58	:		-
LpMDHh59		:	-
LpMDHh60		:	-
LpMDHh61			-
LpMDHh62			
LpMDHh63		:	_
LpMDHh64	:	:	_

		60	*	580	*	600	*	620		
LpMDHh1	:	TCTATTCC	TGAGAAGA	ACATCAGTTGT	TTGACCCGC	CTAGACCATAA	CAGGGCACTT	GGTCA	:	618
LpMDHh2	:								:	-
LpMDHh3	:								:	-
LpMDHh4	:				·				:	-
LpMDHh5	:	TCTATTCC	TGAGAAGA	ACATCAGTTGT	TTGACCCGC	CTAGACCATAA	CAGGGCACTT	GGTCA	:	578
LpMDHh6	:					CTAGACCATAA			:	576
LpMDHh7	:	TCTATTCC	TGANAAGA	ACATNAGTTGT	TTGACCCGC	CTAGACCATAA	CAGGGCACT <mark>N</mark>	GGTCA	:	574
LpMDHh8	:	TCTATTCC	TGAGAAGA.	ACATCAGTTGT	TTGACCCGC	CTAGACCATAA	CAGGGCACTT	GGTCA	:	577
LpMDHh9	:	TCTATTCC	TGAGAAGA	ACATCAGTTGT	TTTGACCCGC	CTAGACCATAA	CAGGGCACTT	GGTCA	:	577
LpMDHh10	:	TCTATTCC	TGAGAAGA	ACATCAGTTG1	TTGACCCGC	CTAGACCATAA	CAGGGCACTT	GGTCA	:	575
LpMDHh11	:	TCTATTCC	TGAGAAGA	ACATCAGTTG'	FTTGACCCGC	CTAGACCATAA	CAGGGCACTT	GGTCA		576
LpMDHh12	:					CTAGACCATAA		GGTCA		574
LpMDHh13	:					CTAGACCATAA				563
LpMDHh14	:					CTAGACCATAA			-	574
LpMDHh15	:					CTAGACCATAA	potent.			574
LpMDHh16	:					CTAGACCATAA	Sec. 9			574
LpMDHh17	:					CTAGACCATAA	From the second			573
LpMDHh18	:					CTAGACCATAA				574
LpMDHh19	:					CTAGACCATAA	p.ess,		•	574
LpMDHh20	•					CTAGACCATAA	144		:	573
LpMDHh21	:					CTAGACCATAA			:	574
LpMDHh22	•	ICIATICC	TGAGAAGA	ACATCAGTTG.	I'I'IGACCCGC	CTAGACCATAA	CAGGGCACTT	GGTCA	•	574
LpMDHh23 LpMDHh24	:	TCTNTTCC	TCACAA						•	525
LpMDHh25	:	Ann. 5		ACATCACATC	TTTCA CCCCN	CTAGACCATAA	CACCCCACTC	CCTCA	:	573
LpMDHh26	:					CTAGACCATAA CTAGACCATAA			:	572
LpMDHh27	:					CTAGACCATAA CTAGACCATAA	4 100		:	573
LpMDHh28	:					CTAGACCATAA	****		:	571
LpMDHh29	:					CTAGACCATAA			:	571
LpMDHh30	•					CTAGACCATAA	***	_	:	572
LpMDHh31	:					CTAGACCATAA			:	570
LpMDHh32	:					CTAGACCATAA			:	572
LpMDHh34	:					CTAGACCATAA			•	571
LpMDHh35	:								:	
LpMDHh36	:	TCTATTCC	TGAGAAGA	ACATCAGTTG'	TTTGACCCGC	CTAGACCATAA	CAGGGCACTI	GGTCA	:	570
LpMDHh37	:	TCTATTC	CTGAGAAGA	ACATCAGTTG'	TTTGACCCGÑ	CTAGACCATAA	CAGGGCACT	GGNCA	:	571
LpMDHh38	:					CTAGACCATAA			:	569
LpMDHh39	:								:	_
LpMDHh40	:				:				:	_
LpMDHh41	:	TCTATTC	CTGAGAANA	ACATCAGNTG'	TTTGACCCGC	CTAGACCATAA	CAGGNCACTC	GGNCA	:	569
LpMDHh42	:	TCTATTC	CTGAGAAGA	ACATCAGTTG'	TTTGACCCGC	CTAGACCATAA	CAGGGCACTT	GGTCA	:	568
LpMDHh43	:	TCTATTC	CTGAGAAGA	ACATCAGTTG	TTTGACCCGC	CTAGACCATAA	.CAGGGCACTT	GGTCA	:	569
LpMDHh44	:					CTAGACCATAA			:	568
LpMDHh45	:					CTAGACCATAA			٤,	567
LpMDHh46	:					CTAGACCATAA			:	568
LpMDHh47	:					CTAÑACCATAA			٤,	565
LpMDHh48	:					CTAGACCATAA			:	561
LpMDHh49	:	TCTATTC	CTGAGAAGA	ACATCAGTTA	TTTGACCCGC	CTAGACCATAA	CAGGGCACTI	'GGTCA	:	564
LpMDHh50	:	TCTATTC	CTGAGAAGA	ACATCAGTTG	TTTGACCCGC	CTAGACCATAA	CAGGGCACTI	GGTCA	:	542
LpMDHh51	:					CTAGACCATAA	4.0	,		525
LpMDHh52	:					CTAGACCATAA				491
LpMDHh53	:					CTAGACCATAA			:	413
LpMDHh54	:					CTAGACCATAA			:	242
LpMDHh55	:					CTAGACCATAA			:	164
LpMDHh56	:					CTAGACCATAA			:	144
LpMDHh57	:	CIATIC	J I GAGAAGA	AACA I CAGI II G	1 1 I GACCCGC	CTAGACCATAA	CAGGGCAC'I'I	.GGTCA	:	140
LpMDHh58 LpMDHh59	:								:	-
LpMDHh60									:	-
LpMDHh61									:	-
LpMDHh62	•									-
LpMDHh63	•								•	_
LpMDHh64	•								•	-
_p. ~ *	-								•	_

		*	640	*	660	*	680	
LpMDHh1 :	GATCTC	TGAGAGAG	CTTGATGNCCA	AGTTAGTGAT	GTGAANAATG	TTATCATCTG	GGCAATC :	680
LpMDHh2 :							::	-
LpMDHh3 :							:	-
LpMDHh4 :							:	_
LpMDHh5 :	GATCTC	TGAGAGA	CTTGATGGCCA	AGTTAGTGAT	GTGAAGAATG	TTATCATCTG	GGCAATC :	640
LpMDHh6 :	GATCTC	TGAGAGA	CTTGATGTCCA!	AGTTAGTGAT	GTGAAGAATG	TTATCATCTG	GGCAATC	638
LpMDHh7 :	GATCTC	TGAGAGAG	CTTNATGTCCA	ANTTAGTGAT	GTGAAÑAATG	TTATCATCTG	GGTAATC :	636
LpMDHh8 :			CTTGATGTCCA					639
LpMDHh9 :			CTTGATGTCCA					639
LpMDHh10 :			CTTGATGTCCA					637
LpMDHh11:			CTTGATGTCCA					638
LpMDHh12 :			CTTGATGTCCA					636
LpMDHh13 :								- .
LpMDHh14:	GATCTO	TGAGAGA	CTTGATGTCCA	AGTTAGTGAT	GTGAAGAATG	TTATCATCTG	GGTAATC :	636
LpMDHh15 :	GATCTC	TGAGAGA	CTTGATGTCCA	AGTTAGTGAT	GTGAAGAATG	TTATCATCTG	GGCAATC	636
LpMDHh16 :	GATCTO	TGAGAGĜ	CTTGATGTCCA	AGTTAGTGAT	GTGAAGAATG	TTATCATCTG	GGTAATC	636
LpMDHh17 :			CTTGATGTCCA					635
LpMDHh18 :			CTTGATGTCCA				65555	636
LpMDHh19 :			CTTGATGTCCA				departs.	636
LpMDHh20 :			CTTGATGTCCA					635
LpMDHh21 :			CTTGATGTCCA					636
LpMDHh22:			CTTGATGTCCA					636
LpMDHh23 :								-
LpMDHh24 :								-
LpMDHh25 :	GATCT	TGAGAGA	CTTGATGTQCA.	AGTTANEGAT	GTGAANAATG	TATCATCTG	GGGANATC	: 635
LpMDHh26:			CTTGATGTČCA					634
LpMDHh27 :			CTTGATGTCCA					: 635
LpMDHh28:			CTTGATGTCCA					633
LpMDHh29			CTTGATGTCCA					633
LpMDHh30 :			CTTGATGTCCA					634
LpMDHh31 :			CTTGÑTÑTCÄA					: 595
LpMDHh32:			CTTGÄTĞTCČA		'GNGAANAATG	TTATCATCTG	GGGCAATC	634
LpMDHh34:	GATCT	CTGAGAGA	CTTGATGTCCA.	AGTTAGTGAT	GTGAAGAATC	TTATCATCTG	GGGCAATC	: 633
LpMDHh35 :								
LpMDHh36 :	GATCT	CTGANAGA	CTTGATGTCCA	AGTTA				: 599
LpMDHh37 :		44667	CTTGATGTCCA		G			: 606
LpMDHh38:			CTTGATGTCCA			TTATCATCTG	GGGCAATC	: 631
LpMDHh39 :								: -
LpMDHh40 :								: -
LpMDHh41 :	GANCT	CTGAGAGA	CNTGATGCCCA	AGNTNGNGNT	GN			: 605
LpMDHh42 :	GATCTO	CTGAGAGA	CTTGATGTCCA	AGTTÄGTGAT	GTGAAGAATG	TTATCATCTG	GGCAAATC	: 630
LpMDHh43 :			CTTGATGTCCA					: 631
LpMDHh44			CTTGATGTCCA					: 630
LpMDHh45			CTTGATGTCCA					: 629
LpMDHh46			CTTGATGTCCA					630
LpMDHh47			CTTGATGCCCA					: 627
LpMDHh48			CTTGATGTCCA					: 623
LpMDHh49			CTTGATGTCCA					: 626
LpMDHh50			CTTGATGTCCA					: 604
LpMDHh51			CTTGATGTCCA					: 587
LpMDHh52	: GATCT	CTGAGAGA	CTTGATGTCCA	AGTTAGTGAT	GTGAAGAATG	TTATCATCTG	GGGCAATC	: 553
-			CTTGATGT <mark>N</mark> CA					: 475
LpMDHh54	: GATCT	CTGAGAGA	CTTGATGT C CA	AGTTAGTGAT	rgtgaagaatc	TTATCATCTG	GGGCAATC	: 304
-	: GATCT	CTGAGAGA	CTTGATGTCCA	AGTTAGTGAT	GTGAAGAATG	TTATCATCTG	GGGĨAATC	: 226
LpMDHh56	GATCT	CTGAGAGA	CTTGATGTCCA	AGTTAGTGAT	GTGAAGAATC	TTATCATCTG	GGGCAATC	: 206
LpMDHh57			CTTGATGTCCA					: 202
LpMDHh58	:						GCAATC	: 6
LpMDHh59	:							: -
LpMDHh60	:							: -
LpMDHh61	:							: -
LpMDHh62	:							: -
LpMDHh63	:							: -
LpMDHh64	:							: -

			700	*	720	*	740		
LpMDHh1	:	ACTCTTNCAGTCA	GTACCCTGAT	GTGAACCAC	GCCACCGTGA	AGACTTCCAGT	'GCCGAGAAG	: 7	742
LpMDHh2	:							:	_
LpMDHh3	:							ŧ	-
LpMDHh4	:				,			:	-
LpMDHh5	:	ACTCTTCCAG						: 6	550
LpMDHh6	:	ACTCTTCCAGTCA						: 6	660
LpMDHh7	:	ACCCTTCCAGTCA	ATACCCTGAT	NTGAACCAC	CCCCCNNAA	AMACTTCCAG-	GGCGA	; (593
LpMDHh8	:	ACTCTTCCAGTC	GTACCCTGAT	GTGAACCAC	GCCACCGTGA	AGACTTCCAGT	GGCGAGAAG	: '	701
LpMDHh9	:	ACTCTTCCAGTCA	GTACCCTGAT	GTGAACCAC	GCCACCGTGA	AGACTTCCAG	GGCGAGAAG	: '	701
LpMDHh10	:	ACTCTTCCAGTC	AGTACCCTGAT	GTGAACCAC	GCCACCGTGA	AKACT		: (584
LpMDHh11	:	ACTCTTCCAGTCA	AGTACCCTGAT	GTGAACCAC	GCCACCGTGA	AGACTTCCAGT	rggcgagaag	;	700
LpMDHh12	:	ACTCTTCCAGTCA	AGTACCCTGAT	GTGAACCAC	GCCACCGTGA	AGACTTNCAG1	CGGCGAGAAG	: (598
LpMDHh13	:						<u></u>	:	-
LpMDHh14	:	ACTCTTCCAGTC							692
LpMDHh15	:	ACTCTTCCAGTC	A Marie						698
LpMDHh16	:	ACTCTTCCAGTC	- Harris						698
LpMDHh17	:	ACTCTTCCAGTC	1994						697
LpMDHh18	:	ACTCTTCCAGTC	N.E.F						698
LpMDHh19	:	ACTCTTNCAGTCA	A PROPERTY AND ADDRESS OF THE PARTY AND ADDRES						698 697
LpMDHh20	:	ACTCTTCCAGTC							697 609
LpMDHh21	:	ACTCTTCCAGTCA ACTCTTCCAGTCA	AGTACCCIGAT	GIGAACCAC	GCCACCG I GA	AGACTICCAG.	CCCCACAAC		698 698
LpMDHh22	:	ACICIICCAGICA	AGIACCCIGAI	GIGAACCAC	GCCACCGIGA	MGACTIMCAG	GGCGAGAAG	:	-
LpMDHh23 LpMDHh24	:							:	_
LpMDHh25	:	ACTCTTMCAGNC	ATACCCTCAT	GTGAACCAC	GCCA CCGMGI	AA C ACŅTNCAC	TGCCNAGAG	:	696
LpMDHh26	:	ACTOTTCCAGTO							646
LpMDHh27	:	ACTCTTÄCAGTC	ATACCCTCAT	GTGAACCAC	GCCACCGTGA	ANACTTTCAG	TGGCGAGAG		697
LpMDHh28	:	ACTCTTCCAGTC							695
LpMDHh29	:	ACTCTTCCAGTC							695
LpMDHh30	:	ACTCTTCCAGTC							696
LpMDHh31	:							:	_
LpMDHh32	:	ACTCTTCCAGTC	AGTACCCTGAT	GTGAACCAC	GCCACCGNGA	AAGACTTCCAG'	rg <mark>n</mark> cgagann	:	696
LpMDHh34	:	ACTCTTCCAGTC	AGTACCCTGAT	GTGAACCAC	GCCACCGTGA	AAGACTTCCAG'	TGGCGAGAAG	:	695
LpMDHh35	:							:	-
LpMDHh36	:							:	-
LpMDHh37	:							:	-
LpMDHh38	:	ACTCTTCCAGTC	AGTACCCTGAT	GTGAACCAC	GCCACCGTGA	AAGACTT I CAG	TGG	:	686
LpMDHh39	:							:	-
LpMDHh40	:							÷	-
LpMDHh41	:							: .	
LpMDHh42	:	ACTCTTCCAGTC.						:	685
LpMDHh43	:	ACTCTTCCAGTC	AGTACCCTGAT	GTGAACCAC	GCCACCGTG/	AAGACTTCCAG	TGGCGAGAAG	:	693
LpMDHh44	:	ACTCTTCCAGTC	AGTACCCTGAT	GTGAACCAC	GCCACCGTG/	AAGACTTCCAG	TGGCGAGAAG		692
LpMDHh45	:	ACTCTTCCAGTC	AATACCCTGAT	GIGAACCAC	GCCACCGTG	AAGACTTNCAG	TGGCGAGAA	:	690
LpMDHh46	:	ACTCTTCCAGTC	A A TACCCIGA'I	GIGAACCAC	GCCACCGTG/	AAGACTTNCAG	IGGCGAGAAG		692
LpMDHh47	:	ACTNTTCCAGTC ACTCTTCCAGTC						•	679 676
LpMDHh48	:	ACTOTTCCAGTO						:	688
LpMDHh49 LpMDHh50	:	ACTCTTCCAGTC ACTCTTCCAGTC	AGTACCCIGAT	CTGAACCAC	CCCACCGIG	AGGACTTCCAG	TGGCGAGAAG	:	666
LpMDHh51	•	ACTOTICCAGIC	ASTACCCIGAT	CTGAACCAC	CCCACCGTC	AAGACTTCCAG	TGGCGAGAAG	;	649
LpMDHh52		ACTOTTCCAGTO	AGTACCCTGAT	TGTGAACCAC	CGCCACCGTG	AAGACTTCCAG	TGGCGAGAAG	:	615
LpMDHh53	:	ACTOTTNCANNO	No TN CCCTGAT	rgňňaňcciic	GCCNCG			:	513
LpMDHh54	:	ACTCTTCCAGTC				AAGACTTCCAG	TGGCGAGAAG	:	366
LpMDHh55	•	ACTCTTCCAGTC						:	288
LpMDHh56	:	ACTCTTCCAGTC						:	268
LpMDHh57	:	ACTCTTCCAGTC						:	264
LpMDHh58	:	ACTCTTCCAGTC						:	67
LpMDHh59	:		-GTACCCTGA	rgrgaacc <u>a</u> (CGCCACCGTG	AAGAC'TTCCAG	TGGCGAGAAG	:	49
LpMDHh60	:						TGGCÄAG-AG	:	14
LpMDHh61	:						GCGAGAAG	:	8
LpMDHh62	:							:	-
LpMDHh63	:							:	-
LpMDHh64	:							:	-

		* 760 * 780 * 800	
LpMDHh1	:	CCTGTTCGCGAACTTGTTAAAGACGATG	770
LpMDHh2	:		: -
LpMDHh3	:		: -
LpMDHh4	:		: -
LpMDHh5	:		: ~
LpMDHh6	:		: -
LpMDHh7	:		: -
LpMDHh8	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGNTCATTGCCACTGTCCA	: 763
LpMDHh9	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAÄGGCTCATTGCCACTGTCCA	: 763
LpMDHh10	:		: -
LpMDHh11	:	CCTGTTC	: 707
LpMDHh12	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 760
LpMDHh13	:		: -
LpMDHh14	:		;
LpMDHh15	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	; 760
LpMDHh16	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 760
	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 759
LpMDHh18	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 760 : 760
LpMDHh19 LpMDHh20	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 760 : 759
-	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTÑAATGCAGGGTTCATTGCCACTGÑCCA	: 759
LpMDHh21 LpMDHh22	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTÄAATGCAGGGTTCATTGCCACTGI9CCA CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTÄAATGCAGGGTTCATTGCCACTGTCCA	; 760 : 760
LpMDHh23	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	. 760
LpMDHh24	:		
LpMDHh25	:		
LpMDHh26	:		•
LpMDHh27	:	CCTGTTCGCGAACT	: 711
LpMDHh28	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 757
LpMDHh29	:		: 757
LpMDHh30	:	CCTGTTCGCGAACTTGÑTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 758
LpMDHh31	:		: -
LpMDHh32	:		: -
LpMDHh34	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 757
LpMDHh35	:		: -
LpMDHh36	:		: -
LpMDHh37	:		: -
LpMDHh38	:		: -
LpMDHh39	:		: -
LpMDHh40	:		: -
LpMDHh41	:		: -
LpMDHh42	:		:
LpMDHh43	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 755
LpMDHh44	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 754
LpMDHh45	:	CCTGTTCG	: 700
LpMDHh46 LpMDHh47	:	CCIGITEG-	: ///
LpMDHh48	:		
LpMDHh49	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 750
LpMDHh50	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 728
LpMDHh51	:	CCTGTTCGCGAACTTGTTAAAGACGAT	: 676
LpMDHh52	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 677
LpMDHh53	:		: -
LpMDHh54	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGCCTAAATGCAGGGTTCATTGCCACTGTCCA	: 428
LpMDHh55	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 350
LpMDHh56	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 330
LpMDHh57	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 326
LpMDHh58	:	${\tt CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCACTGTCCACTGTCCACTGTCCACTGTCCACTGTCACTACTACTACTGTCACTGTCACTGTCACTGTCACTGTCACTGTCACTGTCACTGTCACTGTCACTACACTGTCACTGTCACTGTCACTGTCACTACTGTCACTGTCACTACTACTACTACTACTACTACTACTACTACTACTAC$: 129
LpMDHh59	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 111
LpMDHh60	:	$\texttt{CCTGTTCGCG} \textcolor{red}{\textbf{-}} \texttt{ACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA}$: 75
LpMDHh61	:	CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	: 70
LpMDHh62	:		: -
LpMDHh63	:		: -
LpMDHh64	:		: ~

		*	820	*	840	*	860			
LpMDHh1	:								:	-
LpMDHh2	:								:	-
LpMDHh3	:								:	-
LpMDHh4	:								:	-
LpMDHh5	:								:	-
LpMDHh6	:								:	-
LpMDHh7	:								:	-
LpMDHh8	:	GCAGCGT	GGTGCTGCAA:	TCATCAAAG	CGAG				:	793
LpMDHh9	:	GCAGCGT	GGIGCTGCAA:	FCATCAAAG	NGAGGAAC				:	797
LpMDHh10	:								:	-
LpMDHh11	:								:	-
LpMDHh12	:	GCAGCGT	GGTGCTGCAA	TCATCAAAG	CGAGGAAGCT	CTNCA			:	801
LpMDHh13	:								:,	-
LpMDHh14	:								:	-
LpMDHh15	:	GCAG							:	764
LpMDHh16	:	GCAGCGT	GG						:	769
LpMDHh17	:	GCANCGT	GGTG						٠,	770
LpMDHh18	:	GCAGCGT	GGTGCTGCAA'	TC					:	779
LpMDHh19	:	ACAGCGT	GGTGCTGCAA'	TCATCAAAG	CG				:	788
LpMDHh20	:	ĞCAGCGT	GGTGCTGCAA'	TCATCAAAG	CGAGGAAGC-				:.	794
LpMDHh21	:		'GGTGCTGCÑA'						: •	797
LpMDHh22	:	GCAGCGT	GGNGCTGC-A	TCATCAAAG	CGAGGAAGCT	CTICAGT-			:	802
LpMDHh23	.:								:	-
LpMDHh24	:								:	
LpMDHh25	:								:	-
LpMDHh26	:								:	-
LpMDHh27	:								٠:	-
LpMDHh28	:	GCAGCGT	GGTC						:	768
LpMDHh29	:		GGTGCTGCAA	TCATCAAAC					:	783
LpMDHh30	:	GCAGCGT	GGTGCTGCAA	TCATCAAA	CGAGGAAGCT	CTNCAGTG	G		:	803
LpMDHh31	:								1	-
LpMDHh32	:								:	-
LpMDHh34	:	GCAGCGT	GGTGCTGCAA	TCATA					:	779
LpMDHh35	:								:	-
LpMDHh36									:	_
LpMDHh37	•								:	_
LpMDHh38	•								:	_
LpMDHh39	•								:	_
LpMDHh40	•								:	_
LpMDHh41	:								:	_
LpMDHh42	:								:	_
LpMDHh43	•	GCAGCGT	ie						:	763
LpMDHh44	:		GGTGCTGCAA	TCATCAAA	GCGAGGAAGCT				:	790
LpMDHh45	•					' 			:	-
LpMDHh46	:								:	-
LpMDHh47									:	_
LpMDHh48									:	-
LpMDHh49		GCAGCG	TGGTGCTGCA	TCATCAAA	GCGAGGAAGCT				:	786
LpMDHh50			rggrgcrgca <i>i</i>						:	772
LpMDHh51							• 		:	_
LpMDHh52		GCAGCG'	TGGTGCTGCA	TCATCAAA	GCGAGGAAGCT	CTCCAGTC	CTCTCTCTGC	TGCCAGCT	:	739
LpMDHh53									:	_
LpMDHh54			TGCTGCTGCA	TCATCAAA	GCGAGGAAGCT	TTCCAGTO	CTCTTTTTGC	TGCCAGCT	:	490
LpMDHh55		GCAGCG'	TGGTGCTGCA	TCATCAAA	GCGAGGAAGCT	CTCCAGT	SCTCTCTCTGC	TGCCAGCT	:	412
LpMDHh56							SCTCTCTCTGC		:	392
LpMDHh57							SCTCTCTCTGC		:	388
-		GCAGCG	TGGTGCTGCA	ATCATCA A A	GCGAGGAAGC	CTCCAGTO	GCTCTCTCTGC	TGCCAGCT	:	191
LpMDHh58		GCAGCG	TGGTGCTGCA		GCGAGGAAGCT	'CTCCAGTO	SCTCTCTCTGC	TGCCAGCT	:	173
LpMDHh59							GCTCTCTCTGC		:	137
LpMDHh60							GCTCTCTCTGC		•	132
LpMDHh61									:	~~
LpMDHh63									•	_
Thimuno	•			· -					-	

		*	880	*	900	*	920 *		
LpMDHh1	:							:	-
LpMDHh2	:							:	-
LpMDHh3	:							:	-
LpMDHh4	:							:	-
LpMDHh5	:							:	-
LpMDHh6	:							:	-
LpMDHh7	:							:	-
LpMDHh8	:							:	-
LpMDHh9	:							:	-
LpMDHh10	:							:	-
LpMDHh11	:							:	-
LpMDHh12	:							:	-
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LpMDHh22	•							:	-
LpMDHh23	:							:	-
LpMDHh24	:							:	-
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LpMDHh26	:							:	_
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LpMDHh28	:			- -				:	_
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LpMDHh30	:							:	-
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LpMDHh36	:							•	_
LpMDHh37	:							•	_
LpMDHh38	:							:	-
LpMDHh39	:								_
LpMDHh40	:							:	_
LpMDHh41	:								-
LpMDHh42	:							•	~
LpMDHh43	:							·	_
LpMDHh44	:							•	-
LpMDHh45	:								-
LpMDHh46	:							:	-
LpMDHh47	:							:	_
LpMDHh48	:							•	_
LpMDHh49	:								_
LoMDHh50	:							•	_
LpMDHh51	:							:	_
LpMDHh52	:	CACCAAC	TGACCACATCCGT	'GATT'				:	763
LpMDHh53		-						:	_
LpMDHh54		CTGCTTG	TGACCACATCCGG	GATTGGGT	TCTCGGAACCCC	TGANGGA	ACATTTGTTTCCATG	:	552
LpMDHh55		CTGCTTG	TGACCACATCCGT	GATTGGGT	TCTTGGAACCCC	TGAGGGA	ACATTTGTTTCCATG	:	474
LpMDHh56		CTGCTTG	TGACCACATCCGT	GATTGGGT	TCTCGGAACCCC	TGAGGGAZ	ACATTTGTTTCCATG	:	454
LpMDHh57		CTGCTTC	TGACCACATCCGT	GATTGGGT	TCTCGGAACCCC	TGAGGGA	ACATTTGTTTCCATG		450
LoMDHh58		CTGCTTC	TGACCACATCCGT	GATTGGG	TCTCGGAACCCC	TGAGGGAZ	ACATTTGTTTCCATG	:	253
LpMDHh59		CTGCTTC	TGACCACATCCGT	GATTGGG	TTCTCGGAACCCC	TGAGGGA	ACATTTGTTTCCATG	:	235
LpMDHh60		CTGCTTG	TGACCACATCCG1	GATTGGG	TTCTCGGAACCCC	TGAGGGA	ACATTTGTTTCCATG	:	199
LpMDHh61		CTGCTTG	TGACCACATCCGT	GATTGGG	TCTCGGAACCCC	TGAGGGA	ACATTTGTTTCCATG	:	194
LoMDHh62								:	
LpMDHh63								:	_
	•							-	

		940 * 960	*	980	*		
LpMDHh1	:					:	-
LpMDHh2	:					:	-
LpMDHh3	:					:	-
LpMDHh4	:					:	-
LpMDHh5	:					:	~
LpMDHh6	:					: .	~
LpMDHh7	:					:	-
LpMDHh8	:					:	-
LpMDHh9	:					:	-
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LpMDHh11	:			· · · ·		:	-
LpMDHh12	:					:	-
LpMDHh13	:					:	-
LpMDHh14	:					:	-
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LpMDHh16	:					:	-
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LpMDHh21	:					:	-
LpMDHh22	:					:	-
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LpMDHh24	:					:	-
LpMDHh25	:					:	-
LpMDHh26 LpMDHh27	:					:	-
LpMDHh28	:			,	,	:	-
LpMDHh29	:					:	
LpMDHh29	:					:	-
LpMDHh31	:					:	-
LpMDHh32	:					:	-
LpMDHh34	•					:	-
LpMDHh35	•					:	-
LpMDHh36	:					:	~
LpMDHh37	:					:	-
LpMDHh38	:					:	_
LpMDHh39	:					:	-
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LpMDHh42	:					:	_
LpMDHh43	:					:	_
LpMDHh44	:					:	_
LpMDHh45	:					:	-
LpMDHh46	:					:	-
LpMDHh47	:					:	_
LpMDHh48	:					:	_
LpMDHh49	:						_
LpMDHh50	:					:	_
LpMDHh51	:					:	_
LpMDHh52	:					:	_
LpMDHh53	:					:	-
LpMDHh54	:	GGTGTGTATTCTGATGGNT-ATACNGGGTG	CCTGGTGGGCTT	ATCTACTCCTT)	NCCAGNAAC	: 63	13
LpMDHh55	:	GGTGTGTATTCTGATGGTTCATACGGTGTG	CCTGCTGGGCTT	ATCTACTCCTT	CCCAGTAAC	: 53	36
LpMDHh56	:	GNTGTGTATTCTGATGGTTCATACGGTGTG	CCTGCTGGGCTTA	ATCTACTCCTTC	CCCAGTAAC	: 53	16
LpMDHh57	:	GGTGTGTATTCTGATGGTTCATACGGTGTG	CCTGCTGGGCTT	ATCTACTCCTT	CCCAGTAAC	: 53	12
LpMDHh58	:	GGTGTGTATTCTGATGGTTCATACGGTGTG	CCTGCTGGGCTT	ATCTACTCCTT(CCCAGTAAC	: 3	15
LpMDHh59	:	GGTGTGTATTCTGATGGTTCATACGGTGTG	CCTGCTGGGCTT	ATCTACTCCTT(CCCAGTAAC	: 29	97
LpMDHh60	:	GGTGTGTATTCTGATGGTTCATACGGTGTG	CCTGCTGGGCTT	ATCTACTCCTT(CCCAGTAAC	: 26	61
LpMDHh61	:	GGTGTGTATTCTGATGGTTCATACGGTGTG	CCTGCTGGGCTT	ATCTACTCCTT	CCCAGTAAC	: 2	56
LpMDHh62	:					:	-
LpMDHh63	:					:	-
LpMDHh64	:					:	-

		1000	*	1020	*	1040	*		
LpMDHh1	:							:	-
LpMDHh2	:							:	_
LpMDHh3	•							•	_
LpMDHh4								•	-
LpMDHh5	:								_
LpMDHh6	:							:	_
LpMDHh7	•							:	
LpMDHh8	•							•	-
	:							•	_
LpMDHh9	:							:	-
LpMDHh10	:							:	-
LpMDHh11	:							:	-
LpMDHh12	:							:	-
LpMDHh13	:							:	-
LpMDHh14	:							:	-
LpMDHh15	:							:	-
LpMDHh16	:							:	-
LpMDHh17	:							:	, -
LpMDHh18	:							:	-
LpMDHh19	:							:	· -
LpMDHh20	:							:	-
LpMDHh21	:							:	-
LpMDHh22	:							:	_
LpMDHh23	:							:	-
LpMDHh24	:							:	_
LpMDHh25	:							:	_
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LpMDHh28	:							:	_
LpMDHh29	:							:	_
LpMDHh30	:							:	_
LpMDHh31	•							:	_
T-MOID 3	•							•	_
LpMDHh32	:							:	_
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LpMDHh36	:							:	-
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LpMDHh38	:							:	-
LpMDHh39	:						~~~~~~	:	-
LpMDHh40	:							:	
LpMDHh41	:							:	-
LpMDHh42	:							:	-
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LpMDHh44	:							:	-
LpMDHh45	:							;	-
LpMDHh46	:							:	_
LpMDHh47	:							:	-
LpMDHh48	:							:	_
LpMDHh49	:							:	-
LpMDHh50	:							:	_
LpMDHh51	:							:	_
LpMDHh52	:							:	_
LpMDHh53	:							:	-
LpMDHh54		TTGCTGNGGGGGGG	AATGGAC	AATTGMTCA	AGGCTNCCNA	CNACNAGTT		•	664
LpMDHh55	:	TTGCTGCGGTGGTC						:	598
LpMDHh56	:	TTGCTGCGGTGGT						:	578
LpMDHh57	:	TTGCTGCGGTGGT						:	574
-		TTGCTGCGGTGGTC						:	377
LpMDHh58	:	TTGCTGCGGTGGTC	AAIGGAU	AATIGIICA	AGGGCTCCCGA	rccaccaca	CICAAGAAAGA	-	
LpMDHh59	:							:	359
LpMDHh60	:	TTGCTGCGGTGGTC						:	323
LpMDHh61	:	TTGCTGCGGTGGTC	AATGGAC	AATTGTTCA	GGGCTCCCGA	rogacgagi'il	CTCAAGAAAGA	:	318
LpMDHh62	:				CCTTCCCGA	ANCEGGAGAIA	CITC - HAMMINAG -	:	28
LpMDHh63	:							:	-
LpMDHh64	:							:	-

	1060	*	1080	*	1100	*	
LpMDHh1 :							: -
LpMDHh2 :							: -
LpMDHh3 :							: -
LpMDHh4 : LpMDHh5 :							: -
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LpMDHh27:							: -
LoMDHh28:							: -
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LpMDHh37:							: -
LpMDHh38:							
LpMDHh39:							
LpMDHh40:							: -
LpMDHh41:							: -
LpMDHh42:							: -
LpMDHh43 :							: -
LpMDHh44:							: -
LpMDHh45:							: ~
LpMDHh46:							: -
LpMDHh47:							: ~
LpMDHh48 : LpMDHh49 :							: -
LoMDHh50:							• -
LpMDHh51:							: ~
LpMDHh52:							: -
LpMDHh53:							: -
LpMDHh54:							
LpMDHh55 :	AGATGGATG	CCACAGCCC	AGGAGCTCTCGC	AGGAGAAGG	TOTOCCOT	ACTCGTGCCTCGAG	: 660
LpMDHh56:	AGATGGATG	CCACAGGGG	AGGAGCTCTCGÄ	TAGGAGAAGG(ACTCGTGCCTCGAG	: 640
LoMDHh57:	AGATGGATG	CCACAGCCC	AGGAGCTCTCG	AGGAGAAGG	CTCTCGCCT	ACTCGTGCCTCGAG	: 636
LpMDHh58 :	AGATGGATG	CCACAGCCC	AGGAGCTCTCGC	AGGAGAAGG	TCTCGCCT	ACTCGTGCCTCGAG	: 439
LpMDHh59 :	AGATGGATG	CCACAGCCC	AGGAGCTCTCGC	AGGAGAAGG	TCTTGCCT	ACTCGTGCCTCGAG	: 421
LpMDHh60 :	AGATGGATG	CCACAGCCC	AGGAGCTCTCGC	BAGGAGAAGG	CTCTÖGCCT	ACTCGTGCCTCGAG	: 385
LpMDHh61 :	AGATGGATG	CCACAGCCC	AGGAGCTCTCGC	GAGGAGAAGG	CTCTCGCCT	ACTCGTGCCTCGAG	: 380
LpMDHh62:	aga-ggaĉg	CCACAGCCC	AGGAGCTCTCGC	BAGGAGAAGG	TTNTCGCCT	ACTCGĞGCCTCGAG	: 89
LpMDHh63 :			<u>-</u>	: BAGGAGAAGG	TTCTCGCCT	ACTCGTGCCTCGAG	: 38
LpMDHh64:							

		1120	*	1140	*	•	1160	*	11	
LpMDHh1 :										: -
LpMDHh2 :										: -
LpMDHh3 :										: -
LpMDHh4 :	:									: -
LpMDHh5 :	:									: -
LpMDHh6 :	:									: -
LpMDHh7 :	:									: -
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LpMDHh9 :	:									: -
LpMDHh10:	:									: -
LpMDHh11:	:									: -
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LpMDHh53	:									: -
LpMDHh54	:									: ~
	:	TAACTGCATACC	AGGGAG	CAGCTGCCG	CTCTGA	TGTTTT	GAATAAA	AGGAACAT	TTTGGCTN	: 722
	:	TAACTGCATACC	AGGGAGG	CAGCTGTCG	CTCTGA	TGTTTI	GAATAAA	4-GÏÏACAT	TTTGÑCTN	: 701
	:	TAACTGCATACC	AGGGAG	CAGCTGCCG	CTCT					: 667
	:	TAACTGCATACC	AGGGAG	CAGCTGCCG	CTCTGA	TGTTTT	GAATAAA	AGGAACAT	TTTGGCTC	: 501
LpMDHh59	:	TAACTGCATACC	AGGGAG	CAGCTGCCG	CTCTGA	TGTTTI	GAATAAA	AGGAACAT	TTTGGCTC	: 483
	:	TAACTGCATACC	AGGGAG	CAGCTGCCG	CTCTGA	TGTTTT	GAATAAA	AGGAACAT	TTTGGCTC	: 447
LpMDHh61	:	TAACTGCATACC								l .
	:	TAACTGCATACC								
LpMDHh63	:	TAACTGCATACC	AGGGAG	CAGCTGCCG	CTCTGA	TGTTT	TGAATAAA	AGGAACAT	TTTGGCTC	: 100
LpMDHh64	:									: -

		80 * 1200 * 1220 * 1240		
7 MD77h 7		80 * 1200 * 1220 * 1240		_
LpMDHh1 LpMDHh2	:		:	_
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LpMDHh3 LpMDHh4	:			_
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LpMDHh8	:		:	_
LpMDHh9	•		:	-
LpMDHh10	:		:	_
LpMDHh11	:		:	-
LpMDHh12	:		:	-
LpMDHh13	:		:	-
LpMDHh14	:		:	-
LpMDHh15	:		:	-
LpMDHh16	:		:	-
LpMDHh17	:		:	-
LpMDHh18	:		:	-
LpMDHh19	:		:	-
LpMDHh20	:		:	-
LpMDHh21	:		:	-
LpMDHh22	:		:	-
LpMDHh23	:		:	-
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LpMDHh40	:		:	-
LpMDHh41	:		:	-
LpMDHh42	:		:	-
LpMDHh43	:		:	-
LpMDHh44	:		:	-
LpMDHh45	:		:	-
LpMDHh46	:		:	-
LpMDHh47	:		:	-
LpMDHh48	:		:	-
LpMDHh49	:		:	-
LpMDHh50	:		:	-
LpMDHh51	:		:	-
LpMDHh52	:		:	-
LpMDHh53	:		•	_
LpMDHh54 LpMDHh55	:	CATGAAACTCAT	:	734
LpMDHh56	:		:	705
LpMDHh57			•	-
LpMDHh58	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG	:	563
LpMDHh59	:		:	545
LpMDHh60	:		:	509
LpMDHh61	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG	:	504
LpMDHh62	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG	:	213
LpMDHh63	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG	:	162
LpMDHh64	:		:	-

		* 1260 * 1280 * 1300		
LpMDHh1	:		:	-
LpMDHh2	:		:	-
LpMDHh3	:		:	-
LpMDHh4	:		:	-
LpMDHh5	:		:	-
LpMDHh6	:		:	-
LpMDHh7	:		:	-
LpMDHh8	:		:	-
LpMDHh9	:		:	-
LpMDHh10	:		:	-
LpMDHh11	:		:	-
LpMDHh12	:		:	-
LpMDHh13	:		:	-
LpMDHh14	:		:	-
LpMDHh15 LpMDHh16	:		:	-
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LpMDHh43	:		:	
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LpMDHh46	:		:	-
LpMDHh47	:		:	-
LpMDHh48	:		:	-
LpMDHh49	:		:	-
LpMDHh50	:		:	-
LpMDHh51	:		:	-
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LpMDHh54	:		:	-
LpMDHh55	:		:	-
LpMDHh56	:		:	-
LpMDHh57	:		:	-
LpMDHh58	:	TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG	:	625
LpMDHh59	:		:	607 571
LpMDHh60	:		:	571 566
LpMDHh61	:		:	
LpMDHh62	:	· · · · · · · · · · · · · · · · · · ·	:	275 224
LpMDHh63	:	and the state of t		224 55
LpMDHh64	:	GWAAGWAGCIIIIGIAGCICIAIIIICGCCIGWAGAIIIACAGGACAGG	:	23

		*	1320	*	1340	*	1360		
LpMDHh1	:							: -	
LpMDHh2	:							: -	
LpMDHh3	:							: -	
LpMDHh4	:							: -	
LpMDHh5	:							: -	
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LpMDHh12 LpMDHh13	:							: -	
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LpMDHh54	:							: -	
LpMDHh55	:							: -	
LpMDHh56	:							: -	
LpMDHh57	:							: -	,
LpMDHh58	:		TGGAACAATTTG					: 687	,
LpMDHh59	:		TGGAACAATTTG					: 646	i
LpMDHh60	:		TGGAACAATTTG						i
LpMDHh61	:	GCAGGAAGAI	TGGAACAATTTG	ACGTCTGAT	TAAAACCAAC	CTCTTATTA-		: 616	i
LpMDHh62	:	GCAGGAAGAT	TGGAACAATTTG	ACGTCTGAT	TAAAACCAAC	CTCTTATTAT	TCCTGTGTGTA	: 337	!
LpMDHh63	፡		TGGAACAATTTG					: 265	i
LpMDHh64	:	GCAGGAAGAT	TGGAACAATTTG	ACGTCTGAT	TAAAACCAAC	CTCTTA-TAT	TCCTGTGTGTA	: 116	í

		*	1380	*	1	400	*	1420			
LpMDHh1 :	-								- :		-
LpMDHh2 :									- :		-
LpMDHh3 :	٠								- :		-
LpMDHh4 :	٠								- :		-
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LpMDHh9 :	•								- :		-
LpMDHh10:	•								- :		-
LpMDHh11:									- :		-
LpMDHh12:	•								- :		-
LpMDHhl3:									- :		-
LpMDHh14:											-
LpMDHh15 :											_
LpMDHhl6:									- :		_
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LpMDHh35									- :		_
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LpMDHh56	:								- :		-
LpMDHh57	:							man managara	·- :		740
LpMDHh58	:	TGAATGAGGC	TTTTTGTAG	CTCTATT1				TGATATTGGCAG	<u> </u>		748
- <u>-</u>	:							man ma mmaaaa a	: :	:	
LpMDHh60	:	TGAATGAGGC	T1TTGTAG	CICIAITI	TCGCC1	GATGATI	TACAGGCCA	TGATATTGGCAG	<i>12</i>		695
LpMDHh61	:				meeee		T A C A C C A C 7	TONTATECCOAC	- : - 2		200
- <u>-</u>	:	TGAATGAGGC	TTTTGTAG	CTCTAT"	"I'CGCC'I	GATGATT	TACAGGACA	ATGATATTGGCAG	<u> </u>		399
	:	TC A D TC A CCC	mmmeres e	OTOTA	un/o/c/c/c/c		TACACCCC	ACGATATTGGCAG(- 178
LpMDHh64	:	I GAAL GAGGC	TITIGIAG	CICIAII		CATCALI	IACAGGCCA	COLLEGE TO COLLEGE	• تعد	•	_,,

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LpMDHh6	:		:	_
LpMDHh7	•			_
LpMDHh8	•		:	
LpMDHh9			:	_
LpMDHh10	:		:	_
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LpMDHh27	:	***************************************	:	_
LpMDHh28	:		:	-
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LpMDHh42	:		:	-
LpMDHh43	:		:	-
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LpMDHh45	:	***************************************	:	-
LpMDHh46	:		:	-
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LpMDHh50	:		:	-
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LpMDHh56			:	-
LpMDHh57			:	-
LpMDHh58			:	_
LpMDHh59			:	_
LpMDHh60		GGATTGGAACAATTTGACGCCTGATTAAAACCAACCTCTTATTACTAAAAAAAA	:	750
LpMDHh61			:	_
LpMDHh62		GGATTGGAACAANNANANN	:	418
LpMDHh63			:	_
I DMDUb 64		ሮር እጥጥርር እ አር እ ልጥጥጥር እ ርርርርጥር እጥጥ እ እ አርርር እርርጥርጥጥ እጥጥ እጥጥ እጥጥር ነስ እ እ እ እ እ እ እ እ		226

		*	20	*	40	*	60		
LpMDHi	:	GTNCATAAAGCTGCC	CAAAGCAATN	ICGTGNAATAT	TATCAGTAA	CCTGTCAATI	CTACC	:	60
		*	80	*	100	*	120		
iHGMod		GTACCAATTGCTGCT	• •	AAAAAGCTGG		INCTAAGAGAT			120
- <u></u>	_							•	
		*	140	*	160	*			
T BATTATT	_	CCCCMMCA CA A CATCM	TINTO IN COLORATION IN	יוווים אים אים אים אים אים אים אים אים אים א	maamammia	TATORTOGA COM	TCTNT . 1	77	,

69/241

* 20 * 40 * LpMDHi : XHKAAQSNXXNIISNPVNSTVPIAAEVFKKAGTYNXKRLLGVDNXXMXXTDXALXXRG : 58

LpMDHj	:	* ANAAAGGAGCCGAC	20 GCAGGGGCGCA	* \GAATTCCAT(40 CTGCTNACTC	* TGCCACCACC	60 TAAGTT	:	60
LpMDHj	:	* GGACATGGCGTCAG	80 CTGTTACAATC	* CAGTTCAGTC	100 AGCGCGCAGG	* CCGCTTTGGTT	120 TTCAAA	:	120
LpMDHj	:	* ACCAAGGAACCATG	140 GCAGCACGAGO	* CTACAGTGGC	160 CTAAAGGCAT	* CATCGTCGTCC	180 GATCAG	:	180
LpMDHj	:	· * CTTCGAATCAGGAA	200 CATCATTCCTC	* EGGCAAGACC	220 GCCTCCCTCC	* GGGCAACTGTT	240 TACCAC	:	240
LpMDHj	:	* AAGGGTTGTGCCAA	260 AGGCGAAGTCT	* rgggtcgcag.	280 ATATCGCCTC	* AGGCATCTTAG	300 CAAGGT	:	300
LpMDHj	:	* GGCGGTGCTTGGTG	320 CTGCTGGTGG	* CATCGGTCAA	340 CCACTGGGCC	* TGCTGATCAA	360 SATGTC	:	360
LpMDHj	:	* TCCTCTGGTCTCGG	380 AGCTGCGCCTC	* GTATGATATC	400 GCGAATGTCA	* AGGGCGTCGC		:	420
LpMDHj	:	* TCTCAGCCACTGCA	440 ACACGCCTGC	* ICAGGTCATG	460 GACTTCACTG	* GCCCCGCAGA	480 GCTAGC	:	480
LpMDHj	:	* AGAGTGCTTGAAAG	500 GGTGTGGATGT	.* IGTCGTCATC	520 CCTGCGGGTG	* TCCCAAGGAA	540 GCCAGG	:	540
ьрмонј	:	* CATGACCCGTGATG	560 FACCTTTTAA	* CATNAATGCG	580 GGAATCGNCA	* AGTCGCTTAT	600 TGAGGC	:	600
LpMDHj	:	* TGTTGCAGACAATT	620 FGCCCTGAGGG	* CCTTATTCAT	640 ATCATCAACA	* ACCCCGGTCA	660 AACTCC	:	660
L _Р МОНј	:	CCCT : 664							

LpMDHj	:	* XRSRRRGAEFHLXTLPPE		* SVSAQAAL ¹	40 VSKPRNHGSTSY	* 'SGLKASSSS	60 SIS :	1	60
LpMDHj	:	* FESGTSFLGKTASLRATV			100 YKVAVLGAAGGI	_	.20 CMS :	: :	120
LpMDHj	:	* PLVSELRLYDIANVKGV	LTO		160 ELAECLKGVDVV	_	L80 CPG	: :	180
T:DMDH:i		* MTRDDLFNXNAGTXKSL	. 0 0		220 OTPP : 221				

72/241

		*	20	*	40	*	60		
LpMDHk	:	TNTTTANCCCNCCAA	NTATCCAGN	ANCCACCTGG	CCCTACACAN	AANAAAAACAI	NNAAAA	:	60
			80		100		120		
LoMDHk	:	AACCAGNACGCAAGG		- GGGCGCACGC	100 AGCAATTCCC	ATCTGCTCAC	120 CAACCC		120
p.	•							•	
		*	140	*	160	*	180		
LpMDHk	:	AAGTTGGAGATGGCA	ATCAGCTGTT	ACCATCAGCT(CAGTCAGCGC	GCAGGCCGCT'	TTGGTC	:	180
		*	200	*	220	*	240		
LpMDHk	:	TCGAAACCAAGGAAI		ACAAGCTACA		GGCATCATCA		:	240
-									
		*	260	*	280	*	300		
LpMDHk	:	ATCAGCTTCGAATC	AGGGACATCA:	rtcctgggca:	AGACCGCCTC	TCTTCGGGCG	ACTATC	:	300
		*	320	*	340	*	360		
LpMDHk	:	ACCTCAAGGATTGTC		AAGTCTGGGT		ACCTCAGGCC		:	360
		*	380	*	400	*	420		
трмпнк	:	AAGGTGGCGGTGCTT	rggrgcrgcc	GGTGGCATCG	GTCAACCACT	GGGCCTGCTG	ATCAAG	:	420
		*	440	*	460	*	480		
LpMDHk	:	ATGTCTCCTCTGGT		CGCCTGTATG		TGTCAAGGGA		:	480
		*	500	*	520	*	540		
LpMDHk	:	GCAGATCTCAGCCA	CTGCAACACG	CCTTCTCAGG	TCATGGACTT	CACTGGCCCA	GCAGAA	:	540
		*	560	*	580	*	600		
LpMDHk	:	CTAGCTGACTGCTTC		GATGTTGTCG		GGGTGTCCCA		:	600
		•							
_		*	620	*	640	*	660		
грирнк	:	CCAGGCATGACCCG	rgatgacctt	TTTAACATCA	ATGCGGGCAT	CGTCAAGTCG	CTTATT	:	660
		*	680	*	700	*	720		
LpMDHk	:	GAGGCTGTTGCAGA		GAGGCCTTCA		CAGCAACCCG	_	:	720
T 100 **1-		*	740	*	760	*	780		
тЪмпнк	:	TCCACTGTGCCGAT	TGCTGCTGAG	ATTUTGAAAC	LEDDEDDARDA	CTACAACCCC	AAGAAG	:	780
		*	800	*	820	*	840		
LpMDHk	:	CTCTTCGGGGTTTC		GTTGTCAGAG				:	840
⊺տM∩મՆ		* AACCTCAGCCTCAT	860 Ლ⊄₽Ლ₽₽ Т	* ር ጥርርር አርጥጥር	880 TCGGTGGCCA		900 מרנים מרנים		900
	•							•	

FIGURE 35

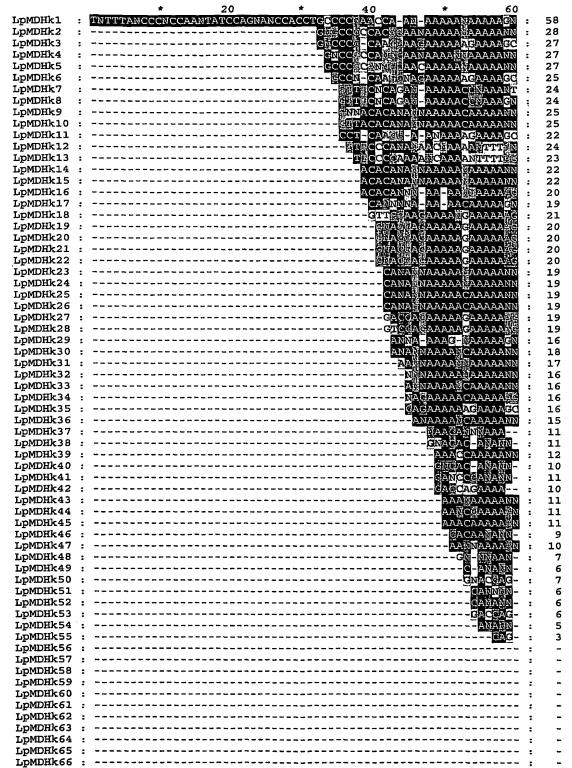
73/241

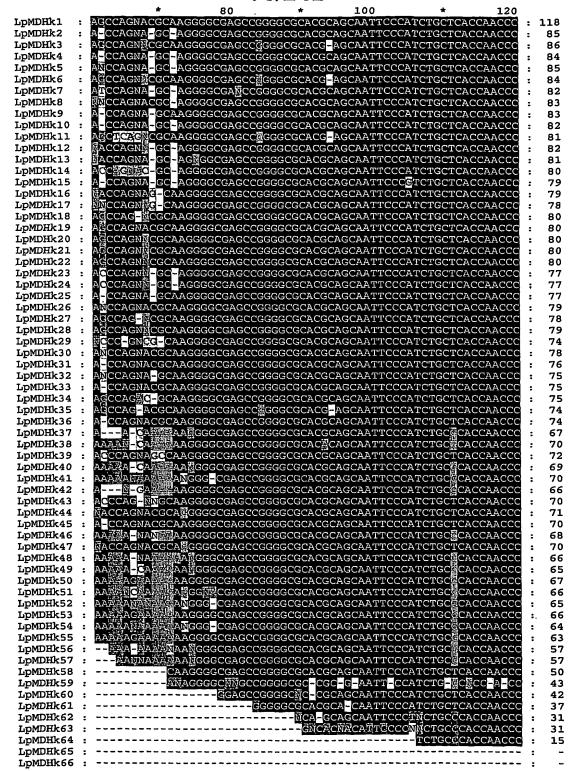
		* 920 * 940 * 960	
LpMDHk	:	CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGGTTCACGGACGAGGAAACTGAACAG	: 960
		* 980 * 1000 * 1020	
LpMDHk	:	CTGACAAAGAGGATACAGAACGCTGGGACAGAGGCGGTGGAGGCGAAGGCTGGTGCTGGC	:1020
		* 1040 * 1060 * 1080	
LpMDHk	:	TCTGCTACTCTGTCCATGGCTTATGCCGCTGCCAGATTTGTTGAGTCATCGCTCCGCGCA	:1080
		* 1100 * 1120 * 1140	
LpMDHk	:	ATGGCTGGTGATCCAGATGTTTACGAGTGCACGTATGTTCAGTCTGAGTTAACAGAGCTT .	:1140
		* 1160 * 1180 * 1200	
LpMDHk	:	CCATTCTTCGCGTCCAGAGTTAAGCTTGGGAAGGACGGNGTTGAGTCCATCATTTCCTCC	:1200
		* 1220 * 1240 * 1260	
LpMDHk	:	GACCTGGAGGAGTGACGAGTACGAGGCCAAGGCGCTTGANGCATTGAAGGCTGAGCTG	:1260

LpMDHk : AAG : 1263

FIGURE 35 (cont.)

		* 20 * 40 * 60		
LpMDHk	:	XLXXQXSXXHLALHXXKTKXNQXARGEPGRTQQFPSAHQPKLEMASAVTISSVSAQAALV	:	60
t.»MD፱៤		* 80 * 100 * 120 SKPRNHGSTSYSGLKASSSSISFESGTSFLGKTASLRATITSRIVPKAKSGSQISPQASY	:	120
дрионк	٠	SKEKNIGDIS IBGEKADDE IDE EDGIDE EGKIADEMILI IDKI VI 161000 STON STON	•	
LpMDHk	:	* 140 * 160 * 180 KVAVLGAAGGIGQPLGLLIKMSPLVSELRLYDIANVKGVAADLSHCNTPSQVMDFTGPAE	:	180
LpMDHk	:	* 200 * 220 * 240 LADCLKGVDVVVIPAGVPRKPGMTRDDLFNINAGIVKSLIEAVADNCPEAFIHIISNPVN	:	240
LpMDHk	:	* 260 * 280 * 300 STVPIAAEILKQKGVYNPKKLFGVSTLDVVRANTFVAQKKNLSLIDVDVPVVGGHAGITI	:	300
LpMDHk	:	* 320 * 340 * 360 LPLLSKTRPSVSFTDEETEQLTKRIQNAGTEAVEAKAGAGSATLSMAYAAARFVESSLRA	:	360
LpMDHk	:	* 380 * 400 * 420 MAGDPDVYECTYVQSELTELPFFASRVKLGKDXVESIISSDLEGVTEYEAKALXALKAEL	:	420
I.nMDHk		K : 421		





			140	*	160	*	180		
LpMDHk1	:	AAGTTGGAGATGGC?						:	178
LpMDHk2	:	AAGTTGGAGATGGC?						:	145
	:	aagttgga <u>@</u> atggc/						:	146
LpMDHk4	:	AAGTTGGAGATGGC <i>i</i>	ATCAGCTGTTAC	CATCAGCTC	AGTCAGCGCG	CAGGCCGCT	TTGGTC	:	144
LpMDHk5	:	AAGTTGGAGATGGC						:	145
LpMDHk6	:	aagttgga <u>@</u> atggc/						:	144
	:	AAGTTGGAGATGGC						:	142
	:	AAGTTGGAGATGGC						:	143
	:	AAGTTGGAGATGGC						:	143
LpMDHk10	:	AAGTTGGAGATGGC			Parent .			:	142
LpMDHk11	:	AAGTTGGNATGGC						:	141
LpMDHk12	:	AAGTTGGGGATGGC						:	142
LpMDHk13	:	AAGTTGGAGATGGC		200				:	141 140
LpMDHk14 LpMDHk15	:	AAGTTGGAGATGGC AAGTTGGAGATGGC						:	139
LpMDHk16	:	AAGTTGGAGATGGC						:	139
LpMDHk17	:	AAGTTGG <mark>EN</mark> ATGGC						:	138
LpMDHk18	•	AAGTTGGAGATGGC.						:	140
LpMDHk19	:	AAGTTGGAGATGGC				100		:	140
LpMDHk20	:	AAGTTGGAGATGGC.						:	140
LpMDHk21	:	AAGTTGGAGATGGC						:	140
LpMDHk22	:	AAGTTGGAGATGGC				100		:	140
LpMDHk23	:	AAGTTGGAGATGGC	ATCAGCTGTTAC	CCATCAGCTC	AGTCAGCGCG	CAGGCCGCT	TTGGTC	:	137
LpMDHk24	:	AAGTTGGAGATGGC	ATCAGCTGTTAC	CCATCAGCTC	AGTCAGCGCG	CAGGCCGCT	TTGGTC	:	137
LpMDHk25	:	AAGTTGGAGATGGC	ATCAGCTGTTAC	CCATCAGCTC	AGTCAGCGCG	CAGGCCGCI	TTGGTC	:	137
LpMDHk26	:	AAGTTGGAGATGGC	ATCAGCTGTTAC	CCATCAGCTC	AGTCAGCGCG	CAGGCCGCT	TTGÄTC	:	139
LpMDHk27	:	AAGTTGGAGATGGC						:	138
LpMDHk28	:	AAGTTGGAGATGGC						:	139
LpMDHk29	:	AAGTTGGGGATGGC						:	134
LpMDHk30	:	AAGTTGGAGATGGC						:	138
LpMDHk31	:	AAGTTGGAGATGGC						:	136
LpMDHk32	:	AAGTTGGAGATGGC						:	135
LpMDHk33	:	AAGTTGGAGATGGC			****			:	135
LpMDHk34 LpMDHk35	:	AAGTTGGAGATGGC AAGTTGGA@ATGGC						•	135 134
LpMDHk36	:	AAGTTGGAGATGGC AAGTTGGAGATGGC						:	134
LpMDHk37	:	AAGTTGGABATGGC						:	127
LpMDHk38	:	AAGTTGGACATGGC	1 7	356	761		\$52- EEE	:	130
LpMDHk39	:	AAGTTGGAGATGGC	in and	248	03.		1999	:	132
LpMDHk40	:	AAGTTGGACATGGC						:	129
LpMDHk41	:	3438	ATCAGCTGTCA(898	198	CAGGCCGC	1037	:	130
LpMDHk42	:	AAGTTGGACATGGC	ATCAGCTGNCA	CCATCAGNTC	CAGTCAGCGC	CAGGCCGC:	retege	:	126
LpMDHk43	:	AAGTTGGAGATGGC	ATCAGCTGTTA	CCATCAGĈTO	CAGTCAGCGCG	CAGGCCGC"	TTGGTČ	:	130
LpMDHk44	:	AAGTTGGAGATGGC	ATCAGCTGTTA	CCATCAGCT	CAGTCAGCGCG	CAGGCCGC	TTTGGTC	:	131
LpMDHk45	:	AAGTTGGAGATGGC	ATCAGCTGTTAG	CCATCAGCTO	CAGTCAGCGCG	CAGGCCGC	TTGGTC	:	130
LpMDHk46	:	AAGTTGGAQATGGC	2.48	della.	200	•	499.0	:	128,
LpMDHk47	:	AAGTTGGAGATGGC	and a		100		mark by	:	130
LpMDHk48	:		ATCAGCTGTGA			CAGGCCGC'	tint 37	:	126
LpMDHk49	:		ATCAGCTGTCA			CAGGCCGC'	粉香 工	:	125
LpMDHk50	:	AAGTTGGACATGGC				CAGGCCGC'	81 E	:	127
LpMDHk51	:	A A CERTACA A TOCAC	ATCAGCTGTGA			CAGGCCGC'		:	126
LpMDHk52 LpMDHk53	:	AAGTTGGAGATGGC	ATCAGCTGTGA	CCATCAGET(CAGTCAGCGC	CAGGCCGC'	rowcere	:	125 126
	:	AAGTTGGAGATGGC AAGTTGGAGATGGC AAGTTGGAGATGGC	ATCAGCGGIGA	CCATCAGRIC	CAGICAGCGC	CAGGCCGC.	POTECTE	:	124
LpMDHk55	:	AAGTTGGAGATGGC	ATCAGCTGTGA	CCATCAGIT	CAGTCAGCGC	CAGGCCGC'	готс	:	123
LpMDHk56	:	AAGTTGGAGATGGC	ATCAGCTGT	CCATCAGTT	CAGTCAGCGC	CAGGCCGC'	retegre	:	117
LpMDHk57	:	AAGTTGGAGATGGC						:	117
LpMDHk58	:	AAGTTGGAGATGGC						:	110
LpMDHk59	:	AAGTTGGAÄATGGC						:	100
LpMDHk60	:	AAGTTGGAGATGG						:	102
LpMDHk61	:	ATTGGAGATGGC	ATCAGCTGTTA	CCATCAGCT	CAGTCAGCGCC	CAGGCCGC'	TTTGGTC	:	95
LpMDHk62	:	A-NTTGGACATGG	ATCAGCTGTĈA	CCATCAGÏT	CAGTCAGCGC	CAGGCCGC	TÖTGGTG	:	90
LpMDHk63	:	-ANTTGGA-ATGG	ATCAGCTGTÇA	CCATCAGTT	CAGTCAGCGC	CAGGCCGC'	PCTGGTG	:	89
LpMDHk64	:	AAGTTGGAGATGG						:	75
LpMDHk65	:							:	-
LpMDHk66	:							:	-

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200
                                                                              220
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         238
LpMDHk1
LpMDHk2
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         205
                  TCGAAACCAAGGAATCATGGCAGCACĜAGCTŢCĘĠTGGCCTAAAGGCATCATCĘĠCGTCG
TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
LpMDHk3
                                                                                                                         206
LpMDHk4
                                                                                                                         204
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
TCGAAACCAAGGAATCATGGCAGCACGAGCTGGGGTGGCCTAAAGGCATCATCGGGCGTCG
TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
LpMDHk5
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LpMDHk6
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LpMDHk7
                                                                                                                         202
LpMDHk8
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LpMDHk9
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TCGAAACCAAGGAATCATGGCAGCACËAGCT∭C@TGGCCTAAAGGCATCATC®∰CGTCG
TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
LpMDHk10
                                                                                                                         202
LpMDHk11
                                                                                                                         201
LpMDHk12
                                                                                                                         202
LpMDHk13
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         201
LpMDHk14
                   {	t TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         200
LpMDHk15
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         199
LpMDHk16
                  {	t TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         199
                                                                                                                         198
LpMDHk17
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                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCGTCG
LpMDHk18
                                                                                                                         200
LpMDHk19
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         200
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         200
LpMDHk20
                  	t TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         200
LpMDHk21
LpMDHk22
                   {	t TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         200
LpMDHk23
                   TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCA@CATCATCGTCG
                                                                                                                         197
LpMDHk24
                   TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         197
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
TCGAAACCAAGGAATC∰TGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         197
LpMDHk25
LpMDHk26
                                                                                                                         199
LpMDHk27
                   TCGAAACCAAGGAATCÄTGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         198
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         199
LpMDHk28
LpMDHk29:
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         194
                   {	t TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         198
LpMDHk30
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
LpMDHk31
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                   TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                          195
LpMDHk32
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LpMDHk33
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                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGCATCATCATCATCGTCG
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TCGAAACCAAGGAATCATGGCAGCACGAGCTGCGGTGGCCTAAAGGCATCATCGGCGCTCG
TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTTAAAGGCATCATCATCGTCG
TCGAAACCAAGGAGTCATGGCAGCACGAGCTGCAGTGGCCTGAAGGCATCATCATCGTCG
TCGAAACCAAGGAGTCATGGCAGCACGAGCTGCAGTGGCCTGAAGGCATCATCATCGTCG
                                                                                                                         195
LpMDHk34
LpMDHk35.
                                                                                                                         194
                                                                                                                         194
LpMDHk36
LpMDHk37
                                                                                                                         187
                                                                                                                         190
LpMDHk38
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTTACAGTGGCCTAAAGGCATCATCGTCG
TCÄAAACCAAGGAÄTCATGGCAGCACĞAGCTÄCAGTGGCCTĞAAGGCATCATCATCGTCG
TCÄAAACCAAGGAĞTCATGGCAGCACĞAGCTĞCAGTGGCCTĞAAGGCATCATCATCGTCG
TCÄAAACCAAGGAĞTCATGGCAGCACĞAGCTÜCAGTGGCCTĞAAGGCATCATCATCGTCG
LpMDHk39
                                                                                                                         192
LpMDHk40
                                                                                                                         189
LpMDHk41 :
                                                                                                                         190
LpMDHk42
                                                                                                                         186
                   TCGAAACCAAGGAÄTCATGGCAGCACÄAGCTÄCAGTGGCCTÄAAGGCATCATCATCGTCG
TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
                                                                                                                         190
 LpMDHk43
 LpMDHk44 :
                                                                                                                         191
                  TCAAACCAAGGAATCATGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
TCGAAACCAAGGAATCATGGCAGCACAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
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TCAAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
TCAAAACCAAGGAATCATGGCAGCACAGAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
 LpMDHk45 :
                                                                                                                         190
                                                                                                                         188
 LpMDHk46:
 LpMDHk47
                                                                                                                         190
 LpMDHk48
                                                                                                                          186
                                                                                                                         185
 LpMDHk49 :
 LpMDHk50 :
                                                                                                                         187
 LpMDHk51 :
                                                                                                                          186
                                                                                       AAGGCATCATCATCGTCG
AAGGCATCATCATCGTCG
                        AAACCAAGGA(ITCATGGCAGCAC
                                                                       CAGTGGCCT
 LpMDHk52:
                                                               AGCT
                                                                                                                         185
                        AAACCAAGGA
                                         TCATGGCAGCAC
                                                               AGCT
                                                                        CAGTGGCCT
                                                                                                                          186
 LpMDHk53
                                         TCATGGCAGCAC
                                                                       CAGTGGCCT
                   TC
                        AAACCAAGGA
                                                               AGCT
                                                                                        AAGGCATCATCATCGTCG
                                                                                                                       : 184
 LpMDHk54 :
                   TCHAAACCAAGGARTCATGGCAGCACGAGCTICAGTGGCCTGAAGGCATCATCATCGTCG
TCHAAACCAAGGARTCATGGCAGCACGAGCTICAGTGGCCTGAAGGCATCATCATCGTCG
TCHAAACCAAGGARTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG
TCGAAACCAAGGARTCATGGCAGCACGAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
TBAAACCAAGGARTCATGGCAGCACGAGCTTCAGTGGCCTTAAGGCATCATCATCGTCG
 LpMDHk55
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 LpMDHk56
                                                                                                                          177
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 LpMDHk57
 LpMDHk58
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 LpMDHk59
                                                                                                                         159
                   TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
 LpMDHk60
                                                                                                                          162
                  TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG
TCÄAAACCAAGGAĞTCATGGCAGCACĞAGCTŢCAGTGGCCTĞAAGGCATCATCATCGTCG
TCÄAAACCAAGGAĞTCATGGCAGCACĞAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG
TCÄAAACCAAGGAĞTCATGGCAGCACĞAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG
                                                                                                                          155
 LpMDHk61 :
 LpMDHk62 :
                                                                                                                          150
 LpMDHk63:
                                                                                                                          149
 LpMDHk64
                                                                                                                          135
 LpMDHk65
 LpMDHk66
```

		* 260 * 280 * 300			
LpMDHk1 :		ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACC <u>A</u> CCTCTCTTCGGGCGACTATC	:	298	
LpMDHk2 :		ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	:	265	
LpMDHk3				266	
LpMDHk4	•	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	:	264	
LpMDHk5	:	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	:	265	
		ATCAGCTTffGAATCAGGGACATCGTTCCTGGGCAAGACffGCCTCGCTffGCGGGCGACTGTT	:	264 262	
LpMDHk7		ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	:	263	
LpMDHk8	:	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	:	263	•
LpMDHk9	•	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	:	262	
LpMDHk11	•	ATCAGCTTijGAATCAGGGACATCĞTTCCTGGGCAAGACĦĠŊĊTCĞCTÄCGGGCGACTĞTŢ	:	261	
LpMDHk12	:	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	:	262	
LpMDHk13	:	ATCAGCTTCGAATCAMGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	:	261	
LpMDHk14	:	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	:	260	
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LpMDHk54	:		:	244	
LpMDHk55	:		:	243 237	
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LpMDHk65	=		:	-	
LoMDHk66	:		:	-	,

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LpMDHk8	:		IGTGCCAAAGGCA IGTGCCAAAGGCA					:	323
LpMDHk9	:		rgtgccaaaggca	220				:	323
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LpMDHk26	:		TGTGCCAAAGGC					:	319
LpMDHk27	:		TGTGCCAAAGGC <i>!</i> TGTGCCAAAGGC <i>!</i>					:	318 319
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LpMDHk30	:.		TGTGCCAAAGGC! TGTGCCAAAGGC!					•	318
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LpMDHk37	:	256 959	TGTGCCAAAGGC			362	3.5	:	307 310
LpMDHk38 LpMDHk39	:		TGTGCCAAAGGC? TGTGCCAAAGGC?					:	312
LpMDHk40	:		TGTGCCAAAGGC			Anna Walt	6200	:	309
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LpMDHk42	:	8017 844	TGTGCCAAAGGC			388	365	:	306
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LpMDHk50	:	888 388	TGTGCCAAAGGC			### C-9	TCTCAC	:	307
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LpMDHk66	:			~				:	_

81/241

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LpMDHk66

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LpMDHk28
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LpMDHk3 :	G	CAGATCT <u>T</u> AGCC	ACTGCAACACGC	CTTCTCAGG	TCATGGACT'	CACTGGCCCG	GCGGAA :		506
LpMDHk4 :		CAGATCTCAGCCA							504 505
LpMDHk5 :	G	CAGATCTCAGCC	ACTGCAACACGC	CTTCTCAGe	TCATGGACT	rcac regette	GCAGAA		5 05
LpMDHk6 :	12	CAGATCTCAGCC	A CTCGA A CA CCC	CTTCTCACC	TO TO TO TO THE	PGA CTCCCCCA	CCAGAA	. ,	502
LpMDHk7 :		CAGATCTCAGCC CAGATCTCAGCC							503
LpMDHk8 :		CAGATCTCAGCC							503
LpMDHk10 :		CAGATCTCAGCC						-	502
LpMDHk11 :	Č	CAGATCTTAGCC	ACTGCAACACGC	CTTCTCAGO	TCATGGACT	TCACTGGCCC	GCGGAA		501
LpMDHk12	Č	CAGATCTCAGCC	ACTGCAACACGC	CTTCTCAGO	TCATGGACT	TCACTGGCCCÄ	GCAGAA	:	502
LpMDHk13 :		GCAGATCTCAGCC.						:	501
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LpMDHk15 :		GCAGATCTCAGCC							499
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LpMDHk19		GCAGATCTCAGCC							500 500
LpMDHk20		ECAGATCTCAGCC ECAGATCTCAGCC							500
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		GCAGATCTCAGCC						:	499
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LpMDHk32		GCAGATCTCAGCC GCAGATCTCAGCC						:	495
LpMDHk33 LpMDHk34		GCAGATCTCAGCC GCAGATCTCAGCC						:	495
LpMDHk35	: 1	GCAGATCT <u>T</u> AGCC	'ACTGCAACACGC	CTTCTCAG	GTCATGGACT	TCACTGGCCC	EGCEGAA	:	494
LpMDHk36		GCAGATCTCAGCC						:	494
LpMDHk37	.	GCGGATCTCAGCC	CACEGCAACACGC	CTGCTCAG	GTCATGGACT	TCACTGGCCC	GCGGAA.	:	487
		GC@GATCTCAGCC						:	490
LpMDHk39		GCAGATCTCAGCC						:	492
LpMDHk40	:	GC@GATCTCAGC(:	489
LpMDHk41	:	GC@GATCTCAGCC				TCACTGGCCC	GCGGAA	:	490
LpMDHk42	:	GCAGATCT <u>T</u> AGC(:	486 490
LpMDHk43	:	GCAGATCTCAGC(GCAGATCTCAGC(:	491
LpMDHk44 LpMDHk45	:.	GCAGATCTCAGC(GCAGATCTCAGC(:	490.
LpMDHk46	•	GC@GATCTCAGC(CACTGCAACACG(CTECTCAG	GTCATGGACT	TCACTGGCCC	GCEGAA	:	488
LpMDHk47	:	GCAGATCTCAGC						=	490
LpMDHk48	:	GCÜGAĞCTCAGC						:	486
LpMDHk49	:	GCCGATCTCAGC	CACTGCAACACG			FTCACTGGCCC		:	485
LpMDHk50	:		CACTGCAACACG			TCACTGGCCC		:	487
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	:	GCCGATCTCAGC	CAC'TGCAACACG(CCTGCTCAC	GTCATGGAC	TTCACTGGCCC	GCGGAA	:	486
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LpMDHk58		GCATATCTCANN	CACTGCAACACG	CCTTCTÑAC	GNCATGGAC	TCACTGGNCC	AÑCAÑAA	:	470
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LpMDHk60		GCAGATCTCAGC	CACTGCAACACG	CCTTCTCAC	GTCATGGAC'	TTCACTGGCCC	AGCAGAA	:	462
LpMDHk61		GCAGATCTCAGC	CACTGCAACACG	CCTTCTCAC	GTCATGGAC	TTCACTGGCCC	AGCAGAA	:	455
LpMDHk62								:	
LpMDHk63		GCCGATCTCAGC	CACTGCAACACG	CCTGCTCAC	GTCATGGAC	TTCACTGGCCC	CGCGGAA	:	-
LpMDHk64		GCCGATCTCAGC	CACTGCAACACG	CCTCCTCAC	-GTCATGGAC	TTCACTGGCCC	CGCGGAA	:	
LpMDHk65		GCÄGATCTCAGC	CACTGCAACACG	CCTGCTCAC	GGCATGGAC	TTCACTGGCCC	CGCGGAA	:	
LDMDHk66	:		C:CTGCAACACG	CCTGCTCAC	ĸĠŖŖĊŔŦĠĠŔĊ	TTCACTGGCCC	CGCGGAA	:	54

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560
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LpMDHk9
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                   CCAGGCATGACCCÄTGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT
CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT
LpMDHk23 :
                                                                                                                                617
LpMDHk24 :
                                                                                                                                617
LpMDHk25
                   CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT
                                                                                                                                617
                   {\tt CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}
LpMDHk26
                                                                                                                                619
LpMDHk27
                   CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT
                                                                                                                                618
                    CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT
LpMDHk28 :
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LpMDHk29:
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LpMDHk30
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                                                                                                                                618
LpMDHk31
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                                                                                                                                616
                    CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT
LpMDHk32 :
                                                                                                                                615
LpMDHk33
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                                                                                                                                615
                   {\tt CCAGGCATGACCCTTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTCGCGGGCATCGTCAAGTCGCTTATTTCGCGGGCATCGTCAAGTCGCTTATTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATTTTAACATCAATGCGGGGCATCGTCAAGTCGCTTATTTTAACATCAATGCGGGGCATCGTCAAGTCGCTTATTTTAACATCAATGCGGGGCATCGTCAAGTCGCTTATTTTAACATCAATGCGGGGCATCGTCAAGTCGCTTATTTTAACATCAATGCGGGGCATCGTCAAGTCGTCAAGTCGCTTATTTTAACATCAATGCAAGTCGGGGCATCGTCAAGTCGTCAAGTCGTCAAGTCGTCAAGTCGTCAAGTCAATGCAAGTCGAAGTCGAAGTCGAAGTCGAAGTCGAAGTCGAAGTCGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAA
 LpMDHk34
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 LpMDHk35
                       <u>fggcatgacficgtgatgacctttttaacatcaatgcgggcatcgtcaagtcgcttatf</u>
                                                                                                                                614
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CCAGGCATGACCCGTGATGACCTTTIITAACATCAATGCGGGCATCGIIICAAGIICGCTTATE
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 LpMDHk39
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CCAGGCATGACCCCTGAGGGCGTTATCAAGACCAACCAAGTCGCTTATE
CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT
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 LpMDHk42 :
 LpMDHk43:
                                                                                                                                610
 LpMDHk44
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 LoMDHk45:
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 LpMDHk46:
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CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTAT
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 LpMDHk48 :
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 LpMDHk49
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                                                                                                                                605
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 LpMDHk51 :
 LpMDHk52 :
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                                                                                                                                606
 LpMDHk53:
 LpMDHk54:
                                                                                                                                604
 LpMDHk55:
                                                                                                                                603
 LpMDHk56:
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                                                                                                                                597
                    CCAGGCATGACCCGTGATGACCTTTTTAACATCÑATGCGGGCATCGTCAAGTCGCTTATC
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 LpMDHk57:
 LpMDHk58:
                          GCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGCCAAGTCGCTTATC
                                                                                                                                579
 LpMDHk59
                                                                                                                                582
 LpMDHk60
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 LpMDHk61 :
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 LpMDHk63
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CCTGGCATGACTGCTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT
CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT
                                                                                                                             : 555
 LpMDHk64:
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 LpMDHk65
 LpMDHk66
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	*	680	*	700	*	720	
LpMDHk1 :	GAGGCTGTTGC	AGACAACTCCCCTG	AGGCCTTCAT	CCATATCATCA	NCNACCC-	:	711
LpMDHk2:	GAGGCTGTTGC					:	647
LpMDHk3 :	GAGGCTGTTGC	AGACAACTGCCCTG	AGGCCTTCAT	CCATATCATCA	GCAACCCG	GTCAAC :	686
LpMDHk4:		AGACAACTGCCCTG.					684
LpMDHk5 :	GAGGCTGTTGC	AGACAACTGCCCTG.	AGGCCTTCAT	CCATATCATCA	GCAACCCG	GTCAAC :	685
LpMDHk6:						:	-
LpMDHk7:						:	_
LpMDHk8 :		AGACAACTCCCCTG				 :	659
LpMDHk9 :		AGACAACTGCCCTG.					683
LpMDHk10 : LpMDHk11 :		AGACAACTGCCCTG					682
LpMDHk12:		AGACAACTGCCCTG. AGACAACTGCCCTG.					681 682
LpMDHk13 :		AGACAACTGCCCTG. AGACAACTGCCCTG.					681
LpMDHk14 :		AGACAACTGCCCTG					680
LpMDHk15 :		AGACAACTGCCCTG					679
LpMDHk16 :		AGACAACTGCCCTG					679
LpMDHk17 :	GAGGCTGTTGC						634
LpMDHk18 :	GAGGCTGTTGC	AGACAACTGCCCTG	AGGCCTTCAT	CCATATCATCA	AGCAACCCG	GTCAAC:	680
LpMDHk19:	GAGGCTGNTGC	AGACAACTGCCCTG.	AGGCCTTCAT	CCATATCATCA	AGCAACCCG	GÑCAAC :	680 ·
LpMDHk20:		AGACAACTGCCCTG					680
LpMDHk21 :		AGACAACTGCCCTG					680
LpMDHk22 :		AGACAACTGCCCTG	AGGCCTTCAT	CCATATCATCA	AGCAACCCG	GTCAAC :	680
LpMDHk23 :	GAGGCTGTTGC					:	628
LpMDHk24 : LpMDHk25 :		'AGACAACTGCCC <mark></mark> 'AGACAACTGCCCTG	ACCCCTTCAT	CCATATCATC	CCAACCC	CTCAAC :	640 677
LpMDHk26:		AGACAAC I GCCC I G AGACAAC I GCCC I G					679
LpMDHk27:	*A*	AGACAACTGCCCTG		14.44			678
LpMDHk28 :		AGACAACTGCCCTG					679
LpMDHk29 :		AGACAACTGCCCTG					674
LpMDHk30 :		AGACAACTGCCCTG					678
LpMDHk31 :	GAGGCTGATGC	AGACAACTGCCCTG	AGGCCTTCAT	CCATATCATCA	AGCAACCCG	GTCAAC :	676
LpMDHk32 :	A349	AGACAACTGCC				:	637
LpMDHk33:	200	AGACAACTGCCCTG					675
LpMDHk34 :		AGACAACTGCCCTG					675
LpMDHk35 :		AGACAACTGCCCTG					674
LpMDHk36		AGACAACTGCCCTG		****			674
LpMDHk37 : LpMDHk38 :		:AGAC <mark>-</mark> ACT -E CCTG :AGACAACTGCCCTG					659
LpMDHk39	#***C	AGACAACTGCCCTG	See the	CCATATEATE			644
LpMDHk40		AGACAACTGCCCTG		CCATATTATC	AGCAACCCG	GTCAAC	669
LpMDHk41 :		AGACAACTGCCCTG					670
LpMDHk42	GAGGCTGTTGC	CAGACAACTGCCCTG	AGGCCTTCAT	CCATATČATC	AGCAACCCG	GTCAAC :	666
LpMDHk43		MGAGANICTA MACEG					637
LpMDHk44 :		AGACAACTGCCCTG					671
LpMDHk45		CAGACAACTGCCCTG			AGCAACCCC	GTCAAC	670
LpMDHk46		CAGACAACTGCCCTG					647
LpMDHk47 : LpMDHk48 :		CAGACAACTGCCCTG CAGACAACTGCCCTG		CCATATCATC			661 640
LpMDHk49		AGACAACTGCCCTG AGACAACTGCCCTG		CCATATTATC	AGCAACCCC	GTCAAC	665
LpMDHk50		CAGACAACTGCCCTG		; 3			667
LpMDHk51	GAGGCTGXTGC	CAGACAACTGCCCTG	SAGGCCTTCAT	CCATATTATC	AGCAACCC	GTCÑA- :	665
LpMDHk52	GAGGCTGTTGC	CAGACAACTGCCCTG	AGGCCTTCAT	CCATATTATC	AGCAACCC	GTCAAC	665
LpMDHk53	: GAGGCTGTTGC	CAGACAACTGCCCTG	AGGCCTTCAT	CCATATTATC	AGCAACCC	GTCAAC :	666
LpMDHk54		CAGACAACTGCCCTG					664
LpMDHk55		CAGACAACTGCCCTG		li di			: 663
LpMDHk56		CAGACAACTGCCCTC					
LpMDHk57	: GAGGCTGNTGC	CAGACAACTGCCCTC	AGGCCTTCAT	CCATATTATC	AGCAACCC	GTCNAC	: 657
LpMDHk58	NACCORORRO		A CCCCCCCC	CCAMAGGAGG	7.007.200	CECA-C	
- F	: MAGGCTGTTG(CAGACAACTCCCTTC CAGACAACTGCCCTC	AGGCCTTCA'	CCATATCATC	AGCAACCCC	GICAAC	639
LpMDHk60 LpMDHk61		CAGACAAC I GCCC I G CAGACAAC I GCCC I G					: 642 : 635
LpMDHk61	:			COATE CATE		CACARO	. 633
	GAGGCTGTTG	CAGACAACTGCCCTG	AGGCCTTCAT	CCATATTATC	AGCAACCC	GTCAAC	629
		CAGACAACTGCCCTG					615
		CAGACAACTGCCCÃG					: 347
LpMDHk66	: GAGGCTGTTG	CAGACAACTGCCCAC	AGGCCTTCAT	CCATATCATC	AGCAACCC	GTCAAC	: 234

		0//2-11	
		* 740 * 760 * 780	
LpMDHk1	:		: -
LpMDHk2	:	TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: -
LpMDHk3	:	TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 746
LpMDHk4	:	TMCACTGT	: 692
LpMDHk5	:	TNCACTGTGA	: 695
LpMDHk6	፡		: -
LpMDHk7	:		: -
LpMDHk8	:		: -
LpMDHk9	:	TMCACTGTGCCGATTGCTGCTGA	: 706
LpMDHk10	:	TCCACTGTGCCGATTGCTGCTGAA	: 706
${ t LpMDHkll}$:	TCCACEGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTNTACAACCCCAAGAAG	: 741
LpMDHk12	:	TNCACTGTG	: 691
LpMDHk13	:	TMCACTGTGCCGATTGCTGCTGAG	: 705
LpMDHk14	:		: -
LpMDHk15	:	TCCACTGTGCCGATTGCTGCTGAGAT	: 705
LpMDHk16	:	TMCACTGTGCCGATTGCTGCTGAGATA	: 706
LpMDHk17	:		: -
LpMDHk18	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 740
LpMDHk19	:	TCCACTGNGCCGATTGCTGCTGANATTCTGAAACANAAGGGCGNNTACAACCCCAANAAG	: 740
LpMDHk20	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 740
LpMDHk21	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 740
LpMDHk22	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 740
LpMDHk23	:		: -
LpMDHk24	:		: -
LpMDHk25	:	TCCACTGTGCCGATTGCTGCT	: 698
LpMDHk26	:	TNCACTGTGCCGATTGCTGCTGAGATTCTGAAAN	: 713
LpMDHk27	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 738
LpMDHk28	٤,	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 739
LpMDHk29	:	TTCACTGTGC	: 684
LpMDHk30	:	TNCACTGTGCCGATTGH	: 695
LpMDHk31	:	TMCACTGTGCCGATTGCTG	: 695
LpMDHk32	:		: ~
LpMDHk33	:		:
LpMDHk34	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGGCGTNT-CGACCCCAAGAAG	: 734
LpMDHk35	:	TCCAC@GTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 734
LpMDHk36	:	TNCACTGTGCCGATTGCTGCTGAGATTCTGAA	: 706
LpMDHk37	:	TGCACGGTGCCGATTGCTGNAAT	: 682
LpMDHk38	:	TCCACGG GCCGATTGNTGCXGAGATTCTGAAACAGAA-GGCGT	: 712
LpMDHk39	:		: -
LpMDHk40	:	TNCACGGTGCCGAT	: 683
LpMDHk41	:	TCCACGGTGCCGATTGCTGCAGAGA	: 695
LpMDHk42	:	TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 726
LpMDHk43	:		: -
LpMDHk44	:	TNCACTGTGCCGATT	: 686
LpMDHk45	:	TNCACTGTGCCGATTGCTGCTG	: 693
LpMDHk46	:	**	: ~
LpMDHk47	:		: -
LpMDHk48	:	mach occupance a remaining	: -
LpMDHk49	:	TCCACGGTGCCGATTG	: 681
LpMDHk50	:	TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 727
LpMDHk51	:	PINCA CCC PROCECCIA IDM	: -
LpMDHk52	:	TMCACGGTGCCGATM	: 680
LpMDHk53	:	TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 726
LpMDHk54	:	TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAG	: 702
LpMDHk55 LpMDHk56	:	TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 723
-	:	TŃCACĞGTGCCGATTGCTGCÄĞAGATTCTGAAACA-AAÄGGCGTCTACAAC	: 707
LpMDHk57 LpMDHk58	•	CONCENSE COATT GRIFGE HAMATTAN GE	: 687
_	:	PMC	:
LpMDHk59	:	TNCTOCACTGTGCCGATTGCTGAGGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 642
LpMDHk60 LpMDHk61	:		: 702
LpMDHk62	:	TNCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAĞCCCCAAGAAG	: 695
-	:	7	: -
LpMDHk63 LpMDHk64	:	TMCACCCCCATTCCCTACACACACACACACACACACACAC	: 630
LpMDHk65	:	TNCACGGTGCCGATTGCTGCAGAGTTCTGAAACAGAAGGGCGTCTACAACCCCAA TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGTGTCTACAACCCCAAGAAG	: 671
LpMDHk66		MOCA CHOMOCOCO MECCHOCODO CA CHOMOCO CA	: 407
-P.:	•	TOCHOTO TOCOMITTO COMONITO CONTACA GARAGOGI, GICIACARCOCCAAGAAG	: 294

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LpMDHk2	:		: -
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LpMDHk4	:		: -
LpMDHk5	:		
LpMDHk6	:		
LpMDHk7	:		
LpMDHk8	:		
LpMDHk9	•		•
LpMDHk10	•		: -
LpMDHk11	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCA¶AANAAN	: 801
LpMDHk12	:		
LpMDHk13	:		
LoMDHk14	:		
LpMDHk15	:		• -
LpMDHk16	:		• -
LpMDHk17	:		• -
LpMDHk18	:	CTCTTCGGGGTTTCCACC	: 758
LpMDHk19	:	CTCTTWGGGGWTTWCACCCTG	: 761
LpMDHk20	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAA	: 772
LpMDHk21	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAN	: 772
LpMDHk22	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAMAAGAAG	: 800
LpMDHk23	:		: -
LpMDHk24	:		-
LpMDHk25	:		
LpMDHk26	:		
LpMDHk27	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGA	: 771
LpMDHk28	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAG	: 773
LpMDHk29	:		: -
LpMDHk30	:		: -
LpMDHk31	:		: -
LpMDHk32	:		: -
LpMDHk33	:		: -
LpMDHk34	:	CTWTTCNGGGNTTACACCCTGGATGTTGGC	: 764
LpMDHk35	:	CTCTTCGGGGNTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCT	: 785
LpMDHk36	:		: -
LpMDHk37	:		: -
LpMDHk38	:		: -
LpMDHk39	:		: -
LpMDHk40	:		: -
LpMDHk41	:		: -
LpMDHk42	:	CTCTTCGGGGTTTMCACCCTGGATGTTGTCAGAGCTAACACATTTGNAGCTCAMAANAAG	: 786
LpMDHk43	:		: -
LpMDHk44	:		: -
LpMDHk45	:		: -
LpMDHk46	:		: -
LpMDHk47	:		: -
LpMDHk48	:		: -
LpMDHk49	:		: -
LpMDHk50	:	CTCTTCGGGGTTTC	: 741
LpMDHk51	:		: -
LpMDHk52	:		: -
LpMDHk53	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGGGCTAACACATT	: 770
LpMDHk54	:		: -
LpMDHk55	=	CTCTTCGGGGTTTCCCCCCTGGATGTTGTCAGGGCTAACACATTTGTAGCTCA	: 777
LpMDHk56	:		: -
LpMDHk57	:	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	: -
LpMDHk58	:		: -
LpMDHk59	:		: -
LpMDHk60	:	$\tt CTCTT\underline{C}GGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG$: 762
LpMDHk61	:	CTCTTA	: 701
LpMDHk62	:		: -
LpMDHk63	:		: -
LpMDHk64	:	***************************************	: -
LpMDHk65	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG	: 467
LpMDHk66	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG	: 354

		*	860	*	880	*	900	
LpMDHk1 :							;	-
LpMDHk2 :							;	; -
LpMDHk3 :				~-~				: -
LpMDHk4 :							;	: -
LpMDHk5 :							:	: -
LpMDHk6 :							:	: -
LpMDHk7 :								: -
LpMDHk8 :								: -
LpMDHk9 :								-
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LpMDHk60	:		:	-
LpMDHk61	:		:	-
LpMDHk62	:		:	_
LpMDHk63	:		:	-
LpMDHk64	;		:	-
LpMDHk65	:		:	-
LpMDHk66	:	AAG	:	777
_p	•	-	•	

		* 20 * 40 * 60		
LpMDH1	:	GNAAACAGNNGCGNCTTTTCCTNCANTGTTGCCGTGCAATCGCTGANAAGTATCCAGAAA	:	60
LpMDHl	:	* 80 * 100 * 120 TCATATACGAGGAAGTAATTATTGATAACTGCTGTATGACGCTCGTGAAGAACCCTGGTA	:	120
LpMDHl	:	* 140 * 160 * 180 CGTTTGATGTATTAGTGATGCCAAATCTATATGGCGACATTATTAGTGATCTATGTGCTG	:	180
LpMDH1	:	* 200 * 220 * 240 GTTTGATCGGAGGCTTGGGCCTAACTCCCAGCTGCAACATTGGTGAAGGTGGCATTTGTC	:	240
LpMDHl	:	* 260 * 280 * 300 TTGCAGAGGCTGTCCATGGCTCTGCACCTGATATATCTGGCAAGAACCTGGCAAACCCAA	:	300
LpMDHl	:	* 320 * 340 * 360 CTGCTCTTATGCTGAGTGCTGTTATGATGTTGCGCCACTTGCAATTNAACGACCAAGCAN	:	360
THOMOST	•	* 380 * 400 * AACGGATCCACAATGCTATCCTCCAGACTATCGNCGAGGGGAAGNACANAACTG : 414		

LpMDHl	:	* KQXXLFXXCCRAIAXKYI	20 PEIIYEEVIID	* NCCMTLVKI	40 NPGTFDVLVMPN	* LYGDIISDI	60 CAG	:	60
LpMDH1	:	* LIGGLGLTPSCNIGEGG	80 ICLAEAVHGSA	* PDISGKNL	100 ANPTALMLSAVM	* MLRHLQXNI	120 DQAX	:	120
TroMDHl		* RIHNAILQTIXEGKXXT	: 137						

99/241

LpMDHm	:	* GNCACCNCCAGNNA	20 CAACTCTGGT	* ACCTCAATTG	40 CTACTCCACA	* CCTCACTACTI	60 CTACC	:	60
		*	80	*	100	*	120		
LpMDHm	:	AATCCACTACACAG		CCCGCCCC		CTACCTCTCC		:	120
LpMDHm	:	* AATCTACAACATGA	140 AGGCAGTCGT	* AGCTGGAGCC	160 GCCGGTGGCA'	* TTGGACAGCCI	180 TTGTC	:	180
LpMDHm	:	* CCTCCTCCTTAAGA	200 ACCTGCCCGCT	* CGTCACTGAG	220 CTCGCCCTAT	* ACGATGTCGT(240 CAACGC	:	240
LpMDHm	:	* CGTCGGTGTCGCGF	260 ACTGACCTCTC	* CCACATCTCC	280 TCGCCCGCGA	* AAGTAACCGG	300 CTACCT	:	300
LpMDHm	:	* GCCGGCAAATGACG	320 GTATGCAGCA	* GCTCTCACT	340 GGCGCCGACA	* TCGTGGTCAT	360 CCCCGC	:	360
LpMDHm	:	* TGGTATTCCCCGC	380 AGCCGGCAT	* GACCCGTGAC	400 CGACCTCTTCA	* AGATCAACGC(420 CGGCAT	•:	420
LpMDHm	:	* TGTCCAGGGTCTC	440 ATCGAGGGTGT	* CGCCAAGCAC	460 CTGCCCAAGG	* CATACGTTCT(480 CGTCAT	.:	480
LpMDHm	:	* CTCCAACCCGTC	500 AACTCGACTGT	* GCCCATCGCC	520 CGCCGAGGTGC	* TGAAGAAGGC	540 CGGTGT	:	540
LpMDHm	:	* CTTCGACCCCAAG	560 AAGCTCTTCGG	* TGTCACCAC	580 CCTCGATGTCG	* TCCGCGCCGA	600 GACCTT	:	600
LpMDHm	:	* CGTTGCCGAGATC	620 ACTGGCGAGAA	* .GGACCCAGC(640 SAAGTTGAACA	* TNCCCGTA :	652		

FIGURE 40

		*	20	*	40	*	60		
LpMDHm	:	XXPXTTLVPQLLLH	TSLLLPIHYT	ASSYPAPAIQ:	rtsp*QIYNM	KAVVAGAAGG	IGQPLS	:	59
		*	80	*	100	*	120		
LpMDHm	:	LLLKTCPLVTELAL	YDVVNAVGVA:	TDLSHISSPAI	KVTGYLPANDO	GMQQALTGAD	IVVIPA	:	119
		*	140	*	160	*	180		
LpMDHm	:	GIPRKPGMTRDDLF	KINAGIVQGL:	IEGVAKHCPK	AYVLVISNPVI	NSTVPIAAEV	LKKAGV	:	179
		*	200	*					
T MIDITI-	_	DDDWWT DOWNING DV	र साम के राज का का विकास	או או אורורועודויטיו	יותע . מוכי				

101/241

		*		20	*	40	*	60		
ToPEPCa	•	GNGTACACGA	AATAGAA'	TCAACGGAAAGC	ANGAAGTG	ATGATTGGGTAT	CAGCATTC	TGG	:	60
DP	•									
		*		80	*	100	*	120		
T.nDFDCa		СУУССУТССТ	ינגררנידידי	тстствстввтт	GGCACTTG	TACAAAGCTCAA			:	120
приниса	•	OAROORIOCI	0000011	.0.0.0.0						
		*	,	140	*	160	*	180		
T.nDWDCa		ጥ እ ለረረጥፕርረር			ייים אריים אייים	TTTCATGGACGA			:	180
пренеса	•	IMMOOTIGGG	.011011001							
		*	,	200	*	220	*	240		
ToDEDCa		тссаасасст			CTATACTO	TCACAACCTCCA	GATACTGT	'CCA	:	240
привиса	•	100111011001								
		*	r.	260	*	280	*	300		
T.DDFDCa		ጥሮሮልጥሮልሮጥፕ	тсссстаа		AAGTCATT	rGAGCAGTCCTTC	CGGAGAGGA	GCA	:	300
пренеси	•	100111011011	.000-11-							
		*	ŧ	320	*	340	*	360		
TINDEPCA		ադունդունարարդ	PAGAACGC		ACAGCTGC	FACTCTTGAACA?	rggtatgca	TCC	:	360
приниса	٠	111010111								
		*	k	380	*	400	*	420		
T _D DEPCa		ACCAATCTCA	ACCTAAAC		CTTTGAT	GGATGAAATGGC	CTTGTTGC	CAC	:	420
PP: D: CG	•	11001111010								
		+	k	440	*	460	*	480		
Loperpoa		AGAGGAATAC	CCGTTCC		BAACCAAG	ATTTGTTGAGTA	TTTCCGCC7	TGC	:	480
-p	•									
		1	*	500	*	520	*	540		
LpPEPCa	:	AACACCAGAG	GCTCGAGT	TATGGTAGGATG	AATATTGG	AAGCAGGCCATC	AAAACGTAA	AGCC	:	540
	-									
		•	*	560	*	580	*	600		
LpPEPCa	. :	AAGCGGAGG!	AATCGAA!	CATTGCGTGCA	ATTCCTTG	GATATTTGCTTG	GACACAGA	CTAG	:	600
		,	*	620	*	640	*	660		
LpPEPCa	. :	ATTCCACCT	GCCAGTG'	FGGCTTGNTTTT	GGTGCGGC	CTTCAAGCATGT	CCTGCAAA	AGGA	:	660
-										
		•	*	680	*	700	*	720		
LpPEPCa	ι :	CATTCGTAN	TCTTCAA	ATCCTTCAGCAG	ATGTACAA	CGAGTGGCCGTT.	TAGGGTTA	CCAT	:	720
-										
			*	740	*	760				
T.かDEDCa		ልልልሮሮፕሮርና ፕ	TGAGATG	GTGTTTGCCAAG	GGCGATCC	AGGTATAGCAGC	T: 769			

FIGURE 42

LpPEPCa	:	* XTRNRINGKXEVMIGYQ	20 HSGKDAGRFSAG	* WHLYKAQE	40 ELIKVAETFGVF	* XTMFHGRG	60 GTV	:	60
LpPEPCa	:	* GRGGGPTHLAILSQPPD	80 TVHGSLRVTVQO	* SEVIEQSFG	100 EEHLCFRTLQRI	* TAATLEHO	120 MHP	:	120
LpPEPCa	:	* PISPKPEWRALMDEMAV	140 VATEEYRSIVF(* QEPRFVEYF	160 RLATPELEYGRI	* MNIGSRPSI	180 KRKP	:	180
LpPEPCa	:	* SGGIESLRAIPWIFAWI	200 'QTRFHLPVWLX	* FGAAFKHVI	220 LQKDIRXLQILQ	* OMANEMbel	240 RVTI	:	240
T. DEDCa		* NI.VEMVFAKGDPGTAA	: 256						

103/241

			20	*	40	*	60		
_		* -~ ~~~ ~ ~~	20 	יי יייטאזיייכיזייכיריי	ጥሬሮ <mark>ል</mark> ሬልሬሮሞሮሮ	CAGCAGATTO	TT:		60
LpPEPCb :	GAAGAAGTT	rgctgatgt	TTTAAGNACATI	INIGICCI	IGCAGAGCICC	C. 10 C. 10 - 1			
				_		"	120		
		*	80	*	100			1	L20
ImPEPCb:	TTGGTGCT	TACATCATC	TCAATGGCAACT	CCCCATC	TGATGTGCTTG	CTGTTGAGC.	1.1.1		-20
11p1									
		*	140	*	160		180		
r-nench	TOTACTOR	састсссат	ATAAAAAAGCC	ATTGAGAGI	TGTTCCACTAT	TTGAAAAGC'	TTG :	J	180
Pbbgbcn:	IGCAGCGG	GAG10CC11							
			200	*	220	*	240		
	·	*	200 CCAGCATCTGT	יי מכולות בילות לייו	ያይያ የአጥጥጥጥር እስጥ እና	ACTGGTACA	TGA :	. :	240
LpPEPCb :	CAGATCTT	GAANCAGC	CCAGCATCIGI	1 GCACGAC	MIIIICAMING	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			
							300		
•		*	260	*	280				300
Imperech :	ATAGAATO	AATGGCAA	260 SCAGGAGGTCAT	GATTGGAT	ACTCAGACTCT	3GGAAGGACG	CIG :	•	300
Dp::									
			•	•					
		*	320	*	340	*	360		
	adadment	TOTAL CALCA	GTGGCAAATGTA	TAAAGCAC	AAGAAGATCTC	ATAAAGGTGG	CAA	:	360
Pbberco:	GGCGTCTC	,1C1GCAGC	G100CHH11011						
					400	*	420		
		*	380	~ ~	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	ርጥጥርርር ር <u>ነ</u> ር አርነልር			420
LpPEPCb :	AGCAATAT	rggagtaaa	GTTAACAATGTT	TCATGGAA	GAGGIGGAACG	GIIGGCHOM		•	
-									
		*	440	*	460	*	480		400
Tabedch .	CTCCTCC	CAGTCATCT	TGCTATATTAT	TCAACCAC	CAGACACGATA	.CAAGGATCA	CTTC	:	480
превесо .	. 0100100	0							
			500	*	520	*	540		
			CGAGGTCATAG	ለረረአረጥሮልባ	ттссасасса	CACTTGTGC	TTCA	:	540
LpPEPCb :	: GTGTAAC	AGTT CAAGG	CGAGGICAIAG	AGCIAC I CIVI					
				-	E00	•	600		
		*	560	*	580				600
LoPEPCb	: GAACTCT	GCAACGTT1	CACTGCAGCTA	CTCTTGAGC	CATGGAATGCAT	CCICCAAII	ICAC	•	000
- F									
		*	620	*	640	*	660		
r DEDCh		י א כו א א ידכוכר כ	3TGCTATAATGG	ATGAGATG	GCTGTAGTGGC?	AACAAAAGAA	TATC	:	660
грьвьср	: CCAAGCC	AGAATOOC	31001						
			C00	•	700	*	720		
	_	-	680	 	_ヤ ッとででででででででで	GCAACACCT		:	720
LpPEPCb	: GATCAAI	TGTCTTCC	AAGAACCACGTT	TIGICGAA	INCTICCOCIC			-	
					560		780		
		*	740	*	760	* ~~~~~~~			700
TIDPEPCh	: CTGAATA	ATGGTCGGA	TGAATATTGGTA	GCCGGCCA	TCAAAGAGAAA	GCCTAGTGGA	AUUUA	:	780
TPI BI CD									
		*	800	*	820	*	840		
		חמטיים מיים	CAATTCCATGG	TCTTTGCT	TGGACACAGAC	AAGGTTTCA:	rcttc	:	840
PDEELCD	: TAGAAT	-9-1-6-16	CULTICOLIGI						
			0.50		880	*	900		
		*	860	~ ~~~~~~~~	VOU ™™™™™™™™™™™				900
LpPEPCb	: CTGTAT	GGCTTGGAI	TTGGTGCAGCG	I'I'CAAACAT	ATCATGCAGAA	CONCAL CAC	OLIVA	•	200

FIGURE 44

PCT/AU2004/000493 WO 2004/089066

104/241

		* 920 * 940 * 960		0.00
ГЪБЕРСР	:	TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCTTGACTTGC	:	960
Lppepcb	:	* 980 * 1000 * 1020 TTGAGATGGTTTTTGCCAAGGGAGATCCAGGAATTGCTTGTTATATGACAAATTGCTTG	:	1020
LpPEPCb	:	* 1040 * 1060 * 1080 TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACTTTGAAGAGACGAAAC	:	1080
LpPEPCb	:	* 1100 * 1120 * 1140 AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC	:	1140
LpPEPCb	:	* 1160 * 1180 * 1200 AGCGTCTGCGGTTGCGTGAGTCATACATCACAACATTGAATGTTTGCCAAGCCNACACCC	:	1200
LpPEPCb	:	* 1220 * 1240 * 1260 TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTCGAAGG	:	1260
LpPEPCb	:	* 1280 * 1300 * 1320 AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG	:	1320
LpPEPCb	:	* 1340 * 1360 * 1380 CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTATTTGCTGTGGAATGCAAA	:	1380
LpPEPCb	:	* 1400 * 1420 * 1440 ACACAGGCTAGGCCAGTTTGCCTATTTGGAATAACTGTCATCCCGTCAGATGGGGCGTGA	:	1440
LpPEPCb	:	* 1460 * 1480 * 1500 ATATGTGTGTCCCCAAATGCTAGTGAACCCTGGAGGCATTTTGGCCACTTACATGCCTT	:	1500
LpPEPCb	:	* 1520 * 1540 * 1560 TTGGTTATGGATGNACTTTGATCTTAATGNCAAGGGTTGTTGAAGCCTGATCTAAATAAA	:	1560
LpPEPCb	:	* 1580 * 1600 * 1620 ATATGGAACAATGATATTCTGGTNGGATCTAATAATTTGCTTGGCTCTGGCATCGNAATA	:	1620
		* 1640		

LpPEPCb : GNGATTTGGAGTNGTTTAAC : 1640

		. 20 " 40 " 60		
LpPEPCb	:	RSCXCFKXIXVLAELPADCFGAYIISMATAPSDVLAVELLQRECHIKKPLRVVPLFEKLA	:	60
LpPEPCb	:	* 80 * 100 * 120 DLEXAPASVARLFSIDWYMNRINGKQEVMIGYSDSGKDAGRLSAAWQMYKAQEDLIKVAK	:	120
LpPEPCb	:	* 140 * 160 * 180 QYGVKLTMFHGRGGTVGRGGGPSHLAILSQPPDTIQGSLRVTVQGEVIEHSFGEEHLCFR	:	180
LpPEPCb	:	* 200 * 220 * 240 TLQRFTAATLEHGMHPPISPKPEWRAIMDEMAVVATKEYRSIVFQEPRFVEYFRSATPET	:	240
LpPEPCb	:	* 260 * 280 * 300 EYGRMNIGSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIMQKDIRNI	:	300
LpPEPCb	:	* 320 * 340 * 360 HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSEDLQPFGEQLRNNFEETKQ	:	360
LpPEPCb	:	* 380 * 400 * 420 LLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAXTLKRIRDPSFEVTPQQAPLSKE	:	420
LpPEPCb	:	* 440 * 460 FADEKEPAELVQLNRGSEYAPGLEDTLILTMKGICCGMQNTG : 462		

	*	20	*	40	*	60	
LpPEPCb1 :	GAAGAAGTTGCTG	ATGTTTTAAGNA	CATTINTGI	CCTTGCAGAG	CTCCCAGCAG.	ATTGTT : 6	0
LpPEPCb2 :							-
LpPEPCb3 :							_
LpPEPCb4:							_
LpPEPCb5 :						:	_
LpPEPCb6:							
PDPERCOG :						:	-
	*	80		100	*	120	
z-nmochi	TTGGTGCTTACAT		A A OBOOOG				^
LpPEPCb1 :	TIGGIGCITACAT	CATCTCAATGGC	AACTGCCCC	AICIGAIGIG	CITGCTGTTG	AGCTTT : 12	U
LpPEPCb2 :						:	-
LpPEPCb3 :						:	_
LpPEPCb4:						:	_
LpPEPCb5:						: '	_
LpPEPCb6 :						:	-
	*	140	*	160	*	180	
LpPEPCb1 :	TGCAGCGGGAGTC	SCCATATAAAAA	AGCCATTGAC	BAGTTGTTCCA	CTATTTGAAA	AGCTTC: 18	0
LpPEPCb2 :						:	-
LpPEPCb3 :						:	-
LpPEPCb4 :						:	
LpPEPCb5:						:	_
LpPEPCb6 :						:	_
-							
	*	200	*	220	*	240	
LpPEPCb1 :	CAGATCTTGAAN(CAGCTCCAGCAT	CTGTTGCAC	GACTATTTCA	ATAGACTGGT	ACATGA: 24	0
LpPEPCb2 :						;	_
LpPEPCb3 :							_
LpPEPCb4:							_
LpPEPCb5:							_
LpPEPCb6:		· ·					_
nprarcuo .						•	
	*	260	*	280	*	300	
LpPEPCbl :	ATAGAATCAATG		TCATCATTC		TCTCCCAACC		١٥
-	AIAGAAICAAIG	CAAGCAGGAGG	ICAIGAIIG	JAIACI CAGAC	CICICCAROC	·	-
LpPEPCb2 :							_
LpPEPCb3 :							_
LpPEPCb4:						:	_
LpPEPCb5 :						;	-
LpPEPCb6 :						:	-
	.4.	200	.4.	240	4.	360	
	*	320	×	340	*		
LpPEPCb1 :	GGCGTCTCTCTG						
LpPEPCb2 :			-GTATAAAG	CACAAGAAGAT	CTCATAAAG	FIGGCAA :	35
LpPEPCb3 :						·:	-
LpPEPCb4 :						: .	-
LpPEPCb5 :	'					:	-
LpPEPCb6 :						·:	-
					_		
	*	380	*	400	*	420	
	AGCAATATGGAG	TAAAGTTAACAA	TGTTTCATG	GAAGAGGTGG <i>I</i>	ACCCTTCCC	AGAGGAG : 42	20
LpPEPCb2 :	AGCAATATGGAG	TAAAGTTAACAA	TGTTTCATG	GAAGAGGTGG <i>I</i>	AACGGTTGĞC <i>i</i>	AGAGGAG:	95
LpPEPCb3 :		AA	TGTTT-NTG	GAAGAGGTGG	AACGGTTGGC	AGAGGAG: 3	37
LpPEPCb4 :					<u></u>	ANAGGAG:	9
LpPEPCb5 :						:	-
LpPEPCb6						:	-

LpPEPCb1 GMGTGCGATCATCTTGCTANTATACTCAACCCAGGACACGATACAAGGATACTTG		*	440)	*	460	*	480	
LpPEPCb2 GRGGTCCGATCATCTTGCTATATTATCTCAACCAGCAACACGATACAGGATACATCT 157 LpPEPCb4 GRGGTCCGATCATCTTGCTATATTATCTCAACCAGGATGCAGGATGCAGGATGCATCTT 157 LpPEPCb5 157	LpPEPCb1 :	GTGGTCCCAGT			TCAACCAC		TACAAGGATCA	ACTTC :	480
Lppepcba	LpPEPCb2 :	GTGGTCCCAGT	CATCTTGC	TATATTATC'	TCAACCAC	CAGACACGAT	TACAAGGATC	ACTTC:	
LpPEPCh5 : LpPEPCh6 : * 500 * 520 * 540 LpPEPCh2 : GTGTARCAGTTCAAGGGGAGGTCATAGAGGACTCATTTGGAGGAGGAACACTTGTGCTTCA : 540 LpPEPCh2 : GTGTARCAGTTCAAGGGGAGGTCATAGAGCACTCATTTGGAGGGGAACACTTGTGCTTCA : 215 LpPEPCh3 : GTGTARCAGTTCAAGGGGAGGTCATAGAGCACTCATTTGGAGGGAACACTTGTGCTTCA : 157 LpPEPCh4 : GTGTAACAGTTCAAGGGGAGGTCATAGAGCACTCATTTGGAGGGAACACTTGTGCTTCA : 152 LpPEPCh5 : LpPEPCh1 : NAACTCTGCAAGGTCACTCATAGGCACTCATTTGGAGGAGAACACTTGTGCTTCA : 129 LpPEPCh1 : NAACTCTGCAAGGTTCACTGCAGCTACTCTTCAGGAGGAGAACACTTGTGCTTCA : 129 LpPEPCh2 : GAACTCTGCAAGGTTCACTGCAGCTACTCTTCAGGATAGCACTCATTTCGC : 600 LpPEPCh3 : GAACTCTGCAAGGTTCACTGCAGCTACTCTTCAGGATAGCACTCACT	LpPEPCb3 :	GTGGTCCCAGT	CATCTTGC	TATATTATC'	TCAACCAC	[AGACACGA]	TACAAGGATC	ACTTC:	
LpPEPCb6 :		GTGGTCCCAGT	CATCTTGC	ratattatc'	TCAACCAC	CAGACACGA'	'ACAAGGATC	CHILC:	.69
Tope=Pcb1								;	_
LppEPCb1 TGTIAACAGTTCAAGGGGAGGTCATAGAGGACCAGTTTTGGAGGGGAACACTTGGGCTCA 540 54	превесов :							•	
LppEPCb1 TGTIAACAGTTCAAGGGGAGGTCATAGAGGACCAGTTTTGGAGGGGAACACTTGGGCTCA 540 54									
LppEpcba CARACCAGATCACACTCAGACCAGAGGCACTCTTTGGAGGGCAACACTTTGGCTTCA 215 125		*			*		*		
LpPEPCb3 : GROTARCAGTTCAAGGCAAGGTCATAGAGGCACTCATTTGGAGAGAACACTTGTGGTTCA : 157 LpPEPCb6 :	-	GTGTAACAGT'	rcaaggcga	GGTCATAGA	GCACTCAT	TTGGAGAGG	AACACTTGTG	CTTCA :	
LpPEPCb5 :	-	GTGTAACAGT	FCAAGGCGA	GGTCATAGA	GCACTCAT	TTGGAGGGG	AACACTTGTG		
LpPEPCb6	-								
Tagastage								:	-
LpPePCb2	-							:	-
LpPepcb GARCICTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCTCCCAATTTCAC 275 LpPepcb GARCICTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC 275 LpPepcb GARCICTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC 217 LpPepcb GARCICTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC 189 LpPepcb CAACCTTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC 189 LpPepcb CAACCTGCAACTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC 189 LpPepcb CAACCAGAATGGCTGCTATAATGGATGGATGGCTGTAGTGGCAGCAAAAGAAAATC 660 CAACCAGAATGGCTGCTATAATGGATGGCTGTATAGTGGCAGCAAAAGAAAATC 660 CAACCAGAATGGCTGCTATAATGGATGGCATGTAGTGGCAACAAAGAATATC 277 LpPepcb CAACCAGAATGGCTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAGAATATC 249 LpPepcb CAACCAGAATGGCTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAGAATATC 249 LpPepcb CAACCACGAATGGCTGCTATAATGGATGGATGGCTGTAGTGGCAACAAAAGAATATC 249 LpPepcb CAACACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTGAGAA 395 LpPepcb CAACAATTGGCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCCGCAACACCTGAGA 337 LpPepcb CAACAATTGGCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCCGCAACACCTGAGA 339 LpPepcb CAACAATTGGTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCCGCAACACCTGAGA 339 LpPepcb CAACAATTGGTTCCAAGAACCACGTTTTGTCGAATACTTCCCCTCGGCAACACCTGAGA 339 LpPepcb CAACAATTGGTCGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LpPepcb CAACAATTGGTCGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGGATGAATATTGGTAGCGGCCATCAAAGAGAAAGCTAGTGGAGCA									
LpPepcb GARCICTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCTCCCAATTTCAC 275 LpPepcb GARCICTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC 275 LpPepcb GARCICTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC 217 LpPepcb GARCICTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC 189 LpPepcb CAACCTTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC 189 LpPepcb CAACCTGCAACTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC 189 LpPepcb CAACCAGAATGGCTGCTATAATGGATGGATGGCTGTAGTGGCAGCAAAAGAAAATC 660 CAACCAGAATGGCTGCTATAATGGATGGCTGTATAGTGGCAGCAAAAGAAAATC 660 CAACCAGAATGGCTGCTATAATGGATGGCATGTAGTGGCAACAAAGAATATC 277 LpPepcb CAACCAGAATGGCTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAGAATATC 249 LpPepcb CAACCAGAATGGCTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAGAATATC 249 LpPepcb CAACCACGAATGGCTGCTATAATGGATGGATGGCTGTAGTGGCAACAAAAGAATATC 249 LpPepcb CAACACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTACTGAGAACACACTGAGAA 395 LpPepcb CAACAATTGGCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCCGCAACACCTGAGA 337 LpPepcb CAACAATTGGCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCCGCAACACCTGAGA 339 LpPepcb CAACAATTGGTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCCGCAACACCTGAGA 339 LpPepcb CAACAATTGGTTCCAAGAACCACGTTTTGTCGAATACTTCCCCTCGGCAACACCTGAGA 339 LpPepcb CAACAATTGGTCGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LpPepcb CAACAATTGGTCGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGCA 345 LPPEPCb CAACAATTGGTCGGATGAATATTGGTAGCGGCCATCAAAGAGAAAGCTAGTGGAGCA		*	56	n	*	580	*	600	
LpPEPCb3 : GARCAGCAGATGCTTCACTGCAGCTACTCTTGAGCATGGATGCATCTCCAATTTCAC : 275 LpPEPCb4 : GAACTCTGCAACCTTTCACTGCAGCTACTCTTGAGCATTGAGATGCATCCTCCAATTTCAC : 217 LpPEPCb5 : LpPEPCb6 :	LoPEPCb1 :	NAACTCTGCA			TCTTGAGC		ATCCTCCAAT		600
Lppepch6 GARCTCTGCAACGTTTCACTGCAGCTACTCTGAGCATGGAATGCATCCTCCAATTTCAC 189	-	GAACTCTGCA	ACGTTTCAC	TGCAGCTAC	TCTTGAGC	ATGGAATGC.	ATCCTCCAAT	TTCAC :	275
LpPEPCb5 : LpPEPCb6 : * 620 * 640 * 660 LpPEPCb1 : CCAARCCAGAATGGCTGTCTATAATGATTGATTGAGTGAGTGAGT	-	GAACTCTGCA	ACGTTTCAC	TGCAGCTAC	TCTTGAGC	ATGGAATGC.	ATCCTCCAAT	TTCAC :	
* 620 * 640 * 660		GAACTCTGCA.	ACGTTTCAC	TGCAGCTAC	TCTTGAGC	ATGGAATGC.	ATCCTCCAAT	TTCAC:	189
# 620 * 640 * 660 LpPEPCb1 : CCAAGCCAGAATGGCTGTATAATGGATGACTGTAGAGGAGGAAAAAAAA								;	: -
LpPEPCb1 CCAARCCAGAATGGCRTGCTATAATGGATGARATGGCTGTACRGGCAGCAAAAGAAAATC 660 1	грькьсре :								•
LpPEPCb1 CCAARCCAGAATGGCRTGCTATAATGGATGARATGGCTGTACRGGCAGCAAAAGAAAATC 660 1									
LpPEPCb2 : CCAAGCCAGAATGGCGTGCTATAATGGATGGATGGCTGTAGTGGCAACAAAAGAATATC : 2335 LpPEPCb4 : CCAAGCCAGAATGGCGTGCTATAATGGATGAGTGGATGAGATGGCACAAAAGAATATC : 249 LpPEPCb5 :		*			*		*		
CAAGCCAGAATGCCTGCTATAATGATGAGTGCTGTAGTGGCAACAAAAGAATATC	-	CCAAÄCCAGA	ATGGCNTGC	TATAATGGA	TGANATGO	CTGTAGNGG	CAGCAAAAGA	AAATC	
LpPEPCb6 CAAGCCAGAATGGCTGCTATAATGGATGGCTGTAGTGGCAACAAAAGAATATC 249	-								
LpPEPCb6									
* 680 * 700 * 720									: -
LpPEPCb1 : GATCAATTGMCTTCCAAGAACCCCMTTTTGMCMAATA									: -
LpPEPCb1 : GATCAATTGMCTTCCAAGAACCCCMTTTTGMCMAATA									
LpPEPCb1 : GATCAATTGMCTTCCAAGAACCCCMTTTTGMCMAATA		*	69	10	*	700	*	720	
LpPEPCb2 : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 395 LpPEPCb3 : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 337 LpPEPCb4 : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 309 LpPEPCb5 :	Loperch1 :	GATCAATTGN			TGNCNAAT				: 697
LpPEPCb5: LpPEPCb6: * 740 * 760 * 780 LpPEPCb1: LpPEPCb2: CTGAATATGGTCGGATGAATATTTGGTAGCCGGCAACACCTAGTGGAGGCA : 455 LpPEPCb3: CTGAATATGGTCGGATGAATATTTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 397 LpPEPCb4: CTGAATATGGTCGGATGAATATTTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 397 LpPEPCb5: CTGAATATGGTCGGATGAATATTTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 369 LpPEPCb6: *** * 800 * 820 * 840 LpPEPCb1: *** LpPEPCb2: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAG	_	GATCAATTGT	CTTCCAAGA	ACCACGTTT	TGTCGAAT	PACTTCCGCT	CGGCAACACC	TGAGA	: 395
LpPEPCb6: * 740 * 760 * 780 LpPEPCb1:	LpPEPCb3 :								
# 740 * 760 * 780 LpPEPCb1: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 455 LpPEPCb2: LpPEPCb3: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 397 LpPEPCb4: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 397 LpPEPCb5: LpPEPCb6: * 800 * 820 * 840 LpPEPCb1: LpPEPCb2: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 515 LpPEPCb3: LpPEPCb4: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 457 LpPEPCb5:	-	GATCAATTGT	CTTCCAAGA	AACCACGT'I'I	rtgircgaa'i	ractrecect	'CGGCAACACC	TGAGA	: 309
* 740 * 760 * 780 LpPEPCb1: LpPEPCb2: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 455 LpPEPCb3: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 397 LpPEPCb4: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 369 LpPEPCb5:		:							:
LpPEPCb1: LpPEPCb2: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 455 LpPEPCb3: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAAGCCTAGTGGAGGCA : 397 LpPEPCb4: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAAGCCTAGTGGAGGCA : 369 LpPEPCb5:	DPFEECDO.								•
LpPEPCb1: LpPEPCb2: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 455 LpPEPCb3: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAAGCCTAGTGGAGGCA : 397 LpPEPCb4: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAAGCCTAGTGGAGGCA : 369 LpPEPCb5: LpPEPCb6: * 800 * 820 * 840 LpPEPCb1: LpPEPCb1: LpPEPCb2: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 515 LpPEPCb3: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 457 LpPEPCb4: LpPEPCb5:					_				
LpPEPCb2: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 455 LpPEPCb3: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAAGCCTAGTGGAGGCA : 397 LpPEPCb4: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAAGCCTAGTGGAGGCA : 369 LpPEPCb5: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAAGCCTAGTGGAGGCA : 369 LpPEPCb6: CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAAGCCTAGTGGAGGCA : 369 LpPEPCb6: CTGAATATGGTCGGATGAATTGGTAGCCGCCATCAAAGAGAAAAGCCTAGTGGAGGCA : 369 LpPEPCb1: CTGAATATGGTCGGATGATTCATGGTAGAAAAGGAAAGG	* mm m m1 - 4	*	74	70	*	760	*	780	
LPPEPCb3 : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 397 LPPEPCb4 : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAAGCCTAGTGGAGGCA : 369 LPPEPCb5 :		CTGAATATGG	TCGGATCA	TATTCCTA	CCCCCCA	CAAAGAGAZ	AGCCTAGTGC	AGGCA	: 455
LPPEPCb4 : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 369 LPPEPCb5 :		CTGAATATGG	TCGGATGA	ATATTGGTA(GCCGGCCA'	rcaaagaga <i>i</i>	AGCCTAGTGC	AGGCA	
LpPEPCb5: LpPEPCb6: * 800 * 820 * 840 LpPEPCb1: LpPEPCb2: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC: 515 LpPEPCb3: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC: 457 LpPEPCb4: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC: 429 LpPEPCb5:		amar marma	magan man						: 369
* 800 * 820 * 840 LpPEPCb1: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC: 515 LpPEPCb2: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACGAGGTTTCATCTTC: 457 LppEPCb4: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACGAGGTTTCATCTTC: 429 LppEPCb5:		:							: -
LpPEPCb1: LpPEPCb2: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 515 LpPEPCb3: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 457 LpPEPCb4: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 429 LpPEPCb5:	LpPEPCb6	:							: -
LpPEPCb1: LpPEPCb2: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 515 LpPEPCb3: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACGAGGTTTCATCTTC : 457 LpPEPCb4: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 429 LpPEPCb5:									
LpPEPCb1: LpPEPCb2: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 515 LpPEPCb3: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 457 LpPEPCb4: TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 429 LpPEPCb5:		,	. 80	00	*	820	*	840	
Lppepcb3 : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACGAGGTTTCATCTTC : 457 Lppepcb4 : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 429 Lppepcb5 :									:
Lppepcb4 : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 429 Lppepcb5 :	LpPEPCb2	* TAGAATCGCT	CCGTGCAA	TTCCATGGA	TCTTTGCT'	TGGACACAGA	ACAAGGTTTC	ATCTTC	
LppepCb5 ::		: TAGAATCGCT	CCGTGCAA	I'I'CCATGGA'	TCTTTGCT	TGGACACAGI	ACGAGGTTTCA	71.C1.1.C	
LppepCb6 ::		: INAIGAMATICECT	CCGIGCAA	I I CCA I GGA	TCITIGC!				. =23
	LpPEPCb6	:							: -

	*	8	60	*	880	*	900
LpPEPCb1 :							: -
LpPEPCb2 :	CTGTATGGCT	TGGATTTG	GTGCAGCGTTC	AAACATA	TCATGCAGAAGGA	CATCAGG	AATA : 575
LpPEPCb3 :					TCATGCAGAAGGA		
LpPEPCb4 :					TCATGCAGAAGGA		
LpPEPCb5 :	Cremiesei		0100.1000110		TCATGGIGITIGGI	CALL CALC	
LpPEPCb6 :				-			
пръвъсле :							: -
	+	9	20	•	940	•	960
LpPEPCb1 :			20	-	340		360
LopePCb2 :	TO CATA CT CT	CAAACAAA	TOTACAATCAC	TOCCOO	TCTTTAGGGTCAC		: car
LpPEPCb3 :	TCCATACTCT	GAAAGAAA	TGTACAATGAC	FIGGCCA1	TCTTTAGGGTCAC	CCTTGAC	TTGC: 577
LpPEPCb4:	TCCATACTCT	GAAAGAAA	TGTACAATGAG	TGGCCAT	TCTTTAGGGTCAC	CCLIGAC	TTCC : 549
LpPEPCb5 :							: -
LpPEPCb6 :							: -
		_			1000		1000
	*	9	80	*	1000	•	1020
LpPEPCb1 :							:
LpPEPCb2 :					CTGCTTTATATGA		
LpPEPCb3 :					CTGCTTTATATG		
LpPEPCb4:					CTGCTTTATATGA		
LpPEPCb5 :	<u>@@#</u>	uning-Cy	AGGGAGATCC-	-GG-ATTC	CTGCTTTATATGA	ACAAATTO	CTTC: 50
LpPEPCb6 :							: -
	*	10	40	*	1060	*	1080
LpPEPCb1 :							 : -
LpPEPCb2 :					MAAACAACTTTG/		
LpPEPCb3 :	TGTCTGAAGA	TCTGCAGC	CCTTTGGGGA	GCAGCTG	GAAACAACTTTG?	AGAGACO	BAAAC : 697
LpPEPCb4	TGTCTGAAGA	TCTGCAGC	CCTTTGGGGA	GCAGCTGA	AGAAACAACTTTG <i>I</i>	AGAGACO	BAAAC : 669
LpPEPCb5 :	TGTCTGAAGA	TCTGCAGC	CCTTTGGGGA	GCÑGCTGA	AGAAACAACTTTG/	AAGAGAC	BAAAC : 110
LpPEPCb6 :							 : -
-							
	*	11	.00	*	1120	*	1140
LpPEPCb1							: -
LpPEPCb2	AGNTACTCTT	TAAGGTTC	TTGNCCACAA	GG			: 785
LpPEPCb3	AGTTACTCCT	TCAGGTTC	TGGCCACAA	GGACGTT	CTTGAAGGGGATC	CTTACCTO	GAAGC: 757
LpPEPCb4	AGTTACTCCT	TCAGGTTC	CTGGCCACAA	GGACGTT	CTTGAĞGGGGATC	CTTACCTO	GAAGC : 729
LpPEPCb5	AGTTACTCCT	TCAGGTTG	CTGGCCACAA	GGACGTT	CTTGAAGGGGATC	CTTACCTO	BAAGC : 170
LpPEPCb6				GGACGTT	CTTGAAGGGGATC	CTTACCTO	GAAGC : 32
-							
•							
	,	11	.60	*	1180	*	1200
LpPEPCb1	:						: -
LpPEPCb2							: -
LpPEPCb3	AGCGTCTGCC	GGTGCGTG	AGTCATAC				: 783
LpPEPCb4	: AGCGTCTGCC	GTTGCGTC	BAGTCATACAT	CACAACA			: 764
LpPEPCb5	: AGCGTCTGC	GTTGCGT	BAGTCATACAT	CACAACA'	TGAATGTTTGCC	AAGCCTA(CACCC : 230
	: AGCGTCTGC	GTTGCGT	BAGTCATACAT	CACAACA'	TTGAATGTTTGCC.	AAGCGNN	CACCC : 92
•							
	1		220	*	1240	*	1260
LpPEPCb1							
LpPEPCb2							
LpPEPCb3	:						: -
	:						: -
LpPEPCb5		TAAGAGAC	CTAGCTTCGA	GGTGACA	CCGCAGCAGGCAC	CTCTGTC	GAAGC: 290
LpPEPCb6					CCGCAGCAGGCAC		

	*	1280	*	1300	*	1320	
LpPEPCb1 :						:	_
LoPEPCb2 :							_
LpPEPCb3 :							
LpPEPCb4 :							
LpPEPCb5 :	AGTTCGCTGATGAC						350
LpPEPCb6:	AGTTCGCTGATGAC	GAAGGAGCCAGC	TGAGCTGGT	GCAACTGAAC	CGTGGGAGCG.	AGTACG:	212
				•			
	*	1340	*	1360	*	1380	
LpPEPCb1 :							_
							_
LpPEPCb2 :						-	_
LpPEPCb3 :						;	_
LpPEPCb4:							
LpPEPCb5 :	CCCCAGGCCTGGAG						409
LpPEPCb6:	CCCCAGGCCTGGA	GGACACCCTCAT	'CCTTACCAT	GAAGGGTAT!	TTGCTGTGGAA	TGCAAA :	272
	*	1400	*	1420	*	1440	
LpPEPCb1 :						:	-
LpPEPCb2 :						:	_
LpPEPCb3 :							_
-						:	· _
LpPEPCb4:	2 G2 G2 GG GT2 GG G	C A COMPONICIONA	mmaa a maa			CCCECA	100
LpPEPCb5:	ACACAGGCTAGGC	CAGTTTGCCTA-	TIGGAATAA	CIGICAL	LGICAGAIGGG	GCGIGA :	468
LpPEPCb6 :	ACACAGGCTAGGC	CAG'I"I"I'GCC'I'A'I	"I"I'GGAA'I'AA	CTGTCATCCC	JGTCAGATT-GG	GCGTGA:	331
	*	1460	*	1480	*	1500	
LpPEPCb1 :						:	-
LpPEPCb2 :						:	-
LpPEPCb3 :						:	_
LpPEPCb4 :							_
LpPEPCb5:	ATATGTGTGTTCC	CCAAATCCTACT	rca a coorde	ACCCATTT	CCCACTTACA	necenn .	528
-							390
LpPEPCb6 :	AIAIGIGIGIICC	CCAMALGCIAG	I GAACCC I GG	ACCCS-111	GGCCACITACA	TOCCII.	330
	*	1500		1540		1560	
	*	1520	*	1540	•	1560	
LpPEPCb1 :						:	-
LpPEPCb2 :						:	-
LpPEPCb3 :						:	
LpPEPCb4 :						:	-
LpPEPCb5 :		NAC-TTGATCT	FAATGNCAAG	GGTTGTTGA	AGCCTGATCTA	: AAATAA	587
LpPEPCb6 :	TTGGTTATGGATG	NACTTTGATCT	raatgicaan	GGTTGTTGA	AGCCTGATCTA	AATÑAA:	450
_							
	*	1580	*	1600	*	1620	
LpPEPCb1						:	_
LpPEPCb2	·					:	_
LpPEPCb3	·						_
-							_
LpPEPCb4	7 = 7 = 667 7 63 7 = 6				COROBOCOCADO	TONTA A TON	646
TDARACD2	ATATGGAACAATG	ATATICIGG-N	GGATCTAATA	ATTIGCTIG	GCICIGGCAIC		646
LpPEPCb6	ATATGGAACAAT	ATATTCTGGTT	Griffichia			:	482
					•		
	*	1640					
LpPEPCb1		:	-				
LpPEPCb2		:	-				
LpPEPCb3		:	_				
LpPEPCb4			-				
	GNGATTTGGAGTN	IGTTTAAC : 6	66				
		. 0	_				
LpPEPCb6	:	:	_				

LpPEPCc	:	AGCANTCTG	* TNCTTNCC.	20 ANCAACCACGTT	* TTTGTNCGA	40 ATACTTNCCGC	* TCGGCAACA	60 CCT	:	60
-		GCACACTGA	* ATATGGTC	80 GGCATGAATAT	* rggtagcce	100 GCCATCAAAGA		120 GTG	:	120
LpPEPCc	:	GAGGCATAG	* BAATCGCTC	140 CGTGCAATTCC	* ATGCATCTI	160 TTGNTTGGACAC		180 TTN	:	180
LpPEPCc	:	ATNTTCCTO	* STATGNCTI	200 GNATTCGNCTC	* CACCNCCA	220 CCCCCNTA : 2	224			

111/241

* 20 * 40 * 60

Lppepcc : XSXLXXNHVLXEYXPLGNTCTLNMVGMNIGSRPSKRKPSGGIESLRAIPCIFXWTQTRXX : 60

Lppepcc : XPVXLXFXSTXTP : 73

		+	20	*	40	*	60		
LpPEPCd	:	GTTNCTGGAACNA	AGGATCTTCTTG	AAGGTGATC	CCTACCTGAAC	CAGCGGCTCC	GCCTC	:	60
						.i.	120		
		*	80	*	100	* ************************************	TZU		120
LpPEPCd	:	CGTGACGCGTACA	TCACCACCATGA	ACGTATGCC	AGGCCTACACA	TTGAAGCGGA	iccgi	•	1.20
					160	*	180		
		*	140	* *	TOO	። ኋርጥጥልጥርርናል ሮል			180
LpPEPCd	:	GACCCAGACTACC	ACGTCGCACTGC	GGCCCCATC	TTTCCAAGGA	3G11A1CCACI			
			222	*	220	*	240		
		AAGCCGGCTTCCG	200 ACCUTCUCACC	። ካፕሮል አርርርርር	CCAGCGAGTA	CGCCCCGGGGC	TGGAG	:	240
Грьевса	:	AAGCCGGCTTCCG	AGCIIGIGACGC	LOPPICCOO	00110001110111				
			262	*	280	*	300		
		GACACCCTCATCI	260 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	 :::::::::::::::::::::::::::::::::::	CCGGTCTGCA	AAACACCGGTT		:	300
грьяьса	:	GACACCCICATCI	IGACCAIGAAGC	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,					
			200	•	340	*	360		
		CAGGAGAGATGCC	320	᠃ᠬᠳᠬᠬᠬ᠘ᡴ᠘ᡣᡳ	₽₽₽ ₽₽₽₡₽₽₫₽₽₽	TGCGATGTTT	TCTTT	:	360
PDEELCO	:	CAGGAGAGATGCC	TGATCACCATC	IIIIIGIAIC	.110712011101				
			200		400	*	420		
		AGTCGTTTGCGG	380	* ~~~~~~~~~~	ያህር ተካልርረጥርር አጥር	TGTCTCCCTG(:	420
LpPEPCd	. :	AGTCGTTTGCGG	[GGGCCTTATAT)	CICICOGACC	TAGCIGGILL	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			
			4.40		460	*	480		
		* GAGGAATAATGG	440	ርጣአጥአጣጥር እና *	ዕሪ ድ በይይልፈጥል ልጣ	AACCGATGTT		:	480
LpPEPCd	۱ :	GAGGAATAATGG	GT ITCGCCCAA	GIAINLIGA.					
			500		520				
	,	* : AGATTTGTTTGT	500 ゕゕ෬ゕゕゕゕヹヸヸ	ար Արդար Արդար ձար 		AAAA : 527			
LIDERPCO	1 :	AGATTTGTTTGT	TWGTWWTTGTTC	**** * ***					

LpPEPCd	:	* VXGXKDLLEGDPYLKQRL	20 RLRDAYITTMN	* VCQAYTLKR	40 IRD	* 60 PDYHVALRPHLSKEVMDTS	:	60
LpPEPCd	:	* KPASELVTLNPASEYAPG	80 LEDTLILTMKG	* VAAGLQNTG	} :	98		

		* 20 * 40 " 60		
LpPEPCe	:	GTTACACGCGCAGTTTGCTTAGCAAGGNAGATGGCTGCTAACTTGTACTTCTCAG	:	60
LpPEPCe	:	* 80 * 100 * 120 ATAGAAGATCTGATGTTTGAGCTCTCTATGTGGCGCTGCAGTGATGAACTTAGGGTCCGT	:	120
LpPEPCe	:	* 140 * 160 * 180 GCAGATGAAGTACATCTGTCCTCAAAAAAAAATCTGCAAAGCATTACATAGAGTTCTGG	:	180
LpPEPCe	:	* 200 * 220 * 240 AAGCAAGTTCCTCCAAATGAACCTTATCGTGTCATACTTGGCGATGTCAGGGATAAACTG	:	240
LpPEPCe	:	* 260 * 280 * 300 TACTATACGCGCGAACGTTCTCGCCACATATTGACAACTGGAATTTCAGACATTCCAGAA	:	300
LpPEPCe	:	* 320 * 340 * 360 GNGTCAACTTTTACTAATGTTGAACTGTTTCTGGAACCTCTTGAGCTGTGCTACAGATCC	·:	360
LpPEPCe	:	* 380 * 400 * 420 TTATCTTNCTGTGGNGACAAANCTATTGCTGANGGAAGCCTTCTTGATTTCTNGCGNNCN	:	420
LpPEPCe	:	* 440 * GNATCNACTTTGTGGGCTTACTCTNGCGAA : 450	;	

LpPEPCe	:	* 20 * VTRAVCLLARXMAANLYFSQIEDLMFELSM	VRC	40 CSDELRVRADEVH	* LSSKKKSAK	60 HYIEFW	:	60
LpPEPCe	:	* 80 * KQVPPNEPYRVILGDVRDKLYYTRERSRHI	LTI	100 TGISDIPEXSTFT	* NVELFLEPI	120 SELCYRS	:	120
LpPEPCe	:	* 140 * LSXCXDKXIAXGSLLDFXXXXXTLWAYSXE	:	150				

LpPEPCf :	GGGGTGGT	* EGCCCTNCT	20 CACCTTGCCTN	* CCTGTCTCA	40 NCCACCAGNCA	* CAATCAACG	60 GAT :	60
LpPEPCf :	CACTCCGG	* GTGACTGTT	80 'CAAGGTGAAGT	* TATTGAGCA	100 GAGCTTTGGGG	* AGGAACACT	120 TGT :	120
LpPEPCf :	GCTTCAGG	* ACGCTGCAG	140 GCGTTTCACAGC	* TGCTACTC	160 TTGAGCATGGGA	* TGCGTCCAC	180 CCA :	180
LpPEPCf	: TTTCACCA	* \AAGCCAGA(200 ETGGCGAGCTCT	* TCTTGATG	220 AGATGGCTGTGG	* TTGCAACT(240 BAGG :	240
LpPEPCf	: AATACCGC	* GTCAATCGT	260 CTTCCAAGAACO	* CACGCTTCG	280 TCGAGTATTTC	* CGCCTTGCA	300 ACAC :	300
LpPEPCf	: CAGAGAC	* AGAGTATGG	320 CAGGATGAATA'	* TAGGAAGCA	340 .GGCCATCAAAG	* AGAAAACCA	360 AGTG :	360
LpPEPCf	: GTGGCAT	* TGAATCACT	380 CCGTGCAATTC	* CATGGATCT	400 TCGCATGGACG	* CAGACACGG	420 TTCC	: 420
LpPEPCf	: ACCTTCC	* AGTCTGGT	440 rgggctttggtg	* GTGCATTC!	460 \AGCATATCCTC	* 'AAGAAGGA	480 CATCA	: 480
LpPEPCf	: GAAATTI	* CCATATGC	500 FCCAGGAGATGT	* !ACAACGAG!	520 TGGCCATTTTTC	* :AGGGTCAC	540 GATCG	: 540
LppepCf	: ATCTTG	* TGAGATGG	560 TGTTCGCCAAG	* GTAACCCT	580 . GGCATTGCTGC	* CTTGTATGA	600 CAGGC	: 600
LpPEPCf	: TCCTGG	* TTTCAGAGG	620 AGCTACAGCCA	* CTGGGTGAC	640 AAGCTGAGG :	644		

LpPEPCf	:	* GGGPXHLAXLSXPPXTI	20 NGSLRVTVQGEV	* /IEQSFGEI	40 EHLCFRTLQRFT	* AATLEHGMR	60 PPI	:	60
Lppepcf	:	* SPKPEWRALLDEMAVVA	80 ATEEYRSIVFQEI	* PRFVEYFR	100 LATPETEYGRMN	* IGSRPSKRK	120 PSG	:	120
LpPEPCf	:	* GIESLRAIPWIFAWTQ	140 FRFHLPVWLGFG	* GAFKHILK	160 KDIRNFHMLQEM	* YNEWPFFRV	180 TID	:	180
LpPEPCf	:	* LVEMVFAKGNPGIAAL	200 YDRLLVSEELQP	* LGDKLR :	214				

118/241

rrMDHa	:	GGCTTCTT	* \AAAACNCA	20 CTAAACTCTTT	* CTATTGTT	40 CCTTATTTCTTC	* GATCTATTT	60 CCA	:	60
TrMDHa	:	ATGGCCAA	* AGACCCAGT	80 TCGTGTTCTTGI	* CACTGGT	100 GCTGCAGGACAA	* ATTGGGTAT	120 GCT	: :	120
TrMDHa	:	CTTGTCCC	* TATGATTGC	140 TAGGGGAGTGAT	* rgctcggc(160 CCTGACCAGCCT	* GTGATCCTC	180 CAC	:	180
TrMDHa	:	ATGCTTGA	* CATTCCACC	200 TGCAGCCGAAT(* CACTCAAC	220 GGTGTTAAAATG	* GAGTTGGT	240 EGAT	:	240
TrMDHa	:	GCTGCATT	* CCCTCTTC1	260 TAAAGGAGTTG	* TTGCTACA	280 ACTGATGTGGT	* rgaggcatgo	300 CACT	: '	300
TrMDHa	:	GGTGTCAA	* .TATTGCCG1	320 TATGGTTGGTG	* GGTTCCCT	340 AGAAAAGAAGG	* PATGGAGAG	360 3AAA	:	360
TrMDHa	:	GATGTGAI	* 'GACAAAAA	380 ATGTCTCTATTT	* ACAAGTCT	400 CAGGCTTCTGC	* CCTTGAAAA	420 ACAT	: ,	420
			*	440 AGGTTCTTGTTG	*	460	*	480	:	480
			*	500 CATCCATTCCTG	*	520	*	540		540
			*	560	*	580	*	600		600
			*	GTCAAATTTCTG	*	640	*	660		
			*	GGAAATNATTCA	YTCAACTC	AMIACCCIGNIC	1TMWCCWCI	CARC	•	
TrMDHa	a	: CGTTAAA	ATCTCCT :	674						

FIGURE 55

rMDHa	:	MAKDPVRVI	* JVTGAAGQI	20 GYALVPMIARG	* VMLGPDQP	40 VILHMLDIPPAA	* ESLNGVKMI	ELVD 60	:	60
CrMDHa	:	AAFPLLKGV	* /VATTDVVE	80 ACTGVNIAVMV	* GGFPRKEG	100 MERKDVMTKNVS	* :IYKSQASAI	120 LEKH	:	120
frMDHa	:	AAANCKVLV	* VVANPANTN	140 JALILKEYAPSI	* PEKNISAL	160 TRLDHNRALGQI	* SERLNVEV	180 SDVK	:	180
TrMDHa	:	NVIIWGKX	* FINSIPXCX	200 XPXNR : 201						

				00	•	40	*	60		
	1		TO THE STATE OF TH	20	TTTCTATTC		CTTCGATCTAT	TTCCA	:	60
TrMDHal	:	Gill I CI I E	MAAACNC	NCIAAMMICII	TICIALIG	TEXT T TEXT T T T T	CTTCGATCTAT	TCCA	:	59
TrMDHa2	:		TAAGCIC	TELEVICINE.		TTCTTATTT	CTTCGATCTAT'	TTCCA	:	57
TrMDHa3	:	74:6	AAAAC-C	ACTAAACICI		TCTTMTTT	CTTCGATCTAT	TTCCA	:	57
TrMDHa4	:	-GCATCTT-	AAAAC-C	ACTAAACICI I	TICIATIG	TTCTTATTT	CTTCGATCTAT	TTCC-	:	55
TrMDHa5	:	CTTCTT	MAAAC-C	ACTAAACTCTT	TICIALIG	TICTIALIT	CTTCGATCTAT	rr-civ	:	54
TrMDHa6	:	C	AAAACNO	ACTAAACTOT		$T_1C_1TY_1T_1$	CTTCGATCTAT	TTCC-	:	45
TrMDHa7	:		· @@	ANTAAACTCT.	LTINIALIG		CTTCGATCTAT	TTCC-	:	45
TrMDHa8	:		医	ANTAAACTCT	TTICIALIG		CTTCGATC-AT	TTCC-	:	41
TrMDHa9	:			ACT-AACTCT			CTTCGATCTAT	TTCC-	:	41
$\mathtt{TrMDHal0}$:			TAAACITCII	TWICTALIG	ᅚᅩ고ᇎᇎᇎᇎ	CTTCGATCTAT	TTCCA	:	41
TrMDHa11	:			<u>AAACICI</u>	LIICIALIG	TICITALL	CIICOIII		•	
			_			100	*	120		
			*	80	TOTONOTO	TECTECAGE	ACAACTTGGGT		: :	120
TrMDHa1	:	ATGGCCAA	AGACCCAC	STICGIGIICI	TGTCMCTGC	TGCTGCAGE	ACAAATTGGGT	ATGCT	:	119
TrMDHa2	:	ATGGCCAA	AGACCCAC	STICGIGIICI	TGTCACTGC	TGCTGCAGC	ACAAATTGGGI	ATGCT	:	117
TrMDHa3	:	ATGGCCAA	AGACCCAC		TGTCACTGC	TRACTORIAN TRACTRACAGE	ACAAATTGGGT	ATGCT	:	117
$\mathtt{Tr}\mathtt{MDHa4}$:	ATGGCCAA	AGACCCAC	GTTCGTGTTCT	TGTCACTGC	TCCTCCACC	ACAAÖTTGGG1	ATGCT	:	115
TrMDHa5	:	ATGGCCAA	AGACCCA	GTTCGTGTTCT	TGTCACTGC	ODADDIDDIE TROPTGCAGE	ACAAGTTGGG1	ATGCT	:	114
TrMDHa6	:	ATGGCCAA	AGACCCA	GTTCGTGTTCT	IGICACIGO	DANDET DE LE TROUTE CAGO	ACAAATTGGGT	ATGCT	:	104
TrMDHa7	:	ATGGCC-A	AGACCCA	GTTCGTGTTCT	TGTCACTGC	TTGCTGCAGC	GACAAATTGGG]	ATGCT	:	103
TrMDHa8	:	ATGGCC-A	AGACCCA	GTTCGTGTTCT	TGT-GCTGC	TUCTUCACO TUCTUCACO	ACAA TTGGGT	ATGCT	:	99
TrMDHa9	:	ATGGCC-A	AGACCCA	GTTCGTGTTCT	TGTEACTG	TTGCTGCAG(BACAAATTGGGT	ATGCT	:	100
TrMDHa10	:	ATGGCC-A	AGACCCA	GTTCGTGTTCT	TGICACIG	CTCCTCCAG(GACAAATTGGG	TATGCT	:	101
TrMDHa11	:	ATGGCCAA	AGACCCA	GTTCGTGTTCI	IGICACIG	31GC1GC1GC	311011111111000			
			*	140	*	160	*	180		
TrMDHa1		CTTCTCCC	TATGATT	GCTAGGGGAGT	GATGCTCG	GNCCTGACC	ANN CTGTGATC	CTMCAC	:	180
TrMDHa1	:	am ²³ amaca	יידי א ביידי א ידידי	ჼႺĊႥჽႺႺႺႺჽႺႤ	rgatigetieg	GCCCTGACC	AGCCIGIGATO	TCCMC	:	179
TrMDHa3	:	COTOCO	ママス マこう マヤ	CCTACGGGAGT	rGATGCTCG	GCCCTGACC.	AGCCTGTGATC	JECCAC	:	177
TrMDHa4	:	CTTCTCCC	דידי מיטידי מיחיר	CCTAGGGGAG	rgatgeteg	GCCCTGACC.	AGCCTGTGATC	CICCAC	:	177
TrMDHa5	:	CTTCTCC	ייד אַ יייר אַ יייר	CCTAGGGGAG	TGATGCTCG	GCCCTGACC	AGCCTGTGATC	CICCAC	:	175
TrMDHa6	•	CTTCTCCC	マアスマススマイ	CCTAGGGGAG	TGATGCTCG	GCCCTGACC	AGCCTGTGATC	CTCCAC	:	174
TrMDHa7	:	CHECECC	בינה עינה עינה עינה עינה עינה עינה עינה ע	CCTAGGGGAG'	rGATGCTCG	GCCCTGACC	AGCCTGTGATC	CICCAC	:	164
TrMDHa8		CTTCTCC	ግጥ ለ ጥርኋ አ ጥባ	CCTAGGGGAG'	FGATGCTCG	GCCCTGACC	AGCCTGTGATC	CTCCAC	:	163
TrMDHa9		CTTCTCC	דידי עיביים עידיי	rcctaccccac'	TGATGCTCG	:GCCCTGACC	AGCCIGIGATC	CICCAC	:	159
TrMDHa10		CTT CTCC	יייי עיייי עיייי	rcctacccac	TGATGCTCG	GCCCTGACC	AGCCTGTGATC	CTCCAC	:	160
TrMDHa11		CTTGTCC	TATGATT	rgctagggag'	TGATGCTCG	GCCCTGACC	AGCCTGTGATC	CTCCAC	:	161
IIMDHaii		CIICICC	01111							
			*	200_	*	220	*	240		202
TrMDHa1		ATGCTTG.	ACATTNC	ACCTGGAG					:	202
TrMDHa2		A TIC CTTC	አ ሶ አ ጥሮ የሶር	Δ CCTGC Δ GCCG	AATCACTG <i>I</i>	\ACGGTGT <u>A</u> }A	AAATGGAGTTG	GTGGAT	:	239
TrMDHa3			7 C7 TTCC	λ CCTCC λ CCCC	A A T C A C T C I	ACGGTGTT	MAAATGGAGIIC	LADULU	•	237
TrMDHa4		A MO COMO	א כא שתככו	A CCTCCACCCC	AATCACTGA	ACGGTGTT	\AAATGGAG1"1C	GTGGAT	:	237
TrMDHa5			$\lambda \subset \lambda \oplus \Box \subset C$	Δ CCTGC Δ GCCG	AATCACLC	\ACGGTG1 <i>1F</i>	AMMAIGGMGIIG	CLOCKI	•	
TrMDHa6		A TO COTTO	א כיא דידיכיכי	Δ CCTGC Δ GCCG	AATCACTC	AACGGTGT1	<u> AAATGGAGTTC</u>	「おりりょう		
TrMDHa7			አርአሞጥሮር	ACCTGCAGCCG	BATCACTC	AACGGTGTT#	\AAATGGAGTTC	LADDITU		
TrMDHa8		A TO COTTO	አ ርአ ሞጥርር	A CCTGCAGCCG	AATCACTC	AACGGTGTT	AAAATGGAGTTC	GTGGA.	:	223
TrMDHa9		A TIC CTUTC	א כא ייייכי	ACCTGCAGCCG	PATCACTC	AACGGTGT"17	AAATGGAGTT	GIGGA.	•	219
TrMDHal				1 A CCTGCAGCCC	ID ATCACTO	AACGGTGTT/	<u>AAAATGGAGTI</u>	ADDIDE	9 :	220
TrMDHal		: ATGCTTC	ACATTCC	ACCTGCAGCCG	BATCACTC	AACGGTGTT	AAAATGGAGTT	GTGGA'	4 :	221

		*	260	*	280	*	300		
TrMDHa1	:							:	-
TrMDHa2	:	GCTGCATTCCCTCTT	CTTAAAGGAGTTG	TTGCTACC	ACTGATGTGGTT	GAGGCATC	CACT	: :	299
TrMDHa3	:	GCTGCATTCCCTCTTC	CTTAAAGGAGTTG	TTGCTACA	ACTGATGTGGTT	GAGGCATG	CACT	: :	297
TrMDHa4	:	GCTGCATTCCCTCTTC	CTTAAAGGAGTTG	TTGCTACA	ACTGATGTGGTT	GAGGCATG	CACT	: :	297
TrMDHa5	:	GCTGCATTCCCTCTTC	CTTAAAGGAGTTG	TTGCTACA	ACTGATGTGGTT	GAGGCATO	CACT	: :	295
TrMDHa6	:	GCTGCATTCCCTCTT						: :	294
TrMDHa7	:	GCTGCATTCCCTCTTC	TTAAAGGAGTTG	TTGCTACA	ACTGATGTGGTT	GAGGCATO	CACT	: :	284
TrMDHa8	:	GCTGCATTCCCTCTTC						:	283
TrMDHa9	:	GCTGCATTCCCTCTT						:	279
TrMDHa10	:	GCTGCATTCCCTCTTC						:	280
TrMDHall	:	GCTGCATTCCCTCTTC	CTTAAAGGAGTTG	TTGCTAC	ACTGATGTGGTT	'GAGGCATO	CACT	:	281
		•	220		340		260		
TrMDHa1			320	<u> </u>	340		360		
TrMDHa2	:	GGGGTCAATATTGCC		COTTOCO		A TOO A CACA	20222	:	- 359
TrMDHa3	:	GGTGTCAATATTGCCC							357
TrMDHa4	:	GGTGTCAATATTGCC							357 357
TrMDHa5	•	GGTGTCAATATTGCC						-	357 355
TrMDHa6	:	GGTGTÑAATATTGÄC					774444		344
TrMDHa7	:	GGTGTCAATATTGCC					GAAA		344
TrMDHa8	:	GGTGTCAATATTGCC							343
TrMDHa9	:	GGTGTCAATATTGCC							339
TrMDHa10	:	GGTGTCAATATTGCC						-	340
TrMDHa11	:	GGTGTCAATATTGCC							341
								-	
m-1mii-1		*	380	*	400	*	420		
TrMDHa1	:							:	_
TrMDHa2	:	GATGTGATGACAAAA						-	419
TrMDHa3	:	GATGTGATGACAAAA							417
TrMDHa4	:	GATGTGATGACAAAA							417
TrMDHa5 TrMDHa6	•	GATGTGATGACAAAA	AAIGICICIATII	ACAAGIC.	L'CAGGCTTCTGCC	.CTTGAAAA	AACAT	:	415
TrMDHa6	:	GATGTGATGACAAAA		12 C2 2 Cmc	207.000000000000		202	:	-
TrMDHa8	:	GATGTGATGACAAAA GATGTGATGACAAAA							404
TrMDHa9	•	GATGTGATGACAAAA GATGTGATGACAAAA							403 399
TrMDHa10	:	GATGTGATGACAAAA							399 400
TrMDHa11	:	GATGTGATGAC-AAA							400
TEMPHATE	•	CHICIONION CONNE	AHIOLCICIALLI	MCAAGIC.	HTW/GCIT MIGN	CTIGAAAA	MCAI	•	400
		*	440	*	460	*	480		
TrMDHa1	:							:	_
TrMDHa2	:	GCTGCTGCAAACTGC						:	479
TrMDHa3	:	GCTGCTGCAAACTGC						:	477
TrMDHa4	:	GCTGCTGCAAACTGC						:	477
TrMDHa5	:	GCTGCTGCAAACTGC	AAGGTTCTTGTTC	STTGCCAA	CCCAGCAAACAC	CAATGCATT	FGATC	:	475
TrMDHa6	:							:	-
TrMDHa7	:	GCTGCTGCAAACTGC							464
TrMDHa8	:	GCTGCTGCAAACTGC						-	463
TrMDHa9	:	GCTGCTGCAAACTGC							459
TrMDHa10	:	GCTGCTGCAAACTGC							460
TrMDHa11	:	GCTGCTGCAAACTGC	AAGGTTCTTGTT(TTGNCAA	CCCACCAAACAC	AATGCATI	'GATC	:	460

		*	500	*	520	*	540	
TrMDHa1	:						:	_
TrMDHa2	:	TTGAAGGAATATGC'	CCATCC	ATTCCTGAGAZ	AAACATTTCTG	CTTTGACTAGATTG	GAC.	539
TrMDHa3	:	TTGAAGGAATATGC'						537
TrMDHa4	:	TTGAAGGAATATGC'						537
TrMDHa5	:	TTGAAGGAATATGC						535
TrMDHa6	:						:	_
TrMDHa7	:	TTGAAGGAATATGC'	TCCATCC	ATTCCTGAGAZ	AAACATTTCTG	CTTTGACTAGATTG	-	524
TrMDHa8	:	TTGAAGGAATATGC'						523
TrMDHa9	:	TTGAAGGAATATGC	CCATCC	ATTCCTGAGAZ	AAACATTTCTG	CTTTGACTAGATTG	GAC .	519
TrMDHa10	:	TTGAAGGAATATGC						520
TrMDHa11	•	TTGAAGGAATATGC'						520
		تهملمتن بالمهرف المناطقة	100	-2		0111011011111111111	<u>.</u>	
		*	560	*	580	*	600	
TrMDHa1	:						:	_
TrMDHa2	:	CATAACAGGGCACT	EGGTCA-				:	559
TrMDHa3	:	CATAACAGGGCACT					:	567
TrMDHa4	:	CATAACAGGGCACT	AGGTCAA	ATTTCTGAAA	ACTAAA		:	575
TrMDHa5	:	CATAACAGGGCACT.				AAGTTTCTGATGTG		595
TrMDHa6	.:						:	_
TrMDHa7	:	CATAACAGGGCACT	AGGTCAA	ATTTCTGAAAC	AC		, :	558
TrMDHa8	:	CATAACAGGGCACT				AAGTTTCTGATGTG	AAA	583
TrMDHa9	:	CATAACAGGGCACT.						577
TrMDHa10	:	CATAACAGGGCACT						580
TrMDHa11	:	CATAACAGGGCACT						580
						سالها فالمنابذ فالمنابذ المنابذ فالمنابذ فالمنابذ		-
		*	620	*	640	*	660	
TrMDHa1	:	*	620	*	640	*	660	_
TrMDHa2	:	*	620 	*	640	*	660 :	- -
TrMDHa2 TrMDHa3	: : :	*	620 	*	640	*	660	-
TrMDHa2 TrMDHa3 TrMDHa4	:	*	620 	*	640	*	660	- - -
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5	: : : : :	*	620	*	640	*	660	- - - - 606
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6		* AATGTTAT-A-AT	620	*	640	*	660	- - - - 606
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7	:::::::::::::::::::::::::::::::::::::::			*	640	*	660	- - - - 606 -
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6	:::::::::::::::::::::::::::::::::::::::	* AATGTTAT-A-AT AATGTTATAATCTG		*	640	*	660	- - - 606 - 599
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa8 TrMDHa9		AATGTTATAATÇTG		*	640	*	660	
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10		AATGTTATAATCTG	GG	*			:	
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa8 TrMDHa9		AATGTTATAATÇTG	GG	* TNATTCATCA			:	- 599
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa12 TrMDHa2		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa1 TrMDHa1 TrMDHa2 TrMDHa2 TrMDHa3 TrMDHa3		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa1 TrMDHa2 TrMDHa2 TrMDHa3 TrMDHa3 TrMDHa3 TrMDHa4 TrMDHa4		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa1 TrMDHa2 TrMDHa3 TrMDHa3 TrMDHa4 TrMDHa4 TrMDHa5 TrMDHa6		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa1 TrMDHa2 TrMDHa3 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa6 TrMDHa7		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa1 TrMDHa2 TrMDHa3 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa6 TrMDHa7 TrMDHa8		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa2 TrMDHa3 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9		AATGTTATAATCTG	GG	* TNATTCATCA			:	599 594
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa1 TrMDHa2 TrMDHa3 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa6 TrMDHa7 TrMDHa8		AATGTTATAATCTG	GGGGAAA	TNATTCATCA			:	599 594

rmDHb :		TTCTCCCAN	* AATCNNGAA	20 AANCGCCCANA	* CATCACACA	40 ACATAACACCT	* TACTCTNCT	60 TTC :	:	60
rrMDHb :	: '	TCTCTNAAC.	* AAAAACTG	80 TTCTTCCTCTC	* TTAATCTTC	100 CCTGTTCGATT	* CCTTCCATI	120 TCT	:	120
TrMDHb :	:	TCAAAAATG	* GCCAAAGA	140 CCCAGTTCGTG	* TTCTCGTC#	160 ACTGGTGCTGC	* \GGGCAAATI	180 GGT	:	180
TrMDHb	:	TATGCACTI	* GTCCCTAT	200 GATTGCTAGGG	* GAGTGATG	220 CTTGGTCCTGA	* CCAACCTGTC	240 SATC	:	240
TrMDHb	:	CTTCACATO	* CTTGATAT	260 TCCTCCAGCAG	* CAGAGTCA	280 TTGAATGGAGT	* raagatgga(300 STTG	:	300
TrMDHb	:	GTCGATGCT	* rgcatttcc	320 ACTTCTTAAAG	* GTGTTGTT	340 GCTACAACTGA	* IGTTGTTGA	360 AGCA	:	360
TrMDHb	:	TGCACTGG	* AGTCAATAT	380 TTGCAGTCATG(* STTGGTGGA	400 TTCCCAAGAAA	* AGAAGGTAT	420 GGAG	:	420
TrMDHb	:	AGGAAGGA'	* TGTGATGT(440 CTAAGAACGTC	* rctattac	460 AAGTCCCAGGC	* TTCTGCCCT	480 TGAA	:	480
TrMDHb	:	AAGCATGC	* TGCTGCCA	500 ACTGCAAGGTT	* TTGGTTGT7	520 GCTAACCCAGO	* 'AAACACCAA	540 TGCA	:	540
TrMDHb	:	TTGATCTT	* 'GAAGGAAT'	560 TTGCTCCATCT	* ATTCCAGA(580 SAAAACATTTO	* CTTGTTTGAC	600 CTAGA	:	600
TrMDHb	:	CTTGATCA	* \CAACAGGG	620 CATTGGGCCAA	* ATTTCTGA	640 AAGATTGAATG	* TTCAAGTTT(660 TGAT		660
TrMDHb	;	: GTAAAGAA	* \TGTCATTA	680 TCTGGGGTAAT	* CATTCATC	700 AACTCAGTATC	* CTGATGTCA	720 ACCAT		720
TrMDHb) :	: GCAACTGT	* TTAACACCC	740 CCGCTGGGGAG	* BAAGCCTGT	760 CCGTGAGCTTG	* TTTCTGATG.	780 ACGCC		780
TrMDHb)	: TGGTTGA	* ATGGAGAA	800 TTCATATCTACO	* CGTTCAACA	820 ACGTGGTGCTG	* CAATTATTA	840 AGGCT		: 840
TrMDH)	: AGAAAGC	* TTTCAAGC(860 GCACTATCCGC	* IGCTAGCGC	880 TGCTTGCGACO	* ACATTCGCG	900 ATTG		: 900
TrMDHL	5	: GTTCTTG	* GAACTCCC	920 CAGGGCACCTT	* CGTTTCAAI	940 GGGAGTGTATT	* 'CTGATGGTT	96 CTTA		: 960

PCT/AU2004/000493 WO 2004/089066

124/241

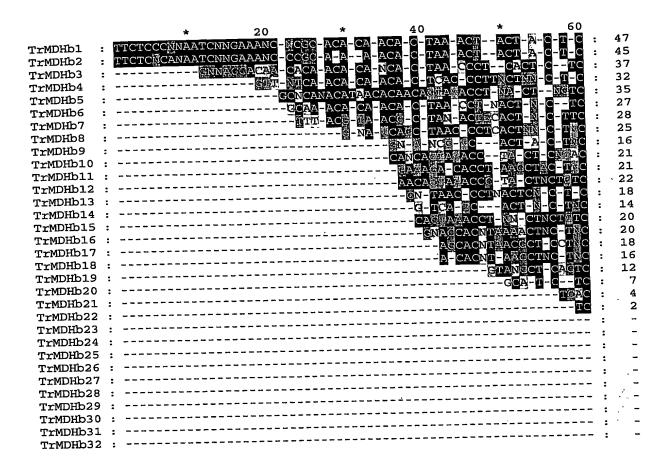
* 1020 1000 980

TYMDHD : AACGTACCAGCTGGACTCATCTATTCATTCCCTGTCACCACTGCTAATGGGGAATGGAAA : 1020

TrMDHb : ATTGTTCAAGGACTTTCAATTGACGAGTTCTCAAGGAAGAAGTTGGACTTGACAGCTGAA : 1080

* 1100 TrMDHb : GAGTTATCCGAGGAAAAGAGTTTGGCATACT : 1111

mMDUb		* MAKDPVRVLVTGAAGQI	20 GYALVPMIARGV	* /MLGPDQPV	40 /ILHMLDIPPA	* AESLNGVKME	ELVD 60	:	60
TYMDHO	•	MAKDIVIVIO							
TrMDHb	:	* AAFPLLKGVVATTDVVI	80 EACTGVNIAVMVO	* GGFPRKEGN	100 MERKDVMSKNV	* SIYKSQASAI	120 SEKH	:	120
TrMDHb	:	* AAANCKVLVVANPANTI	140 NALILKEFAPSI	* PEKNISCL	160 TRLDHNRALGÇ	* ?ISERLNVQV	180 SDVK	:	180
TrMDHb	:	* NVIIWGNHSSTQYPDV	200 NHATVNTPAGEK	* PVRELVSDI	220 DAWLNGEFIST	* TVQQRGAAII	240 KARK	:	240
TrMDHb	:	* LSSALSAASAACDHIR	260 DWVLGTPQGTFV	* SMGVYSDG	280 SYNVPAGLIY	* SFPVTTANGE	300 WKIV	:	300
TrMDHb	:	* QGLSIDEFSRKKLDLT	320 AEELSEEKSLAY	: 328					



			*	.80		*	100_			120		
TrMDHbl	:	TCT	AAAGAA	ACTGTTC	CTTCCTCT	CTTAA:	CTTCCCTG?	CTTGATT	CCTTCC	AGTTCT	:	104
TrMDHb2		TCT	aaadaa	ACTGTTC	TTCCTCT	CTTAA'	CTTCCCTG:	rt <u>r</u> gatt	CCTTCC	AGTTCT	:	102
TrMDHb3	:	TŅĀ	AACAAA	AACTGTTC	TTCCACT	CTTAA	rcttccctg:	FTCGATT	CCTTCI	ATTTCT	:	94
TrMDHb4	:	TCT	: NAACAAA	CTATTC	CTTCATCT	'CTTAA'	rcttc@c@g:	TTCGATT	CCTTCC	THICL	:	91
TrMDHb5	:	TCT	-N-AA-NAA	AACTGTTC	CTTCCTCT	'CTTAA'	rcttcccig:	I'T <u>I</u> GAT'T	CCTTCC	GIRICAL	:	91
TrMDHb6	:	TCT	NANGAA	AACTÄTTC	CTTCATCT	'CTTAA'	rcttc#ceg:	ITCGATT	CCTTCC	eg@TCT	:	84
TrMDHb7	:	II ŠIN	AACAAA	AACTÄTTC	CTTNATCT	'CTTAA'	rcttckceg	TTCGATT	CCTTCC	TTTCT	:	85
TrMDHb8	:	TCT	- NNAACAAA	AACTÄTTC	CTTC <u>H</u> TCT	'CTTAA'	rcttc g cgg'	TTCGATT	CCTTCC	TTTCT	:	84
TrMDHb9	:	TCN	AACAAA	AACTGTT	CTTCC-CT	'CTTAA	rcttccccc	TTCGATT	CCTTC	ATTTCT	:	72
TrMDHb10	:	TCT	CA-AAC-AA	AACTGNT	CTTCCTCT	CTTAA	-CTTCCCTG	TTCGATT	CCTTCC	ACTION	:	78
TrMDHb11	:	TCT	CTNAAC-AA	AACTGTT(CTTCCTCT	CTTAA	TCTTCCCTG'	TTEGATT	CCTTCC	A@TTCT	:	80
TrMDHb12	:	TCT	CT-NAACAA	AACTGTT(CTTCCTCT	CTTŅA	TCTTCCCTG	TTCGATI	CCTTCC	ACTUCE	:	81
TrMDHb13	:	TCT	-N-AANAA	AACTITT(CTT – ŠTCT	CTTAA	TCTTCECEG	TTCGATT	CCTTCC	gTTTCT	:	75
TrMDHb14	:	正以C	AANAAA	AACTGTT	CTTCCACT	CTTAA	TCTTCCCTG	TTCGATT	'CCTTC顯	ATTTCT	:	71
TrMDHb15	:	TCT	CT-AAACAA	AACTGTT	CTTCCTCI	CTTAA	TCTTCCCTG	TTCGATT	CCTTCC	ACTITICIT	:	79
TrMDHb16	:	TCI	CTNAAC-AA	AACTGTT	CTTCCTCI	CTTMA	TCTTCCCTG	TT_GATT	CCTTCC	- GIMICH	:	78
TrMDHb17	:	TCT	-CAAACAAA	AACTGTT	CTTC - @CI	CTTAA	TCTTCCCTG	TTCGATT	CCTTC	ATTTCT	:	76
TrMDHb18	:	TCT	CT <mark>C</mark> AAC-AA	AACTGTT	CTTCCTCT	CTTAA	TCTTCCCTG	TTÆGATI	CCTTCC	- 線INICH	:	74
TrMDHb19	:	TCT	-NNAACAAA	AACTGTT	cite-ĝci	CTTAA	TCTTCCCTG	TTCGATT	CCTTC	ATTTCT	:	70
TrMDHb20	:	TNZ	<mark>AACAAA</mark>	AACTGTT	CTT - CNCT	CTTAA	TCTTCCCTG	TTCGATT	rccttc	ATTTCT	:	63
TrMDHb21	:	ÇC1	CTNAACAAA	AACTGTT	CTTCCTC	CTTNA	TCTTCCCTG	TTTGATT	rccttcc	-@IMCI	:	63
TrMDHb22	:	TCT	NAACAAA	AACTGTT	CTTC-[GCI	rcttna	TCTTCCCTG	TTCGAT	CCTTC	ATTTCT	:	59
TrMDHb23	:		CAAA	aactg <mark>c</mark> t	CTTCCTCI	$\Gamma CTTNA$	TCTTCCCTG	TTCGAT:	rccttcc		:	51
TrMDHb24	:		AA	AACTGTT	CTTCCTCI	$\Gamma CTTNA$	TCTTCCCTG	TTCGAT"	rccttcc	-Chilet	:	49
TrMDHb25	:			CNN	CTTCCTCT	ICTT C A	ECTTCCCTG	TTTGAT'	rccttcc	AGTTCT	:	46
TrMDHb26	:			GGTT	CTTC-GC	rcttaj	NCTTCCCTC	TTCGAT"	rccttc	ATTTCT	:	44
TrMDHb27	:				-TTCCTC	ICTTÑ#	TCTTCCCTC	TTTGAT	rccttcc	- Sinch	:	39
TrMDHb28	:										:	-
TrMDHb29	:										:	-
TrMDHb30	:										:	-
TrMDHb31	:										:	-
TrMDHb32	:										:	_

		•	140		100		<u> 100</u>		
TrMDHb1	:	TCAAAAATGGCCAA						:	164
TrMDHb2	:	TCAAAAATGGCCA						:	162
TrMDHb3	:	TCAAAAATGGCCA	AAGACCCAGTTC	GTGTTCTCGTC	ACTGGTGCT	GCAGG[CAAA]	TGGT	:	154
TrMDHb4	:	TCA A ATGCCA						:	151
TrMDHb5	:	TCAAAAATGGCCA						:	151
TrMDHb6	:	TCAĞĞAATGGCCA	AAGACCCAGTTC	GTGT@CTCGT	ACTGGTGCT	GCAGGGCAAA'	TTGGT	:	144
TrMDHb7	•:	TCALIDAATGGCCA						:	145
TrMDHb8	:	TCAGUAATGGCCA						:	144
TrMDHb9	:	TCAAAAATGGCCA	AAGACCCAGTTC	GTGTTCTCGTC	CACTGGTGCT	rgcagg@caaa	TTGGT	÷	132
TrMDHb10	:	TCAAAAATGGCCÑ						:	138
TrMDHb11	:	TCAAAAATGGCCA						:	140
TrMDHb12	:	TCAAAAATGGCCA						:	141
TrMDHb13	:	TCAĞĞAATGGCCA						:	135
TrMDHb14	:	TCAAAAATGGCCA						:	131
TrMDHb15	:	TCAAAAATGGCCA						:	139
TrMDHb16	:	TCAAAAATGGCCA	AAGACCCAGTTC	GTGTTCTCGT	CACTGGTGC	rgcagggcaaa'	TTGGT	:	138
TrMDHb17	:	TCAAAAATGGCCA	AAGACCCAGTTO	GTGTTCTCGT	CACTGGTGC'	rgcagggcaaa	TTGGT	:	136
TrMDHb18	:	TCAAAAATGGCCA	AAGACCCAGTTO	GTGTTCTCGT	CACTGGTGC'	rgcagggcaaa'	TTGGT	:	134
TrMDHb19	:	TCAAAAATGGCCA	AAGACCCAGTTO	CGTGTTCTCGT	CACTGGTGC'	rgcagggcaaa	TTGGT	:	130
TrMDHb20	:	TCAAAAATGGCCA	AAGACCCAGTT(CGTGTTCTCGT	CACTGGTGC'	rgcagg@caaa	TTEGT	:	123
TrMDHb21	:	TCAAAAATGGCCA	AAGACCCAGTT	CGTGTTCTCGT	CACTGGTGC'	IGCAGGGCAAA	TTGGT	:	123
TrMDHb22	:	TCAAAAATGGCCA	AAGACCCAGTT(CGTGTTCTCGT	CACTGGTGC'	rgcagg@caaa	TTGGT	:	119
TrMDHb23	:	T <mark>-</mark> NAAAATGGCCA	AAGACCCAGTT	CGTGTTCTCGT	CACTGGTGC'	TGCAGGGCAAA	TTGGT	:	110
TrMDHb24	:	TCÄAAAATGGCCA						:	109
TrMDHb25	:	TCAAAAATGGCCA	AAGACCCAGTT	CGTGTTCTCGT	CACTGGTGC'	TGCAGGGCAAA	TTGGT	:	106
TrMDHb26	:	T-NAAAATGGCCA	AAGACCCAGTT	CGTGTTCTCGT	CACTGGTGC	TGCAGGGCAAA	TIGGT	:	103
TrMDHb27	:	TC-AAAATGGCC-	AAGACCCAGTT	CGTGTTCTCGT	CACTGGTGC	TGCAGGGCAAA	TTGGT	:	97
TrMDHb28	:							:	_
TrMDHb29	:							:	-
TrMDHb30	:							:	-
TrMDHb31	:							:	-
									_

		π	200		*	220			240		
TrMDHb1	:	TATGCACTTGTC	CCTATGAT	TGCTAGGGG	AGTGAT	GCTTGGT	CCTGAT	CAACCTO	TGATC	:	224
TrMDHb2		TATGCACTTGTC								:	222
TrMDHb3		TATGCACTTGTC								:	214
TrMDHb4	:	TATGCACTTGTC	CCTATGAT	TGCTAGGGG	AGTGAT	GCTTGGT	CCTGAT	CAACCTO	GTGATC	:	211
TrMDHb5	:	TATGCACTTGTC								:	211
TrMDHb6	:	TATGCACTTGTC								:	204
TrMDHb7	:	TATGCACTTGTC								:	205
TrMDHb8	:	TATGCACTTGTC								፡	204
TrMDHb9	:	TATGCACTTGTC	CCTATGAT	TGCTAGGGG	BAGTGAT	GCTTGGT	CCTGAT	CAACCT	GTGATC	:	192
TrMDHb10	:	TATGCACTTGTC	CCTATGAT	TGCTAGGGG	AGTGAT	GCTTGGT	CCTGAT	CAACCT	GTGATC	:	198
TrMDHb11	:	TATGCACTTGTC								:	200
TrMDHb12	:	TATGCACTTGTC								:	201
TrMDHb13	:	TATGCACTTGTC								:	195
TrMDHb14	:	TATGCACTTGTC								:	191
TrMDHb15	:	TATĢCACTTGTC								:	199
TrMDHb16	:	TATGCACTTGTC								:	198
TrMDHb17	:	TATGCACTTGTC								:	196
TrMDHb18	:	TATGCACTTGTC								:	194
TrMDHb19	:	TATGCACTTGTC								:	190
TrMDHb20	:	TATGCACTTGTC								:	183
TrMDHb21	:	TATGCACTTGTO								:	183
TrMDHb22	:	TATGCACTTGTC								:	179
TrMDHb23	:	TATGCACTTGTC								:	170
TrMDHb24	:	TATGCACTTGTC								:	169
TrMDHb25	:	TATGCACTTGT								:	166
TrMDHb26	:	TATÄCACTTGTO								:	163
TrMDHb27	:	TATGCACTTGT	CCTATGAT	TGCTAGGG	GAGTGAI	GCTTGG	CCTGAT	CAACCT	GTGATC	:	157
TrMDHb28	:			- GGG (GAGTGAT	GCTTGG:	rcctgat	-MACCT	GTGATC	:	34
TrMDHb29	:									:	_
TrMDHb30	:									:	-
TrMDHb31	:									:	-
m 1777- 2 0											_

			*	260	*	280		300		
TrMDHb1	:	CTACACA:	TGCTTG.	ATATTCC	ACCGGCAGCA	GAGTCATTGA	ATGGAGTTA	AGATGGAGATG	:	284
TrMDHb2		CTÄCACA	TGCTTG	ATATTCC	ACCCGCAGCA	GAGTCATTGA	ATGGAGTTA	AGATGGAGTTG	:	282
TrMDHb3	:	CTTCACA	TGCTTG	ATAT@CC	TCCAGCAGCA	GAGTCATTGA	ATGGAGTTA	AAATGGAGTTG	:	274
TrMDHb4	:	CTTCACA'	TGCTTG	ATATCCC	TCCAGCAGCA	GAGTCATTGA	ATGGAGTTA	AMATGGAGTTG	:	271
TrMDHb5	:	CTTCACA'	TGCTTG	ATATTCC	TCCAGCAGCA	GAGTCATTGA	ATGGAGTTA	AGATGGAGTTG	:	271
TrMDHb6	:	CTTCACA'	TGCTTG	ATATŐCC	TCCAGCAGCA	GAGNCATTGA	ATGGAGTTA	AMATGGAGTTG	:	264 265
TrMDHb7	:	CTTCACA'	TGCTTG	ATATQCC	TCCAGCAGCA	GAGTCATTGA	AT'GGAGT'TA	ATGGAGTTG	:	265
TrMDHb8	:	CTTCACA'	TGCTTG	ATATICO	CTCCAGCAGCA	GAGTCATTGA	ATGGAGTTA	AZATGGAGTTG	:	264 252
TrMDHb9	:	CTT ACA	TGCTTG	ATATTEC	CTCCAGNAGNA	GAGTNATTGA	ATGGAG@TA	AMATGGAGCTG	:	252
TrMDHb10	:	CTACACA	TGCTTG	ATATTCC	CACCEGCAGCA	GAGTCATTGA	AATGGAGTTA	AGATGGAGTTG	:	260
TrMDHb11	:	CTTCACA	TGCTTG	ATATTCO	CTCCAGCAGCA	GAGTCATTGA	ATGGAGTTA	AGATGGAGTTG	:	261
TrMDHb12	:	CTECACA	TGCTTG	ATATTCO	Caccagg Cagca	AGAGTCATTG	AATGGAGTTA	AGATGGAGTTG	•	255
TrMDHb13	:	CTTCACA	TGCTTG	ATATACC	CTCCAGCAGC	AGAGTCATTGA	AATGGAGTTA	AMATGGAGTTG	:	255
TrMDHb14	:	CTTCACA	TGCTTC	ATATTCO	CTCCAGCAGCA	AGAGTCATTGA	AATGGAGTTA	ANATGGAGTTG	•	251
TrMDHb15	:	CTACACA	TGCTTC	ATATTCO	CACCAGCAGCA	AGAGTCATTGA	AATGGAGTTA	AGATGGAGTTG	:	258
TrMDHb16	:	CTKCACA	TGCTTG	BATATTCO	CACCAGCAGCA	AGAGTCATTG	AATGGAGTTA	AGATGGAGTTG	:	256
TrMDHb17	:	CTTCACA	TGCTTC	BATATTCO	CTCCAGCAGC	AGAGTCATTG	AATGGAGTTA	AMATGGAGTTG	:	254
TrMDHb18	:	CTTCACA	TGCTTC	BATATTCO	CTCCAGCAGC	AGAGTCATTG	AATGGAGTTA	AGATGGAGTTG	:	254
TrMDHb19	:	CTTCACA	TGCTTC	BATATTC	CTCCAGCAGC	AGAGTCATTG	AATGGAGTTA	AZATGGAGTTG	•	243
TrMDHb20	:	CTTCACA	TGCTTC	BATATTC	CTCCAGCAGC!	AGAGTCATTG.	AATGGAGTTA	AMATGGAGTTG	:	243
TrMDHb21	:	CTTCACA	TGCTTC	BATATTC	CTCCAGCAGC	AGAGTCATTG	AATGGAGTTA	AGATGGAGTTG	:	239
TrMDHb22	:	CTTCACA	TGCTTC	BATATTC	CTCCAGCAGC	AGAGTCATTG.	AATGGAGTTA	AMATGGAGTTG	:	239
TrMDHb23	:	CTECACA	TGCTT	BATATTC	CACCAGCAGC	AGAGTCATTG.	AATGGAGTTA	AGATGGAGTTG	:	229
TrMDHb24	:	CTSCACA	ATGCTTO	GATATTC	CZCCZGCAGC	AGAGTCATTG	AATGGAGTTA	AGATGGAGTTG	•	226
TrMDHb25	:	CTTCACA	TGCTT	BATATTC	CT CAGCAGC	AGAGTCATTG	AATGGAGTTA	AGATGGAGTTG	•	223
TrMDHb26	:	CTTCACA	ATGCTT	GATATTC	CTCCAGCAGC:	AGAGTCATTG	AATGGAGTTA	AMATGGAGTTG	:	223
TrMDHb27	:	CTTCACA	ATGCTT(GATATTC	TTCCAGCAGC	AGAGTCATTG	AATGGAGTTA	AGATGGAGTTG		93
TrMDHb28	:	CTT-ÑC	ATGCTT	GATATCC	CTCCAGCAGC	AGAGTCATTG	AATGGAGTTA	AAATGGAGTTG	•	93 45
TrMDHb29	:			-MTATTC	CINCNGCAGC	NGAGT - NITIG	AATGGAG-TA	AGATGGAGTTG	:	
TrMDHb30	:			TATTC	CT-C@GCAGC	AGAGT - NTTG	AATGGAG-TA	AGATGGAGTTG	:	43
TrMDHb31	:								•	-
TrMDHb32	•								:	-

		*	320		×	340	••	300		
TrMDHb1	:	G <mark>N</mark> CGATGCTGNA	TNNCACTI	GTTAAAGG	NGANGETG	CT			:	323
TrMDHb2	:	GTCGATGCTGCA'	FTTCCACTI	GTTAAAGG	TGNTGATO	NTACAA	CTGATGATG	NGAGGNA	:	342
TrMDHb3	:	GTĞGATGCTGCA'	ITTCCACTI	CTTAAAGG	TGTTGTTG	GCTACAA(CTGATGTTGT	TGAAGCA	:	334
TrMDHb4	:	GTEGATGCTGCA'	TTTCCACTT	CTTAAAGG	@GTTGTTC	GCTACAA(CTGATGTTGT	TGAAGCA	:	331
TrMDHb5	:	GTCGATGCTGCA'	TTTCCACT1	CTTAAAGG	TGTTGTTC	CTACAA	CTGATGTTGT	TGAGGCA	:	331
TrMDHb6	:	GT GATGCTGCA	TTTCCACTI	rcttaaagg	GGTTGTTC	CTACAA	CTGATGTTGT	TGAAGCA	:	324
TrMDHb7	:	G@GGATGCTGCA'	TTTCCACT1	rcttaaagg	#GTTGTTC	3CTACAA	CTGATGTTGT	TGAAGCA	:	325
TrMDHb8	:	GTEGATGCTGCA	TTTCCACT:	rcttaaagg	GGTTGTTC	CTACAA	CTGATGTTGT	TGAAGCA	:	324
TrMDHb9	:	CGEGATGCTGNA'	TTMNAACT:	ſĊŦŦĄĠĠĠĠ		GCTACGA	CTGATGCTG	_ ⊌AA@CA	:	312
TrMDHb10	:	GTCGATGCTGCA	TTTCCACT	rcttaaagg	TGTTGTT	GCTACAA	CTGATGTTGT	TGAGGCA	:	318
TrMDHb11	:	GTCGATGC'TGCA	TTTCCACT	rcttaaagg	TGTTGTT	GCTACAA	CTGATGTTGT	TGAGGCA	:	320
TrMDHb12	:	GTCGATGCTGCA	TTTCCACT	rcttaaagg	TGTTGTT	GCTACAA	CTGATGTTGT	TGAGGCA	:	321
TrMDHb13	:	GTGGATGCTGCA	TTTCCACT	ICTTAAAGG	E GTTGTT	GCTACAA	CTGATGTTG1	'I'GAAGCA	:	315
TrMDHb14	:	GTEGATGCTGCA	TTTCCACT	ICTTAAAGG	TGTTGTT	GCTACAA	CTGATG1"IG1	"IGAAGCA	:	311
TrMDHb15	:	GTCGATGCTGCA	TTTCCACT	ICTTAAAG0	TGTTGTT	GCTACAA	CTGATGTTGT	TGAEGCA	:	319
TrMDHb16	:	GTCGATGCTGCA	TTTCCACT'	TCTTAAAGG	TGTTGTT	GCTACAA	CTGATGTTG1	"I'GAGGCA	:	318
TrMDHb17	:	GTĞGATGCTGCA	TTTCCACT'	TCTTAAAGC	TGTTGTT	GCTACAA	CTGATGTTGT	"I'GAAGCA	:	316
TrMDHb18	:	GTCGATGCTGCA	TTTCCACT'	TCTTAAAGG	TGTTGTT	GCTACAA	CTGATGTTG1	TGA@GCA	:	314
TrMDHb19	:	GTEGATGCTGCA	TTTCCACT	TCTTAAAGG	TGTTGTT	GCTACAA	.CTGATGTTG1	"TGAAGCA	:	310
TrMDHb20	:	GTEGATGCTGCA	TTTCCACT	TCTTAAAGO	TGTTGTT	GCTACAA	CTGATGTTGT	."I'GAAGCA	:	303
TrMDHb21	:	GTCGATGCTGCA	TTTCCACT	TCTTAAAGO	TGTTGTT	GCTACAA	CTGATGTTG1	."I'GAGGCA	:	303
TrMDHb22	:	GTEGATGCTGCA	TTTCCACT	TCTTAAAGO	STGTTGTT	GCTACAA	CTGATGTTG'	"I'GAAGCA	:	299
TrMDHb23	:	GTCGATGCTGCA	TTTCCACT	TCTTAAAGO	STGTTGTT	GCTACAA	CTGATGTTG	"TGAGGCA	:	290
TrMDHb24	:	GTCGATGCTGCA	TTTCCACT	TCTTAAAGO	TGTTGTT	GCTACAA	CTGATGTTGT	'TGAGGCA	:	289
TrMDHb25	:	GTCGATGCTGCA	TTTCCACT	TCTTAAAG(STGTTGTT	GCTACAA	CTGATGTTGT	TGAGGCA	:	286
TrMDHb26	:	GTGGATGCTGCA	TTTCCACT	TCTTAAAG	STGTTGTT	GCTACAA	CTGATGTTGT	rtgaagca:	:	283
TrMDHb27	:	GTCGATGCTGCA	TTTCCACT	TCTTAAAG	STGTTGTT	GCTACAA	ACTGATGTTGT	rtgaggca	:	277
TrMDHb28	:	GTGGATGCTGCA	TTTCCACT	TCTTAAAG	GCATTGTT	GCTACAA	ACTGATGTTG	FTGAAGCA	:	153
TrMDHb29	:	GTCGATGCTGC	TTTCCACT	TCTTAAAG	GTGTTGTT	'GCTACAF	ACTGATGTTGT	rtgaggca	:	105
TrMDHb30	:	GTCGATGCTGCA	TTTCC-CT	TCTTAAAG	STGTTGTT	GCTACA?	ACTGATGTTG	I'TGAGGCA	:	102
TrMDHb31	:								:	-
TrMDHb32	:								:	_

			*	380	-	400	J		420		
TrMDHb1	:									:	- 350
TrMDHb2	:	TNNNCTG	<u> </u>					7077000	magna.	:	394
TrMDHb3	:	TGCACTG	GAGTC	AATATTGCAG:	rcatggtt	GGTGGATTC	CCAAGAAA	AGAAGGIA	TGGAG	-	391
TrMDHb4	:	TGCACTG	GAGTC	AATATTGCAG	CATGGTT	GGTGGATTC	CCAAGAAA	AGAAGGIF	TIGGAG	፡	391
TrMDHb5	:	TGCACTG	GAGTC	AATATTGCAG:	rcatggi'i	GGTGGATTC	CCAAGAAA	AGAAGG I F	DADDI	:	384
TrMDHb6	:	TGCACTG	GAGTO	AATATTGCAG	rcatggtt	GGTGGATTC	CCAAGAAA	AGAAGGIA	ATGGAG	:	385
TrMDHb7	:	TGCACTG	GAGTO	AATATTGCAG	TCATGGTT	GGTGGATTC	CCAAGAAA	AGAAGGTA	ATGGAG	:	384
TrMDHb8	:	TGCACTG	GAGTO	AATATTGCAG'	rcatggtt	GGTGGATTC	CCAAGAAA	AGAAGGTA	AIGGAG	:	.333
TrMDHb9	:	TGCECTG	CA-CC	CATATNICNN					T C C T T	:	ددد. 378
TrMDHb10	:	TGCACTG	GAGTO	AATATEGCAG	TCATGGTT	GGTGGATTC	CCAAGAAA	AGAAGGTA	ATGGAN	:	380
TrMDHb11	:	TGCACTG	GAGTO	'AATAT TGCAG'	TCATGGTT	GGTGGATTC	CCAAGAAA	ALDDAADA	AIGGAG	•	381
TrMDHb12	:	TGCACTG	GAGTO	'AATAT@GCAG'	TCATGGTI	GGTGGATTC	CCAAGAAA	AGAAGGIA	AIGGAG	:	375
TrMDHb13	:	TGCACTG	GAGT	AATATTGCAG	TCATGGTT	GGTGGATTC	CCAAGAAA	AGAAGGTA	ATGGAG	:	371
TrMDHb14	:	TGCACTG	GAGT	CAATATTGCAG	TCATGGT'I	GGTGGATTC	CCAAGAAA	AGAAGGT	DAUDIA	•	379
TrMDHb15	:	TGCACTG	GAGT	CAATAT	TCATGGTL	GGTGGATTC	CCAAGAAA	AGAAGGIA	DADDIA	:	378
TrMDHb16	:	TGCACTG	GAGT	AATAT GCAG	TCATGGTI	'GGTGGATTC	CCAAGAAA	AGAAGGT	DADDIA	•	376
TrMDHb17	:	TGCACTG	GAGT	CAATATTGCAG	TCATGGT1	'GGTGGATTC	CCAAGAAA	AGAAGGIA	AIGGAG		374
TrMDHb18	:	TGCACTG	GAGT	CAATATTGCAG	TCATGGT'I	'GGTGGATTC	CCAAGAAA	AGAAGGI	AIGGAG	:	370
TrMDHb19	:	TGCACTG	GAGT	CAATATTGCAG	TCATGGTI	'GG'I'GGA'I'I'C	CCAAGAA	AGAAGGT	ATGGAG	:	363
TrMDHb20	:	TGCACTG	GAGT	CAATATTGCAG	TCATGGTT	'GGTGGA'I"I'C	CCAAGAAA	AGAAGGT	NTCCAC	:	363
TrMDHb21	:	TGCACTO	GAGT	CAATATTGCAG	TCATGGT	'GGTGGATTC	CCAAGAAA	AGAAGGT.	AIGGAG	•	359
TrMDHb22	:	TGCACTG	GAGT	CAATATTGCAG	TCATGGTT	'GGTGGA'I'TC	CCAAGAA	AAGAAGGT.	ATGGAG	•	350
TrMDHb23	:	TGCACTO	GAGT	CAATATAGCAG	TCATGGT	'GGTGGATTC	CCAAGAA	AAGAAGGT.	ATGGAG	:	349
TrMDHb24	:	TGCACTO	GAGT	CAATATEGCAG	TCATGGT'	GGTGGATTC	CCAAGAA	AAGAAGGT.	ATGGAG	:	345
TrMDHb25	:	TGCACTO	GAGT	CAATATTGCAG	TCATGGT'	rggTggATTC	CCAAGAA	AAGAAGGT.	AIGGAG	:	
TrMDHb26	:	TGCACTO	GAGT	CAATATTGCAG	TCATGGT'	rggrggatic	CCAAGAA	AAGAAGGT	ATGGAG	:	343
TrMDHb27	:	TGCACTO	GAGT	CAATATTGCAG	TCATGGT	rggrggattc	CCAAGAA	AAGAAGGT	ATGGAG	:	
TrMDHb28	:	TGCACTO	GAGT	CAATATTGCAG	TCATGGT	rggTggATTC	CCAAGAA	AAGAAGGT	ATGGAG	:	213
TrMDHb29	:	TGCACTO	GAGT	CAATATTGCAC	TCATGGT	rggrggattc	CCAAGAA	AAGAAGG'I'	ATGGAG	:	165
TrMDHb30	:	TGCACTO	GAGT	CAATATTGCAC	TCATGGT	TGGTGGATTC	CCAAGAA	AAGAAGGT	ATGGAG	:	162
TrMDHb31	. :								GGAG	:	4
m~MDIJb 2 2									NNNN	:	4

			*	440	*	460	*	480		
TrMDHb1	:								:	-
TrMDHb2	:								:	
TrMDHb3	: .	AGGAAGG	ATGTGATG	CTAAGAAIIG	TCTCTATT	PACAAGTCCC.	AGGCTTCTGCCC'	I'I'GAA	-	454
TrMDHb4	:	AGGAAGG.	ATGTGATG	CTAAGAA <u>I</u> G	TCTCTATT:	FACAAGTCCC.	AGGCTTCTGCCC'	I'I'GAA	-	451
TrMDHb5	:						AGGCTTCTGCCC'		•	451
TrMDHb6	:						AGGCTTCTGCCC'		-	444
TrMDHb7	•	AGGAAGG.	ATGTGATG	CTAAGAAUG	TCTCTATT'	FACAAGTCCC	AGGCTTCAGCCC	I'TGAA	•	445
TrMDHb8	:	AGGAAGG	ATGTGATG	CTAAGAATG	TCTCTATT'	TACAAGTCCC	AGGCTTCTGCCC	T'T'GAA	:	444
TrMDHb9	4								:	-
TrMDHb10	:	AGGAAGG	ATGTTATGT	TCTAAGAACG	TCTCTATT'	TACAAGTCCC	AAGCTTCTGCCC	TTGAA	-	438
TrMDHb11	:	AGGAAGG	ATGTGATG	CTAAGAACG	TCTCTATT'	TACAAGTCCC	AGGCTTCTGCCC	TTGAA	-	440
TrMDHb12	:	AGGAAGG	ATGT ATG	CTAAGAACG	TCTCTATT	TACAAGTCCC	AAGCTTCTGCCC	TTGAA	-	441
TrMDHb13	:	AGGAAGG	ATGTGATG	CTAAGAAIIG	TCTCTATT	TACAAGTCCC	AGGCTTCTGCCC	TTGAA	-	435
TrMDHb14	:	AGGAAGG	ATGTGATG	CTAANAA	TCTCTATT	TACAAGTCCC	AGGCTTCTGCCC	TTGAA	-	431
TrMDHb15	:	AGGAAGG	ATGT ATG:	FCTAAGAACG	TCTCTATT	TACAAGTCCC	AÄGCTTCTGCCC	TTGAA	-	439
TrMDHb16	:	AGGAAGG	ATGT ATG	rctaagaacg	TCTCTATT	TACAAGTCCC	AAGCTTCTGCCC	TTGAA	-	438
TrMDHb17	•	AGGAAGG	ATGTGATG	CTAAGAA	TCTCTATT	TACAAGTCCC	AGGCTTCTGCCC	TTGAA	-	436
TrMDHb18	:	AGGAAGG	ATGTGATG	rctaagaa <u>c</u> g	TCTCTATT	TACAAGTCCC	AGGCTTCTGCCC	TTGAA	-	434
TrMDHb19	:	AGGAAGG	ATGTGATG	CTAAGAA	TCTCTATT	TACAAGTCCC	AGGCTTCTGCCC	TTGAA	:	430
TrMDHb20	:	AGGAAGG	ATGTGATG	CTAAGAN	TCTCTATT	TACAANANN	AGNCTTNTGNCC	TTGAA	:	423
TrMDHb21	:	AGGAAGG	ATGTGATG	ICTAAGAACG	TCTCTATT	TACAAGTCCC	AGGCTTCTGCCC	TTGAA	:	423
TrMDHb22	:	AGGAAGC	ATGTGATG	CTAAGAA	TCTCTATT	TACAAGTCCC	CAGGCTTCTGCCC	TTGAA	:	419
TrMDHb23	:	AGGAAGG	ATGTTATG	TCTAAGAACG	TCTCTATT	TACAAGTCCC	CANGCTTCTGCCC	'T'TGAA	:	410
TrMDHb24	:	AGGAAGG	ATGTTATG	TCTAAGAACG	STCTCTATT	TACAAGTCCC	CAMGCTTCTGCCC	TTGAA	:	409
TrMDHb25	:	AGGAAGG	ATGTGATG	TCTAAGAACG	STCTCTATI	TACAAGTCCC	CAGGCTTCTGCCC	TTGAA	:	406
TrMDHb26	:	AGGAAGO	ATGTGATG	CTAAGAA	STCTCTATI	TACAAGTCCC	CAGGCTTCTGCCC	TTGAA	:	403
TrMDHb27	:	AGGAAGG	BATGTGATG	TCTAAGAACO	TCTCTATI	TACAAGTCC	CAGGCTTCTGCCC	CTTGAA	:	397
TrMDHb28	:	AGGAAGG	SATGTGATG	CTAAGAA	GTCTCTAT'I	TACAAGTCC	CAGGCTTCTGCCC	TTGAA	:	273
TrMDHb29	:	AGGAAGO	SATGTGATG	TCTAAGAACO	GTCTCTATI	TACAAGTCC	CAGGCTTCTGCCC	TTGAA	:	225
TrMDHb30	:	AGGAAGO	GATGTGATG	TCTAAGAACO	GTCTCTATI	TACAAGT CC	CAGGCTTCTGCCC	CTTGAA	:	222
TrMDHb31	:	AGGAAGO	GATGTGATG	TCTAAGAAC	GTCTCTATT	TACAAGTCC	CAGGCTTCTGCCC	TTGAA	:	64
TrMDHb32	:	NNGNANC	SNNGTGATG	TCTAAÑAAC	GTCTCTATI	TACAAGTCC	CAGGCTTCTGCC	CTTGAA	:	64

		*	500	*	520	-	540		
TrMDHb1	:							:	-
TrMDHb2	:							:	
TrMDHb3	:	AAGCATGCTGCC/	AACTGCAAGGTT?	rtggttat'	IGCTAACCCAG	CAAATACCA	ATGCA	•	514
TrMDHb4	:	AAGCATGCTGCTA	AACTGCAAGGTTT	rTGGTT <u>級</u> T"	IGCTAACCCAG	CAAAHACCA.	ATGCA	•	511
TrMDHb5	:	AAGCATGCTGCC	AACTGCAAGGNT:	rtggttg <u>n</u>	rgctaaccca <u>i</u>	C-AACACCA.	ATGCA	-	510
TrMDHb6	:	AAGCATGCTGCCA	AACTGCAAGGTT'	rtggtt//t	IGCTAACCCAG	CAAAJACCA	ATGCA	-	504
TrMDHb7	:	AAGCATGCTGCC2	AACTGCAAGGTT:	rtggttat'	IGCTAACCCAG	CAAA ACCA	ATGCA	-	505
TrMDHb8	:	AAGCATGCTGCC	AACTGCAAGGTT	rtggtt <u>a</u> t	TGCTAACCCAG	CAAAŢACCA	ATGCA	:	504
TrMDHb9	:							:	_
TrMDHb10	:	AAGCATGCTGCC2	AACTGCAAGGTT'	TTGGTTGT'	TGCTAACCCAG	CAAACACCA	ATGCA	-	498
TrMDHb11	:	AAGCATGCTGCC2	AACTGCAAGGTT'	TTGGTTGT'	TGCTAACCCAG	C-AACACCA	ATGCA	:	499
TrMDHb12	:	AAGCATGCTGCTGCC	AACTGCAAGGTT'	TTGGTT <u>Ģ</u> T'	TGCTAACCCAG	CAAACACCA	ATGCA	:	501
TrMDHb13	:	AAGCATGCTGCC			TGCTAACCCAG	CAAA!RACCA	ATGCA	:	495
TrMDHb14	:	AAGCATGCTGCC.	AACTGCAAGGTT'	TTGG				:	462
TrMDHb15	:	AAGCATGCTGCC	AACTGCAAGGTT'	TTGGTTGT	TGCTAACCCAG	CAAACACCA	ATGCA	:	499
TrMDHb16	:	AAGCATGCTGCTGCC.	AACTGCAAGGTT'	TTGGTTGT	TGCTAACCCAG	CAAACACCA	ATGCA	:	498
TrMDHb17	:	AAGCATGCTGCTGCC	AACTGCAAGG <u>N</u> T	TTGGGTÄT	TGCTAACCCAN	CAAATACCA	ATGCA	:	496
TrMDHb18	:	AAGCATGCTGCTGCC.	AACTGCAAGGTT'	TTGGTTGT	TGCTAACCCAG	C-AACACCA	ATGCA	:	493
TrMDHb19	:	AAGCATGCTGCC	AACTGCAAGGTT	TTGGTTÄT	TGCTAACCCAG	CAAATACCA	ATGCA	:	490
TrMDHb20	:	AANGATNCTG						:	433
TrMDHb21	:	AAĞCATĞCTGCTGCC	AACTGCAAGGTT	TTGGTTGT	TGCTAACCCAC	CAAACACCA	ATGCA	:	483
TrMDHb22	:	AAGCATGCTGCC	AACTGCAAGGTT	${ m TTGGTT}_{ m A}{ m T}$	TGCTAACCCAC	CAAATACCA	ATGCA	:	479
TrMDHb23	:	AAGCATGCTGCTGCC	AACTGCAAGGTT	TTGGTTGT	TGCTAACCCAG	CAAACACCA	ATGCA	:	470
TrMDHb24	:	AAGCATGCTGCTGCC	AACTGCAAGGTT	TTGGTTGT	TGCTAACCCAG	CAAACACCA	ATGCA	:	469
TrMDHb25	:	AAGCATGCTGCTGCC	AACTGCAAGGTT	TTGGTTGT	TGCTAACCCAC	CAAACACCA	ATGCA	:	466
TrMDHb26	:	AAGCATGCTGCC	AACTGCAAGGTT	TTGGTTÃI	TGCTAACCCAC	CAAAMACCA	ATGCA	:	463
TrMDHb27	:	AAGCATGCTGCC	AACTGCAAGGTT	TTGGTTGT	TGCTAACCCAC	CAAACACCA	AATGCA	:	457
TrMDHb28	:	AAGCA\(\frac{\delta}{3}\)GCTGCTGCC	AACTGCAAGGTT	TTGGTTÃŢ	TGCTAACCCAC	CAAAMACCA	AATGCA	:	333
TrMDHb29	:	AAGCATGCTGCC	AACTGCAAGGTT	TTGGTTGT	TGCTAACCCAC	CAAACACC	AATGCA	:	285
TrMDHb30	:	AAGCATGCTGCTGCC	AACTGCAAGGTT	TTGGTTGT	TGCTAACCCAC	GCAAACACC <i>I</i>	AATGCA	:	282
TrMDHb31	:	AAGCATGCTGCTGCC	AACTGCAAGGTT	TTGGTTGT	TGCTAACCCAC	GCAAACACCA	AATGCA	:	124
TrMDHb32	:	AAGCATGCTGCTGCC	AACTGCAAGGTT	TTGGTTGT	TGCTAACCCAC	GCAAACACCA	AATGCA	:	124

		*	560	*	580	*	600		
TrMDHb1	:						:		-
TrMDHb2	:						:	_	
TrMDHb3	:	TTGATCTTGAA	GGAGTTTGCTC	CATCTATTCC	AGAGAAAAACA	ATTTCAGGTTTGA	CTAGA :	_	574
TrMDHb4	:			CATCTATTCC	AGAGAAAAACA	\TTTCÄĞĞTTTGA	CTAGA:	_	571
TrMDHb5	:	TTGATCTTGNA					:	_	531
TrMDHb6	:	TTGATCTTGAA	GGAGTTTGCTC	CATCTATTCC	AGAGAAAAACA	ATTTCÄGGTTTGA	CTAGA :	_	564
TrMDHb7	:	TTGATCTTGAA	GGAĞTTTGCTC	CATCTATTCC	AGAGAAAAACA	\TTTCAĞĞTTTGA	CTAGA:	_	565
TrMDHb8	:	TTGATCTTGAA	GGAGTTTGCTC	CCATCTATTCC	'AGAGAAAAACA	ATTTCÄĞĞTTTGA	CTAGA:		564
TrMDHb9	:						:		
TrMDHb10	:					ATTTCTTGTTNGA			558
TrMDHb11	:					ATTTCTTGTTTGA		_	559
TrMDHb12	:	TTGATCTTGAA	GGAATTTGCTO	CCATCTATTCC	'AGAGAAAAAC	ATTTCTTGTTTGA	CTAGA:		561
TrMDHb13	:	TTGATCTTGAA	GGAGTTTGCT	CCATCTATTCC	'AGAGAAAAACA	ATTTCÄGGTTTGA	(CIIVA(G/A) :		555
TrMDHb14	:						:		
TrMDHb15	:	TTGATCTTGAA	GGAATTTGCT	CCATCTATTCC	CAGAGAAAAAC	ATTTCTTGTTTGA	CTAGA:		559
TrMDHb16	:	TTGATCTTGAA	GGAATTTGCT	CCATCTATTCC	CAGAGAAAAACA	ATTTCTTGTTTGA	CTAGA:		558
TrMDHb17	:	TTGATCTTGAA	GGAGTTTGCT	CCATCTATTCC	AGANAAAAAA	ATTTCA <mark>N</mark> CTTTG	:		550
TrMDHb18	:	TTGATCTTGAA	GGAATTTGCT	CCATCTATTCC	CAGAGAAAAAC	ATTTCTTGTTTGA	CTAGA:		553
TrMDHb19	:	TTGATCTTGAA	GGAGTTTGCT	CCATCTATTCC	CAGAGAAAAAC	ATTTCÄĞĞTTTGA	ACTAGA:		550
TrMDHb20	:							:	
TrMDHb21	:	TTGATCTTGAA	GGAATTTGCT	CCATCTATTC	CAGAGAAAAAC	ATTTCTTGTTTG	ACTAGA:	-	543
TrMDHb22	:	TTGATCTTGA	GGAGTTTGCT	CCATCTATTC	CAGAGAAAAAC	ATTTCÄGGTTTGA	ACTAGA:		539
TrMDHb23	:					ATTTCTTGTTTG		-	530
TrMDHb24	:	TTGATCTTGAA	GGAATTTGCT	CCATCTATTC	CAGAGAAAAAC.	ATTTCTTGTTTG	ACTAGA	-	529
TrMDHb25	:	TTGATCTTGA	AGGAATTTGCT	CCATCTATTC	CAGAGAAAAC.	ATTTCTTGTTTG	ACTAGA:	-	526
TrMDHb26	Ξ	TTGATCTTGA	AGGAĞTTTGCT	CCATCTATTC	CAGAGAAAAAC.	ATTTC AGGTTTG/	ACTAGA:	-	523
TrMDHb27	:	TTGATCTTGA	AGGAATTTGCT	CCATCTATTC	CAGAGAAAAC.	ATTTCTTGTTTG	ACTAGA:	-	517
TrMDHb28	:	TTGATCTTGA	AGGAĞTTTGCT	CCATCTATTC	CAGAGAAAAAC	ATTTCAGGTTTTG/	ACTAGA:	-	393
TrMDHb29	:					ATTTCTTGTTTG		-	345
TrMDHb30	:					ATTTCTTGTTTG!		-	342
TrMDHb31	:	TTGATCTTGAZ	AGGAATTTGCT	CCATCTATTC	CAGAGAAAAAC	ATTTCTTGTTTG	ACTAGA .	-	184
TrMDHb32	:	TTGATCTTGA	AGGAATTTGCT	CCATCTATTC	CAGAGAAAAAC	ATTTCTTGTTTG	ACTAGA	:	184

			*	620	*	640	*	660		
TrMDHb1	:								:	-
TrMDHb2	:								:	
TrMDHb3	:	CTTGATC		<u></u>					-	585
TrMDHb4	:	CTTGATC	ACAACAG	GGCATTGG					:	593
TrMDHb5	:								:	
TrMDHb6	:	CTTGATC	AC						:	573 603
TrMDHb7	:	CTTGATC.	ACAACAC	GGCATTGGG(CCAAATTTCTG	AAAG			:	597
TrMDHb8	:	CTTGATC	ACAACA(GGCATTGGG	CCAAATTTCT-				:	ועכ
TrMDHb9	:		<u></u>						:	567
TrMDHb10	:	CTTGATC							:	569
TrMDHb11	:	CTTGATC	ACC						•	592
TrMDHb12	:	CTTGATC	ACAACA(GGGCATTGGG	CCAAATTT				:	585
TrMDHb13	:	CTTGATC	ACAACA(GGGCA'T'I'GGG	CCAAATT				:	505
TrMDHb14	:								:	573
TrMDHb15	:	CTTGATC	ACAACA			A A A C A TTC A A	G		•	603
TrMDHb16	:	CTTGATC	ACAACA	GGGCATTGGG	CCAAATTTCTG	AAAGAIIGAA			•	-
TrMDHb17	:		7 67 7 67	20007 55000		222C			:	591
TrMDHb18	:	CTTGATC	ACAACA	GGGCATTGGG	CCAAATTTCTG	21212C			•	571
TrMDHb19	:	CTTGATC	:ACAACA	GGGCATTG					•	
TrMDHb20	:	CERT CARE	12 C2 2 C2	CCCCATTCCC	CCAAATTTCTG	AAAGATTG			:	585
TrMDHb21	:	CTTGATC	ACAACA	GGGCAI IGGG CCCCATTCCC	CCAAATTTCTG	AAAGATTGAA	TATTCAAGTT'	TCTGAT	:	599
TrMDHb22	:	CTTGATC	ACAACA	GGGCAIIGGG CCCCNTTCCC	CCAAATTTCTG	AAAG			:	568
TrMDHb23	:			GGGCATTGGG GGGCATTGGG					:	558
TrMDHb24	:	CTIGATO	ACAACA AD A AD A C	CCCCATTGGG	CCAAATTTCTG	AAAGATTGAA	TGTTCAAGTT	TCTGAT	:	586
TrMDHb25	:	CMIGAIC	ACAACA	CCCCATTCCC	CCAAATTTCTG	AAAGATTGA	ТТСААGTT	TCTGAT	:	583
TrMDHb26	:	CIIGAIC	ACAACA TA CA A CA	CCCCATTCCC	CCAAATTTCTC	AAAGATTGA	ATGTTCAAGTT	TC	:	573
TrMDHb28	•	CIIGAIC	LACAACA TACAACA	CCCCATTCCC	CCAAATTTCTG	AAAGATTGAA	ATÄTTCAAGTT	TCTGAT	:	453
TrMDHb28	:	CTIGATO	CACAACA	CCCCATTGÑG	CCAAATTTCTC	AAAGATTGA	ATGTÜCAAGTT	TCTGAT	:	405
TrMDHb30	•	CTTCATC	CACAACA	CCCCATTCEC.	CCAAATTTCTG	AAAGATTGA	ATGTCCAAGTT	TCTGAT	:	402
TrMDHb30	:	CTTGAT	CAACA	GGGCATTGGC	CCAAATTTCTC	AAAGATTGA	ATGTTCAAGTT	TCTGAT	:	244
LEMDHD3T	•	CTTGAT		GGGCATTGGG	CCAAATTTCTC	EAAAGATTGA	ATGTTCAAGTT	TCTGAT	:	244

			*	680	*	700	*	720		
rrMDHb1	:								:	-
rrMDHb2	:								:	-
TrMDHb3	:								:	-
TrMDHb4	:								:	~
rrMDHb5	:								:	-
TrMDHb6	:								:	-
TrMDHb7	:								:	-
TrMDHb8	:								:	-
TrMDHb9	:								:	-
TrMDHb10	:								:	-
TrMDHb11	:								:	-
TrMDHb12	:								:	-
TrMDHb13	:								:	-
TrMDHb14	:								:	_
TrMDHb15	:								:	. –
TrMDHb16	• :								:	_
TrMDHb17	:		,						:	. –
TrMDHb18	:								: '	-
TrMDHb19	·:								:	-
TrMDHb20	:								:	-
TrMDHb21	:								:	
TrMDHb22	:	GTAAAGA	ATGT						:	610
TrMDHb23	:								:	-
TrMDHb24	:								:	
TrMDHb25	:	GTAAAGA	ATGTCATTA	TCTGGGGTAATC	ATTCATCA	ACTCAGTATCCT	GATGTCA	ACCAT	:	646
TrMDHb26	:								:	-
TrMDHb27	:								:	
TrMDHb28	:	GTAAAGA	ATGTCATTA	TCTGGGGTAATC	ATTCATCA	ACTCAGTATCCT	'GATGTCAA	ACCAT	:	513
TrMDHb29	٠:	GTAAAGA	ATGTCATTA	TCTGGNGTAATC	ATTCATCA	ACTCAG ATCCI	'GATGTCA!	ACCAT	:	465
TrMDHb30	:	GTAAAGA	ATGTCATTA	TCTGGGGTAATC	ATTCATCA	ACTCAGTATCCI	GATGTCA	ACCAT	:	462
TrMDHb31	:	GTAAAGA	ATGTCATTA	TCTGGGGTAATC	ATTCATCA	ACTCAGTATCCI	'GATGTCA	ACCAT	:	304
TrMDHb32	:	GTAAAGA	ATGTCATTA	TCTGGGGTAATC	ATTCATCA	ACTCAGTATCCT	GATGTCA	ACCAT	:	304

			*	740	*	760	*	780		
TrMDHb1	:								:	-
TrMDHb2	:								:	-
TrMDHb3	:								:	-
TrMDHb4	:								:	-
TrmDHb5	:								:	-
TrMDHb6	:								:	-
TrMDHb7	:								:	-
TrMDHb8	:								:	-
TrMDHb9	:								:	-
TrMDHb10	:								:	-
TrMDHb11	:								:	-
TrMDHb12	:								:	
TrMDHb13	:								:	-
TrMDHb14	:								:	_
TrMDHb15	:								:	_
TrMDHb16	:		. 						:	-
TrMDHb17	:								:	-
TrMDHb18	:								:	-
TrMDHb19	:								:	-
TrMDHb20	:								:	-
TrMDHb21	:								:	_
TrMDHb22	:								:	-
TrMDHb23	:								:	-
TrMDHb24	:								:	
TrMDHb25	:	GCAACTG'	TTAACACCC	CCGCTGGGGAGA	AGCCTGTC	CGTGAGCTTGTT	TCTGATGA	CGCC	:	706
TrMDHb26	:								:	_
TrMDHb27	:								:	
TrMDHb28	:	GCAACTG'	TTAACACCC	CCGCGGGGGAGA	AGCCTGTC	CGTGAACTTGTT	<u></u>		:	562
TrMDHb29	:	GCAACTG'	TTAACACCC	CNCGCTGNNGAGA	AGCCTGNC	CGTGAGCTMGTT	TC		:	515
TrMDHb30	:	GCAACTG'	TTAACACC	CCGCTGGGGAGA	AGCCTGTC	CGTGAGCTTGTT	TCTGATGA	CGCC	:	522
TrMDHb31	:	GCAACTG'	TTAACACC	CCCGCTGGGGAGA	AGCCTGTC	CGTGAGCTTGTT	TCTGATGA	CGCC	:	364
TrMDHb32	:	GCAACTG'	TTAACACCC	CCCGCTGGGGAGA	AGCCTGTC	CCGTGAGCTTGTT	'TCTGATG <i>P</i>	ACGCC	:	364

			*	800	*	820	*	840		
TrMDHb1	:								:	-
TrMDHb2	:				·				:	-
TrMDHb3	:								:	_
TrMDHb4	:								:	_
TrMDHb5	:								:	_
TrMDHb6	:								:	_
TrMDHb7	:									_
TrMDHb8	:								:	_
TrMDHb9	:								:	_
TrMDHb10	:								•	_
TrMDHb11	:								:	_
TrMDHb12	:								:	
TrMDHb13	:								:	_
TrMDHb14	:								:	_
TrMDHb15	:								:	
TrMDHb16	:								:	_
TrMDHb17	:								:	_
TrMDHb18	:								•	_
TrMDHb19	:								:	_
TrMDHb20	፡								-	_
TrMDHb21	:								:	_
TrMDHb22	:								:	_
TrMDHb23	:								:	_
TrMDHb24	:				mmc2 2 C2 2	COMOCHCOTO		-	:	752
TrMDHb25		TGGTTGA	ATGGAGAA'I	"ICATATCTACCG	TTCAACAA	CGTGGTGCTG			:	
TrMDHb26									:	_
TrMDHb27									:	_
TrMDHb28									:	_
TrMDHb29						COTCOTCOTCO	እ አጥጥ አጥጥ እ	ACCCT	:	582
TrMDHb30		TGGTTGA	ATGGAGAAT	TCATATCTACCG	TTCAACAA	ACGTGGTGCTGC	, v . d. d. s.	AGGCT	:	424
TrMDHb31		TGGTTGA	ATGGAGAAT	"TCATATCTACCG	FTTCAACA	ACGTGGTGCTGC	<u> </u>	ACCCT	:	424
TrMDHb32	:	TGGTTGA	ATGGAGAAT	TTCATATCTACCC	FTTCAACAA	ACGTGGTGCTGC		70.00 T	•	127

			*	860		880	*	900		
TrMDHb1	:								:	-
TrMDHb2	:								:	_
TrMDHb3	:								:	-
TrMDHb4	:								:	-
TrMDHb5	:								:	-
TrMDHb6	:								:	-
TrMDHb7	:								:	-
TrMDHb8	:								:	-
TrMDHb9	:								:	-
TrMDHb10	:								:	-
TrMDHb11	:								:	-
TrMDHb12	:								:	-
TrMDHb13	:								:	-
TrMDHb14	:								:	-
TrMDHb15	:								:	-
TrMDHb16	:								:	
TrMDHb17	:								:	-
TrMDHb18	:								:	-
TrMDHb19	:								:	-
TrMDHb20	:								:	-
TrMDHb21	:								:	
TrMDHb22	:								:	-
TrMDHb23	:								:	-
TrMDHb24	:								:	-
TrMDHb25	:								:	-
TrMDHb26	:								:	_
TrMDHb27	:								:	-
TrMDHb28	:								:	-
TrMDHb29	:								:	
TrMDHb30	:	AGAAAGC'	TTTCAAGTG						:	598
TrMDHb31	:	AGAAAGC'	TTTCAAGCG	CACTATCCGCTG	CTAGCGCI	GCTTGCGACC	ACATTCGCC	ATTGG	:	484
TeMDUb 2 2		A CA A A CC	TTTCAACCC	CACTATCCGCTC	CTAGCGCI	GCTTGCGACC	'ACATTCGCC	}ATTGG	:	484

			*	920	*	940	*	960		
TrMDHbl	:								:	-
TrMDHb2	:								:	-
TrMDHb3	:								:	-
TrMDHb4	:								:	_
TrMDHb5	:								:	-
TrMDHb6	:								:	-
TrMDHb7	:								:	_
TrMDHb8	:								:	-
TrMDHb9	:								:	-
TrMDHb10	:								:	-
TrMDHb11	:								:	-
TrMDHb12	:								:	-
TrMDHb13	:								:	
TrMDHb14	:								:	-
TrMDHb15	:								:	-
TrMDHb16	:								:	_
TrMDHb17	:								:	-
TrMDHb18	:								:	-
TrMDHb19	:								:	-
TrMDHb20	:								:	-
TrMDHb21	:								:	-
TrMDHb22	:								:	-
TrMDHb23	:								:	-
TrMDHb24	:								:	-
TrMDHb25	:								:	-
TrMDHb26	:								:	-
TrMDHb27	:								:	-
TrMDHb28	:								:	
TrMDHb29	:								:	-
TrMDHb30	:								:	
TrMDHb31	:	GTTCTT	GGAACTCC	CCAGGGCACC'	TTCGTTTC <i>i</i>	AATGGGAGTGTA	TTCTGATGG'	TTCTTAC	:	544
TrMDHb32	•	GTTCTT	GGAACTCC	CCAGGGCACC'	TTCGTTTC	AATGGGAGTGTA	TTCTGATGG	TTCTTAC	:	544

			*	980	*	1000	*	1020		
TrMDHb1	:								:	_
TrMDHb2	:								:	-
TrMDHb3	:								:	
TrMDHb4	:								:	-
TrMDHb5	:								:	-
TrMDHb6	:								:	-
TrMDHb7	:								:	-
TrMDHb8	:								:	-
TrMDHb9	:								:	-
TrMDHb10	:								:	-
TrMDHb11	:								:	_
TrMDHb12	:								:	-
TrMDHb13	:								:	-
TrMDHb14	:								:	_
TrMDHb15	:								:	-
TrMDHb16	:								:	_
TrMDHb17	:								:	-
TrMDHb18	:								:	-
TrMDHb19	:								:	_
TrMDHb20	:								:	_
TrMDHb21	:								:	-
TrMDHb22	:								:	-
TrMDHb23	:								:	-
TrMDHb24	:								:	-
TrMDHb25	:								:	_
TrMDHb26	:								:	_
TrMDHb27	:								:	-
TrMDHb28	:								:	-
TrMDHb29	:								:	-
TrMDHb30	:								:	-
TrMDHb31	:	AACGTAC	CCAGCTGGA	CTCATCTATTCA'	TTCCCTGT	CACCACTGCTAA	rggggaa'	IGGAA -	:	603
TrMDUA32		AACGTAC	CAGCTGGA	CTCATCTATTCA'	TTCCCTG:	CACCACTGCTAA	I'GGGGAA'	IGGAAA	:	604

			*	1040	*	1060	*	1080		
TrMDHb1	:								:	-
TrMDHb2	:								:	_
TrMDHb3	:								:	-
TrMDHb4	:								:	-
TrMDHb5	:								:	-
TrMDHb6	:								:	-
TrMDHb7	:								:	-
TrMDHb8	:								:	-
TrMDHb9	:								:	-
TrMDHb10	:								:	
TrMDHb11	:								:	-
TrMDHb12	:								:	_
TrMDHb13	:								:	_
TrMDHb14	:								:	-
TrMDHb15	:								:	-
TrMDHb16	:								:	-
TrMDHb17	:								:	-
TrMDHb18	:								:	-
TrMDHb19	:								:	-
TrMDHb20	:								:	-
TrMDHb21	:								:	-
TrMDHb22	:								:	-
TrMDHb23	:								:	-
TrMDHb24	:								:	-
TrMDHb25	:								:	-
TrMDHb26	:								:	-
TrMDHb27	:								:	-
TrMDHb28	:								:	-
TrMDHb29	:								:	_
TrMDHb30	:								:	-
TrMDHb31	:								:	-
Trempine 3		ATTCTTC	A AGGACT	TTCAATTGACGAG	TTCTCAA	GGAAGAAGTTGGA	CTTGACA	GCTGAA	:	664

		*	1100	*		
TrMDHb1	:				:	-
TrMDHb2	:				:	-
TrMDHb3	:				:	-
TrMDHb4	:				:	-
TrMDHb5	:				:	-
TrMDHb6	:				:	-
TrMDHb7	:				:	-
TrMDHb8	:				:	-
TrMDHb9	:				:	-
TrMDHb10	:				:	-
TrMDHb11	:				:	-
TrMDHb12	:				:	-
TrMDHb13	:				:	_
TrMDHb14	:				:	-
TrMDHb15	:				:	-
TrMDHb16	:				:	-
TrMDHb17	:				:	-
TrMDHb18	:				:	-
TrMDHb19	:				:	-
TrMDHb20	:				:	-
TrMDHb21	:				:	-
TrMDHb22	:				:	-
TrMDHb23	:				:	-
TrMDHb24	:				:	_
TrMDHb25	:				:	_
TrMDHb26	:				:	-
TrMDHb27	:				:	-
TrMDHb28	:				:	_
TrMDHb29	:				:	-
TrMDHb30	:				:	-
TrMDHb31	:				:	
TWMDUD 2 2		CACTTATCCCACGA	AAAGAGTTTGGCA	TACT	:	695

145/241

TrMDHc :	:	AAAGNGAAT	* TGGAATAT	20 ACGACACTCCA	* ITCCATACI	40 TTCCATTCCNT	* ACTTTGCTTT	60 CTC	:	60
TrMDHc :	:	GCTCTCTCT	* CTCTTTAT	80 ICTCGAAAAGC	* FTTTTCAG(100 CCAACAACGGA		120 AGG	:	120
TrMDHc	:	CCGTCGATC		140 CGTCCAATCAG	* CCGTCTCC	160 CGCGCCTCTTC	* CACCTAACC	180 CGC	:	180
TrMDHc	:	CGTGGCTAT		200 ACCAGTTCCAG	* AACGCAAG	220 GTGGCCATTCT	* CGGCGCTGCC	240 CGGC	:	240
TrMDHc	:	GGGATCGG	* CCAGCCTCT	260 CTCTCTTCTCA	* TGAAGCTC	280 AACCCTCTCGT	* TTCAACCCT#	300 ATCT	:	300
TrMDHc	:	CTTTATGA:	* TATTGCTGG	320 AACCCCTGGTG	* TCGCCGCT	340 GATGTCAGCCA	* CATCAACTC	360 CAGA	:	360
TrMDHc	:	TCTGAGGT	* AACTGGGTA	380 .TGCAGGTGAAG	* SAAGAGCTT	400 GGAAAAGCTTT	* 'GGAGGGTGC'	420 IGAT	:	420
TrMDHc	:	GTTGTTAT	* AATTCCTG(440 CTGGTGTGCCCA	* \GAAAGCCT	460 GGAATGACTCG	* !TGATGATCT'	480 TTTC	:	480
TrMDHc	:	AATATTAA	* .CGCTGGCAT	500 TTGTCAAGTCAC	* CTTGCCACT	520 GCTATTTCTAA	* AGTACTGCCC	540 CCAT	:	540
TrMDHc	:	GCCCTTGT	* TAACATGA:	560 FAAGCAACCCTO	* GTGAACTCC	580 CACCGTTCCCAT	* TTGCTGCAGA	600 GGTT	:	600
TrMDHc	:	TTCAAGAA	* \GGCAGGGA	620 CATATGACGAGA	* AAGAGATTO	640 STTTGGGGTTAG	* CAACCCTTGA	660 TGTA	:	660
TrMDHc	:	GTCAGGGC	* :AAAAACTT	680 ICTATGCCGGG	* AAAGCTAA!	700 AGTTCCAGTTG	* CCGAGGTCAA	720 TGTA	:	720
TrMDHc	:	CCTGTTA	* PAGGAGGCC	740 ATGCAGGAGTT	* ACTATTCT	760 FCCATTATTTT	* NTCAGGCAAC	780 ACCT	:	780
TrMDHc	:	: CAAGCCA!	* ATCTGGGTG	800 ATGATACCCTT	* AAGGNTTT	820 AACGGNANGGA	* CACAAGATGO	840 BAGGA		840
TrMDHc	:	: ACAGAAG	* TTGNGACCG	860 CCAAGGCTGGA	* AAGGGTTC	880 TGCAACTTTGT	* CAATGGCTT!	900 ATGCT		900
m-MDII-		GGA GGGA	*	920	* ያል ል ርረርአየርጥ	940 Саатссасттс	* CAGATGTTA	960 TTGAG		960

FIGURE 61

		*	980	*	1000	*	1020		
rMDHc	:	TGCTCATATGT	GCAATCCAATATCA	TCTCTGACC	TTCCTTTCTT	TGCTTCCAAG(STGAGG	:	1020
rmDHc	:	* ATTGGGAAGAA	1040 TGGTGTGGAAGAAA	* TTCTGGGC1	1060 TAGGTTCTCT	* CACAGATTTC	1080 GAGCAA	:	1080
		*	1100 AAACCTCAAGGCTG	* !>\	1120 "Catctattca	* ^ ^ ^ ^ ^ ^ ^ ^ ^ ^ ^	1140 AAATTT		1140
FrMDHC	:	CAAGGCCTTGA	AAACCTCAAGGCTG	AACICAAA.	CAICIAIIGA	Philodoinii o		•	
rmDHc	:	* GCCTCCCAGTA	1160 ATCGAACATGTCAT	* CACATTACT	1180 GATTTTTCCA	* .TTTAGAACCA	1200 GATCAA	:	1200
TrMDHc	:	* ATTTTGCAAAT	1220 TCAGAACAATTGTT	* TGTAATGT'	1240 IGCCGGTAGGI	* 'ATACCCCTAG	1260 ATTTAA	:	1260
TrMDHc	:	* TAAGTAAATCI	1280 GCGAGAGCAGTTTA	* ATTGCTGCA	1300 GGGACTGAAAI	* TAAAACCAGI	1320 TTTAGG	:	1320
TrMDHc	:	* TTGGCCTTTC	1340 CATTCGTAATGGCCC	* CTTCATTGT	1360 TGCATGNTTTC	* CATATAATGCA	1380 ATTGAA	:	1380
т∽м∩нс		*	1400 CANCGATACACANC	CCCC : 14	08				

			*	20	*	40	*	60		
rMDHc	:	MRPSMLRSV	QSAVSRASS	HLTRRGYATEP	VPERKVAI	LGAAGGIGQPL	SLLMKLNPI	VST	:	60
TrMDHc	:	LSLYDIAGI	* PGVAADVSI	80 HINSRSEVTGYA	* AGEEELGKA	100 LEGADVVIIPA	* \GVPRKPGMT	120 TRDD	:	120
[rMDHc	:	LFNINAGIV	* /KSLATAIS!	140 KYCPHALVNMIS	* ENPVNSTVI	160 PIAAEVFKKAGI	* TYDEKRLFG	180 /TTL	:	180
IrMDHc	:	DVVRAKTF		200 AEVNVPVIGGHA	* AGVTILPLI	.220 FXQATPQANLGI	* DTLKXLTX	240 XTQD	:	240
TrMDHc	:	GGTEVXTA	* KAGKGSATL	260 SMAYAGAIFADA	* AXLKXLNG	280 VPDVIECSYVQ	* SNIISDLPF	300 FASK	:	300
ጥ ታ MDዘር	:	VRTGKNGV		320 TDFEQQGLENL	* KAELKSSI	340 EKGIKFASQ :	345	-		

```
60
                                                            40
                60
          AAAGNGAATTGGAATNT-CGAC-CTCCATTCCNTACT
TrMDHc1
                                                                                               59
TrMDHc2
                                                                                                42
TrMDHc3
                                           -----<mark>G</mark>MACT-CCATTCCNTACTTTM<mark>T</mark>TMCC
                                                                                               30
TrMDHc4
                                                      GCATCC TTCCNTACTTT NTT TTCGCT
--CNTCCATCCCNTACTTT-NTTCNTCGCT
                                                                                                27
TrMDHc5
                                                        CNTCCATCCCNTACTTT-NTTENTCGCT
                                                                                                27
TrMDHc6
                                                                                                27
TrMDHc7
                                                         TECCATTCCNTACTTTNTTTATTN
                                                                                                27
TrMDHc8 : --
TrMDHc9 : -----TCCATTCCNTACT@T-ATTTNTCGCT
                                                                                                25
TrmDHc10 : -----TCC-TTCCTTACTTTCATCGCT
                                                                                                25
TrMDHc11 : -----
TrMDHc12 : -----
TrMDHc13 : -----
TrMDHc14 : --
TrMDHc16 : -----
                                                       100
                                80
              CTCTCTCTCTTATTCTCGAAAAGCTTGTTCAGCCAACAACG-AGAGAATAATGAGGCCGTCG
TrMDHc1 :
             CTCTCTCT_T_TATTCTCGAAAAGCTTTTTCAGCCAACAACG_AGAGAATAATGAGGCCGTCG
CTCTCTCTTTTTATTCTCGAAAAGCTTTTTCAGCCATCAACGGAGAGAATTATGAGTCGTCG
CTCTCTCTCTCTCTATTCTCGAAAAGCTTTTTCAGCCC_ACAACG_AGAGAATTATGAGGCCGTCG
TrMDHc2
                                                                                            : 105
TrMDHc3
                                                                                                91
TrMDHc4 :
              CTCTCTC<mark>--</mark>TTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGGCCGTCG
                                                                                                88
TrMDHc5 :
TrMDHc7 : CTCTCTCTTTATTCTCGAAAAGCTTTTT_AGCCAACAACGGAGAGAATTATGAGGCCGTCG
TrMDHc8 : CTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGGCCGTCG
TrMDHc9 : CTCTCTCTTTATTCTCGAAAAGCTTTTTTAGCCCAACAACG_AGAGAATTATGAGGCCGTCG
                                                                                                87
                                                                                                89
                                                                                                87
TrMDHc10 : CTCTCTC--TTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAAATTATGAGGCCGTCG
                                                                                                86
                   48
                                                                                                46
 TrMDHc12 :
 TrMDHc13 :
 TrMDHc14:
 TrMDHc15 :
 TrMDHc16 : --
 TrMDHc17 : -----
                                                                             180
              ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT
 TrMDHc1 :
 TrMDHc2 :
              ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT
                                                                                               182
              ATGCTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT
ATGCTCAGATCTGTCCAATCAGCCGTTTCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT
                                                                                             : 168
 TrMDHc3
                                                                                             : 154
 TrMDHc4
                                                                                             : 151
                   TCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT
 TrMDHc5
                  TCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT
                                                                                                150
 TrMDHc6 :
              ATG TCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTTCTCTCACCTAACCCGCCGTGGCTAT
ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCCTCTTCTCACCTAACCCGCCGTGGCTAT
ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT
ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT
                                                                                             : 153
 TrMDHc7
                                                                                             : 152
 TrMDHc8
                                                                                             : 150
 TrMDHc9
                                                                                             : 149
 TrMDHc10 :
              ATG TCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT
ATGCTCAGATCTGTCCATCAGCCGTATCCCGCGCCTCCTCTCACCTAACCCGCCGTGGCTAT
ATGCTCAGATCTGTCCAATCAGCCGTATCCCGCGGCCTCCTCTCACCTAACCCGCCGTGGCTAT
                                                                                               111
 TrMDHc11:
                                                                                                108
 TrMDHc12:
                                                                                                111
 TrMDHc13 :
 TrMDHc14 :
 TrMDHc15
 TrMDHc16
 TrMDHc17 :
```

```
240
                   200
           GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG
GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG
                                                                              : 248
TrMDHc1
                                                                              : 245
TrMDHc2
: 231
TrmDHc4 : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGÄGCTGCCGGCGGGATCGGÄCAG
                                                                              : 217
           GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG
                                                                              : 214
TrMDHc5 :
TrMDHc6
           GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGC<u>CGGCGGGATCGGCCAG</u>
                                                                                213
           GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGATCGGCCAG
GCTACCGAACCAGTTCCAGAACGCAÄGGTGGCCATTCTCGGÄGCTGCÄGGGCGGGATCGGÄCAG
TrMDHc7
                                                                              : 216
                                                                              : 215
TrMDHc8
           GCTACCGAACCAGTTCCAGAACGCAÄGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG
TrMDHc9 :
           GCTACCGAACCAGTTCCAGAACGCAAGGÄGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG
                                                                              : 212
TrMDHc11: GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG
                                                                              : 174
TrMDHc12 : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCTGGCGGGATCGGCCAG
                                                                                171
           GCTACCGAACCAGTTCCAGAACGCAAGGNGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG
                                                                                1.74
TrMDHc13 :
TrMDHc14:
TrMDHc15 : --
TrMDHc16 : ------
TrMDHc17 :
                                     280
                                                          300
TrmDHc1 : CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
                                                                              : 311
TrmDHc2 : CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTATGATATTGCT
TrmDHc3 : CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
                                                                              : 308
                                                                                294
TrMDHc4 :
           \mathtt{CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT}
                                                                              : 280
TrMDHc5 : CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
                                                                              : 277
TrmDHc6 : CCTCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
                                                                              : 276
TrmDHc7 : CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
           \mathtt{CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
                                                                               : 278
TrMDHc8
TrMDHc9 :
           \tt CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
                                                                               : 276
TrMDHc10 : CCTCTCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
                                                                               : 275
TrmDHc11: CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
                                                                               : 237
TrmDhc12: CCTCTCTCTCTCTCATGAAGCTCAAAGCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
                                                                                 234
TrmDHc13: CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT
                                                                                 237
TrMDHc14 :
TrMDHc15 :
TrMDHc16 :
TrMDHc17 : ------
                                   340
                                                       360
           GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
TrMDHc1 :
                                                                                374
TrmDhc2 : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
                                                                               : 371
TIMDHc3 : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
                                                                                 357
TrMDHc4
           GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
                                                                                 343
            GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
                                                                                340
TrMDHc5
           GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
TrMDHc6
           GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
                                                                               : 342
TrMDHc7
           GGAACCCCTGGTGTCGCCGCTGA<u>TGTCAGCCACATCAACTCCAGATCTGAGGTAACTG</u>GGTA<u>T</u>
                                                                                 341
TrMDHc8
TrMDHc9
            GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
                                                                                 339
            GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
                                                                               : 338
TrMDHc10 :
            GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
TrMDHc11 :
            GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
                                                                               : 297
 TrMDHc12 :
            GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT
                                                                                 300
 TrMDHc13 :
            ------GNGTGTCGCCGCTGNNGTCAGCCACATCAACTCCANANCTGA-GTAACTGGGTAT
GNTGATGT-NGCC-CAT-AACTCC-GATCTGAGGTAACTGGGTAT
 TrMDHc14 :
                                                                                  54
                                                                                  41
 TrMDHc15 :
 TrMDHc16 :
 TrMDHc17 :
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440
                                                      420
            80
                                400
            GCAGGTGAAGAAGACCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT
                                                                                : 437
TrMDHcl :
                                                                                : 434
TrMDHc2 :
           GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT
TrmDHc3 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTAAATTCCTGCGGGT
TrMDHc4 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTATAATTCCTGCTGGT
TrMDHc5 : GCAGGTGAAGAAGAGCTTTGGAAGAGGGTGCTGATGTTATAATTCCTGCTGGT
                                                                                 : 406
TrmDHc6 : GCAGGTGAAGAAGACTTGGAAAAGCTTTGGAGGGTGCTGATGTTATAATTCCTGCGGGT
TrmDHc7 : GCAGGTGAAGAAGAGCTTTGGAAGAGGGTGCTGATGTTATAATTCCTGCGGGT
                                                                                 : 405
TrMDHC8 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT
                                                                                 : 404
TrMDHc9 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTATAATTCCTGCCGGT
TrMDHc10 : GCAGGTGAAGAAGAGCTTTGGAAAAGCTTTGGAGGGTGCTGATGTTATAATTCCTGCCGGT
                                                                                   402
                                                                                 : 401
                                                                                 : 363
TrMDHc11: GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTATAATTCCTGCGGGT
            {	t GCAGGTGAAGAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT}
                                                                                   360
TrMDHc12 :
            GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT
                                                                                 : 363
TrMDHc13 :
            {	t GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT}
TrMDHc14 :
TrMDHc15 : GCAGGTGAAGAAGACTTTGGAAAAGCTTTGGAGGGTGCTGATGTTATAATTCCTGCTGGT
                                                                                   104
TrMDHc16: --
TrMDHc17:
                                                   480
                             460
            GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG
TrMDHc1 :
            {	t GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCT}{	t TTTCAATATTAACGCTGGCATTGTCAAG}
TrMDHc2 :
         TrMDHc4 :
TrMDHc5
TrMDHc6
TrMDHc7 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 468
TrMDHc8 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 467
TrMDHc9 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTTAAG : 465
TrMDHc10 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG
                                                                                 : 464
            GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG
                                                                                  : 426
 TrMDHc11 :
TrMDHc12 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG
                                                                                 : 423
 TrMDHc13 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG
             GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG
                                                                                 : 180
 TrMDHc14 :
 TrMDHc15 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG
 TrMDHc16 :
 TrMDHc17 :
             TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATG
 TrMDHc1 :
             TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 560
 TrMDHc2 :
 TrMDHc3 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 546
             TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 532
 TrMDHc4
                                                                                 : 529
             TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT
 TrMDHc5
             TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT
                                                                                  : 528
 TrMDHc6
            {	t TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT}
                                                                                  : 531
 TrMDHc7
         * TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT
                                                                                  : 530
 TrMDHc8
             TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT
                                                                                  : 528
 TrMDHc9
             TCACTTGCCACTGĞTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT
                                                                                  : 527
 TrMDHc10 :
                                                                                  : 489
             TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT
 TrMDHc11 :
             TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT
                                                                                  : 486
 TrMDHc12 :
 TrmDHc13 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT
                                                                                  : 489
             TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT
 TrMDHc14 :
             TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT
                                                                                  : 230
 TrMDHc15
                                                                                       3
 TrMDHc16
 TrMDHc17:
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		*	580	*		600	*	6:	20	*		
TrMDHc1 :	: •									:		-
TrMDHc2 :	:	GTGAACTC	CACCGTTCC	CATTGCT	GCAGAG	GTTTTCAAC	SAAGGC	AGGG		:		808
TrMDHc3 :	:	GTGAACTC	CACCGTTCC	CATTGCT	GCAGG-					:		575 563
TrMDHc4	:	GTGAACTC	CACCGTTCC	CATTGCT	GCAGAG	G						583
TrMDHc5	:	GTGAACTC	CACCGTTCC	CATTGCT	'GCAGAG	GTTTTCAAC	SAAGGC	AGGGACA	IIAII	;		591
TrMDHc6	:	GTGAACTC	CACCGTTCC	CATTGCT	'GCAGAG	GTTTTCAA	BAAGGC	AGGGACA	TATGACG.	AGAAG		591 594
TrMDHc7	:	GTGAACTC	CACCGTTCC	CATTGCT	'GCAGAG	GTTTTCAA	JAAGGC.	AGGGACA	TATGACG.	AGAAG	-	556
TrMDHc8	:	GTGAACTC	CACCGTTCC	CCATTGCT	GC					;	-	591
TrMDHc9	:	GTGAACTC	CACCGTTCC	CCATTGCT	'GCAGAG	GTTTTCAA	BAAGGC.	AGGGACA	TATGACG	AGAAG		590
TrMDHc10	:	GTGAACTC	CACCGTTCC	CCATTGCT	GNAGAG	GTTTTCAA	JAAGGC	NGGGACA	TATGACN	AGAAN :		552
TrMDHc11	:	GTGAACTC	CACCGTTC	CCATTGCT	'GCAGAC	GTTTTCAA	JAAGGC.	AGGGACA	TATGACG	AGAAG		549
TrMDHc12	:	GTGAACTC	CACCGTTC	CCATTGCI	'GCAGAC	GTTTTCAA	JAAGGC.	AGGGACA	TATGACG	AGAAG		552
TrMDHc13	:	GTGAACTC	CACCGTTC	CATTGCI	'GCANAC	GTTTTCAA	JAAGGC.	AGGGACA	TAIGACN	AGAAG		306
TrMDHc14	:	GTGAACTC	CACCGTTC	CCATTGCT	GCAGAG	GTTTTCAA	JAAGGC.	AJAĐĐĐA AJAGOA	TAIGACG	AGAAG		293
TrMDHc15	:	GTGAACTC	CACCGTTC	CCATTGCT	'GCAGAG	GTTTTCAA	GAAGGC	AGGGACA	MAIGACG	AGAAG		-
TrMDHc16	:										•	_
TrMDHc17	:										•	
		ϵ	540	*	660)	*	680		*		
TrMDHc1	:										: .	_
TrMDHc2	:										:	-
TrMDHc3	:										:	_
TrMDHc4	:										:	_
TrMDHc5	:										:	598
TrMDHc6	:	AGATTGT							aggggg?	AACCT	-	657
TrMDHc7	:	AGATTGT:	TTGGGGTTA	CAACCCT"	TGATGT	AGTCAGGGC	GAAAAC	TIT _I LIA.	rected F	MAGCI	:	657
TrMDHc8	:								ragacca	AACCT	•	654
TrMDHc9	:	AGATTGT	TTGGGGTTA	CAACCCT'	TGATGT	AGTCAGGGC	GAAAAC	TTTCTA.	raccaca	AAGCI	-	652
TrMDHc10	:		TTGGGGTT-				JAAAAÇ		LGCCGGG	MAAGC I	-	577
TrMDHc11	:	AGATTGT'	TTGGGGTTA	.CAACCC'I"	TG			TGT.			-	594
TrMDHc12	:	AGATTGT'	TTGGGGTTA TTGGGGTTA	.CAACCCT	TGATGT	agreadace agge	JAAAAA.		reenegg	AAACCT		615
TrMDHc13	:	AGATTGT	TTGGGGTTA TTGGGGTTA	"LOODAAO.	TGATGI	AGMCAGGGC	. Д.Д.Д. Е.С.	ᅺᅭᅭᆹᇇᅭᄽ	rgerigge?	AAAGCT	_	369
TrMDHc14	:	AGATTGT	TTGGGGTTA TTGGGGTTA	CAACCCT	TGAIGI.	AGTCAGGGC	./ 1 ./		TGCTGGG	AAACCT	:	356
TrMDHc15	:	AGAT"IGT	TTGGGGTTA	CAACCCT.	TGAIGI.	AGICAGGGC	, AMAMA	JITICIA			:	-
TrMDHc16	:										:	_
TrMDHc17	:										•	
		700		*	720	*		740	*			_
TrMDHc1	:										•	_
TrMDHc2	:										•	_
TrMDHc3	:										:	_
TrMDHc4	:										:	_
TrMDHc5	:				-						:	_
TrMDHc6	:		CAGTTGCCC		moma co		an GGCC	ATGCAGG	ACTTACT	Δ The Market Δ	:	720
TrMDHc7	:	AAAG'I"I'C	CAGTTGCCC	JAGGTCAA	ITGTACC	TGTT	JAGGCC.	AIGCAGE	AGIIACI		:	.20
TrMDHc8	:		GR GRRGGGG		TOTA C						•	682
TrMDHc9	:	AAAGTTC	CAGTTGCC	JAGGICAA		TOTAL	TAGGGG	TGC-NO	AG-TNCT	ATT - NT	•	711
TrMDHc10	:	AAAG'I"I'C	CAGTTGCCC		TGMMCC						•	-
TrMDHc11	:										•	_
TrMDHc12	:	A A A COURT	CAGTTGCC		TC ZACC	тсттатас	GAGGCC	ATGCAGO	AGTTACT	ATTCTN	:	678
TrMDHc13		AAAGTTC	CAGTTGCC(CCAGTTGCC(TIGEACC	TOTTATAC	GAGGCC	ATGCAGO	AGTTACT	ATTCTC	•	432
TrMDHc14		AAAGTTC	CAGTTGCCC	SAGGICAA SAGCTICA	TGTACC	TOTIATAG	GAGGCC	ATGCAGG	AGTTACT	ATTCTC	:	419
TrMDHc15		AAAGTTC	CAGITGCCC	JAGG I CAA	AIGIACC						:	
TrMDHc16											:	_
TrMDHc17	:			 -							-	

		760	*	780	*	800		* 82		
TrMDHc1 :	:								:	-
TrMDHc2	:								:	-
TrMDHc3	:								:	-
TrMDHc4	•								:	-
TrMDHc5	:								:	-
TrMDHc6	•								:	-
TrMDHc7		CCATTATTTT	ITÄAGG-AAC	CACCTNAAC	CCAATNT	GGNTGATGAZ	ACCCTTNA	GGNTTTAACG	: 1	782
TrMDHc8	•								:	-
TrMDHc9	:								:	-
TrMDHc10	:	CCGTTTTTT	TEAGG-GAN	INCCT-NAN	CCANT - T	NGGNGATNA?	A-CCTTAA	GGGTTT-ACG	: '	769
TrMDHc11	:								:	-
TrMDHc12	:								:	-
TrMDHc13	:	CCATTATTTT	NTNAGGCAAC	CACCTNAAC	CCAATNI	GGGTGANGAT	NCCCTTAA	GGNTTTAACG	-	741
TrMDHc14	:	CCATTATTTT	TCAGGCAAC	CACCTCAAC	CCAATCI	'GGNTGATGA'I	'ACCATTAA	.GG@T@TAACG	-	495
TrMDHc15	:	CCATTATTTT	TCAGGCAA	CACCTCAAC	CCAATCT	GGÄTGATGAT	'ACCATTAA	GGGTCTAACG	: 4	482
TrMDHc16	:								:	-
TrMDHc17	:				- 				:	-
								222		
		0	* 84	40	*	860	*	880		
$\mathtt{TrMDHc1}$:								:	-
TrMDHc2	:								:	_
TrMDHc3	:								:	
TrMDHc4	:								:	-
TrMDHc5	:								:	-
TrMDHc6	:					2566677667			:	- 827
TrMDHc7	:	GNANGGGCNC	AAGATGGGG	GAACNGAA	- TTGNGA	CCGCCAAGGG			•	02/
TrMDHc8	:								:	_
TrMDHc9	:								:	001
TrMDHc10	:	G <mark>C</mark> -NNGCCNC	'AAAANG-GG	GAACAAAA	-NTINGA	2			:	801
TrMDHc11	:								:	_
TrMDHc12	:								:	801
TrMDHc13	:	GNANGGACCC	'AANANGGAG	GAACANAA	NTTNNGA	CCCCCANGG-	TGG-AAGG	GTTNT-NNACT	:	558
TrMDHc14	:	GCAAGGACAC	'AAGATGGAG	GAACAGAA	GTTGTGA	CCGCCAAGGC	TGGAAAGG(GTTCTGCAACT	:	545
TrMDHc15	:	GGAAGGACAC	CAAGATGGAG	GAACAGAA	GTTGTGA	CCGCCAAGGC	TGGAAAGG	GTTCTGCAACT	:	343
TrMDHc16	:								:	_
TrMDHc17	:								:	_
		*	900		*	920	*	940		
TrMDHc1									:	-
TrMDHc1	:								:	_
TrMDHc3	:								:	-
TrMDHc3	:								:	_
TrMDHc5	:								:	_
TrMDHc6	:								:	-
TrMDHc7	:								:	-
TrMDHc8	:								:	_
TrMDHc9	:								:	_
TrMDHc10	:								:	_
TrMDHc11	•								:	_
TrMDHc12	•								:	-
TrMDHc13	:	TT-NNAATG	2N						:	811
	:	TTCTCAATC	CTTATCCTC	GAGCCAT	TTTGCTC	ATGCTTGCCT	CAAAGGTC	TGAATGGAGTT	:	621
TrMDHc14 TrMDHc15	:								:	557
	:	- I GLCAAI C				NTGCTNGCCT	-NANGGNO	TGAATGGAGTT	:	34
TrMDHc16	:				· ·			ENGNGTH		7
TrMDHc17	•							Secret Control of Control	, ,	•

		*	960	*		980	*	1000			
rrMDHc1	:		960 							:	-
TrMDHc2	:									:	-
TrMDHc3										:	-
TrMDHc4	:									:	-
TrMDHc5	:									:	_
TrMDHc6	•										_
	:									:	_
TrMDHc7	:									•	_
TrMDHc8	:									•	_
TrMDHc9	:									•	_
TrMDHc10	:									:	_
TrMDHc11	:									:	-
$\mathtt{TrMDHc}12$:									:	-
TrMDHc13	:									:	<u>-</u>
TrMDHc14	:	CCAGATGTT	'ATTGAGTGC'	CATATG'	TGCAATC	CAATATCAT	CTCTGA	CCTTNCTTI	CTTTGCT	:	684
TrMDHc15	:									:	-
TrMDHc16	:	-CNGANGT'I	ATTGAACTC ATNGAGTGC	CATATG'	TGCAATC	CAATATCAT	CTNTGA	CCTTCCTTI	CTTTGCT	:	96
TrMDHc17	:	CCAGATGTT	'ATNGAGTGC'	-NTATG	TGC-AT-	CNATAT-NT	CTCTGA	CCTTCCTTI	CTTTGCT	:	66
		* 1	020	*	1040	1	*	1060	*		
TrMDHc1			.020							:	-
TrMDHc2	:									•	_
	•									•	_
TrMDHc3	•									:	_
TrMDHc4	:									:	_
TrMDHc5	:									:	_
TrMDHc6	:									•	_
TrMDHc7	:									•	_
TrMDHc8	:									•	_
TrMDHc9	:									:	_
TrMDHc10	:									:	-
TrMDHc11	:					·				:	-
TrMDHc12	:			-						:	-
TrMDHc13	:									:	-
TrMDHc14	:	TCCAAGGT	GAGGATTGGG	AANAATG	GTGTGG	TAANAA				:	722
TrMDHc15	:									:	-
TrMDHc16	:	TCCAAGGNI	NNGGATTGGG	AAGAATG	GTGTGG	AGAGATTC'	<u>rg</u>			:	138
TrMDHc17	:	TCC-AGGT	GAGGATTGGG	AAGAATG	GTGTGG	AGAÄATTC'	rgggct'	PAGGTTCTC	FCACAGAT	:	128
		108	0 -	*	1100	*	1:	L20	*		
TrMDHc1	:									:	
TrMDHc2	:									:	_
TrMDHc3										:	-
TrMDHc4	:									:	_
TrMDHc5	:									•	-
TrMDHc6	•									•	_
	•									:	_
TrMDHc7	:									:	_
TrMDHc8	:									•	_
TrMDHc9	:						-				_
TrMDHc10										:	_
TrMDHc11	:										-
TrMDHc12	:									:	-
TrMDHc13	:									:	-
TrMDHc14	:										-
TrMDHc15	:									:	-
TrMDHc16											-
		TTCGAGCA	ACAAGGCCTT	GAAAAC	TTCAAGG	CTGAACTCA	AATCAT	CTATTGAAA	AGGGAATC	:	191

		1140	*	1160		*	1180	*	1		
TrMDHc1 :		1140					_	- 		:	-
TrMDHc2 :										:	-
TrMDHc3 :										:	-
TrMDHc4 :										:	-
TrMDHc5 :										:	-
TrMDHc6 :										:	-
TrMDHc7 :										:	-
TrMDHc8 :										:	-
TrMDHc9 :										:	-
TrMDHc10:										:	-
TrMDHc11 :										:	-
TrMDHcl2										:	-
TrMDHc13										:	-
TrMDHc14										:	-
TrMDHc15	•									:	-
TrMDHc16	•									:	-
TrMDHc17	:	AAATTTGCCTCCC	AGTAAT	CGAACATGT	CATACA	TACTGG	ATTTTTCC	ATTTAG	AACCAG <u>AT</u>	:	254
	-										
		_				10		•	1260		
		200 *		1220	*		40		1260		_
TrMDHc1	:									:	_
TrMDHc2	:									:	_
TrMDHc3	:									:	_
TrMDHc4	:									:	_
TrMDHc5	:									:	_
TrMDHc6	:									•	_
TrMDHc7	:									•	_
TrMDHc8	:									•	_
TrMDHc9	:									•	_
TrMDHc10	:									•	_
TrMDHc11	:									•	_
TrMDHc12	:									•	_
TrMDHc13	:									:	_
TrMDHc14	:										_
TrMDHc15	:									•	_
TrMDHc16	:	CAAATTTTGCAA					CONTROL	A CCCCT	$A \subset A \cap A$		317
TrMDHc17	:	CAAATTTTGCAA	ATTCAG.	AACAA'I''I'G'I''I	TGTAAT	GIIGCC	JG I AGG I A I	ACCCCI	MAIIIADA.	•	31,
		*	12	80	*	1300		*	1320		
TrMDHc1	:									•	_
TrMDHc2	:									. :	_
TrMDHc3	:									•	_
$\mathtt{TrMDHc4}$:									•	_
TrMDHc5	:										_
TrMDHc6	:										_
TrMDHc7	:									•	_
TrMDHc8	:									:	_
TrMDHc9	:										-
TrMDHc10	:										_
TrMDHc11	:										_
TrMDHc12	:										_
TrMDHc13	:										_
TrMDHc14	:										-
TrMDHc15	:									•	-
TrMDHc16	:							7.002.00	TOTACCTE	- :	200
TrMDHc17	:	TAAGTAAATCTG	CGAGAG	CAGTTTATT	GCTGCA	GGGAC'I'C	AAATTAAA	ACCAG1	TTAGGTT	털 :	380

		*	1340	,	*	1360	*	1380		
TrMDHc1	:								:	-
TrMDHc2	:								:	-
TrMDHc3	:								:	_
TrMDHc4	:								:	_
TrMDHc5	:								:	_
TrMDHc6	:								:	_
TrMDHc7	:									_
TrMDHc8	:								•	_
TrMDHc9	:								•	_
TrMDHc10	:								•	
TrMDHc11	:								•	
TrMDHc12	:									
TrMDHc13	:								•	_
TrMDHc14	:									
TrMDHc15	:									_
TrMDHc16	:					G MCNTHER		A ATTCA A CCCTCA		443
TrMDHc17	:	GCCTTTCCAT	TCGTAATGGCCC'I	ΓTCP	VITGITIG	CATGNT111	CATATAAIGC	AATTGAAGGGTG1	•	44-
			1400							
muserit 4		*	1400		_					
TrMDHc1	:	*	1400	:						
TrMDHc2	:	*	1400	:	- -					
TrMDHc2 TrMDHc3	: :	*	1400	: : : : : : : : : : : : : : : : : : : :	-					
TrMDHc2 TrMDHc3 TrMDHc4	: : :	*	1400	: : : : : : : : : : : : : : : : : : : :	- - -					
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5	: : : :	*	1400	: : : :	-					
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6	: : : : :	*	1400	: : : : : : : : : : : : : : : : : : : :	-					
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6 TrMDHc6	: : : : : :	*	1400	: : : : : : : : : : : : : : : : : : : :						
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6 TrMDHc7 TrMDHc8	: : : : : : : : : : : : : : : : : : : :	*	1400	: : : : : : : : : : : : : : : : : : : :	-					
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6 TrMDHc7 TrMDHc8 TrMDHc9	: : : : : : : : : : : : : : : : : : : :	*	1400	: : : : : : : : : : : : : : : : : : : :						
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6 TrMDHc7 TrMDHc8 TrMDHc9 TrMDHc10		*	1400	: : : : : : : : : : : : : : : : : : : :						
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6 TrMDHc7 TrMDHc8 TrMDHc9 TrMDHc10 TrMDHc11	:	*	1400							
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6 TrMDHc7 TrMDHc8 TrMDHc9 TrMDHc10 TrMDHc11 TrMDHc11	:	*	1400							
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6 TrMDHc7 TrMDHc8 TrMDHc9 TrMDHc10 TrMDHc11 TrMDHc11 TrMDHc12	:	*	1400							
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6 TrMDHc7 TrMDHc8 TrMDHc9 TrMDHc10 TrMDHc11 TrMDHc11 TrMDHc12 TrMDHc13 TrMDHc14	:	*	1400							
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6 TrMDHc7 TrMDHc9 TrMDHc10 TrMDHc11 TrMDHc11 TrMDHc12 TrMDHc13 TrMDHc14 TrMDHc14 TrMDHc14	:	*	1400							
TrMDHc2 TrMDHc3 TrMDHc4 TrMDHc5 TrMDHc6 TrMDHc7 TrMDHc8 TrMDHc9 TrMDHc10 TrMDHc11 TrMDHc11 TrMDHc12 TrMDHc13 TrMDHc14	:		1400		465					

			*	20	*	40	*	60		
TrMDHd	:	GGGTAGGC	GGAGATTTN	AACCCATTTTCC	TCTTAAA!	rctctctcaa(CTTCTCTTTC	CATT	:	60
TrMDHd	:	CCCATTAC	* CATTCATTC	80 CCAGAGGTCGAC	* GATGGCAG	100 CATCAGCAGC	* AGCTACTTTT	120 ACTA	:	120
TrMDHd	:	TTGGAACT	* 'GCCCAAAC!	140 AGGGAGGCCACT	* ICCTCAAT	160 CAAACCCTTT	* TGGTTTGAAA	180 GTCA	:	180
TrMDHd	:	ATTCCCAG	* GTTAATTT	200 FAAGACCTTCTC	* TGGTCTCA	220 AGGCCATGTC	* ATCTCTAAGA'	240 TGCG	:	240
TrMDHđ	:	AGTCTGA	* \TCATCTTT	260 CTTTGGCAACGA	* AACTAGTG	280 CTGCTCTGCG	* TGCAACTTTT	300 GCAC	:	300
TrMDHd	:	CCAAAGCT	* CCAAAAGGA	320 AAACCAAAACAT	* CAACCGCA	340 ATTTGCATCO	* TCAGGCATCC	360 TACA	:	360
TrMDHd	. :	AAGTGGC	* GGTTCTTGG	380 TGCTGCAGGAGG	* BAATTGGTO	400 CAGCCACTGGC	* CACTTCTCATI	420 AAGA	:	420
TrMDHd	l :	TGTCGCC	* TTTGGTTTC	440 CGACCTGCATCT	* TTATGAT?	460 ATCGCGAATGI	* TTDADDGAATT	480 GCTG	:	480
TrMDHd	l :	CTGATAT	* CAGTCATTG	500 CAACACTCCTTC	* CAAAGGTT	520 ITGGATTTCA	* CAGGTGCTTCT	540 GAGT	:	540
Ͳ≁MDHċ		• таасала	* TTGTTTGAP	560 AGGTGTGGATG	* PAGTTGTT	580 ATACCTGCTG	* GTGTTCCCAG	AAA :	5	98

rrMDHd	:	* MAASAAATFTIGTAQTGI	20 RPLPQSNPFGLI	* KVNSQVNFK	40 CTFSGLKAMSSLI	* RCESESSFE	60 FGNE :	:	60
rrMDHd	:	* TSAALRATFAPKAQKEN	ONINKNTHÞÓY: 80	* SYKVAVLGA	100 AAGGIGQPLALL	* IKMSPLVSI	120 DLHL	: :	120
r~M⊓ud		* VDIANVKGVAADISHCN	140 TPSKVI:DFTGA:	* SELANCLKO	160 EVDVVVIPAGVP	R : 169			

TrMDHd1	:	GÑGTAGG	* CGGAGATTT	20 NAACCCATTTTC	* CTCTTAAA	40 PCTCTCTMAAC	* TTCTCTTTC	60 CATT :	:	60
TrMDHd2	:	-GITAGG	CGGAGATTÑI	NAACCCATTTTC NAACCCATTTTC	CTCTTAAA'	TCTCTCTC-AC	TTCTCTTTC	CATT :	:	58 52
			*	80 CCCAGAGGTCGA	*	100	*	120 ACTA	. :	120
	: :	CCCATTA	CCATTCATT	CCCAGAGGTCGA CCCAGAGGTGGA CCCAGAGGTIIGA	GATGGCAG	CATCAGCAGCA	GCTACTTTT	'ACTA	: :	118 112
								100		
TrMDHd1	:	TTGGAAC	* TGCCCAAAC	140 AGGGAGGCCACT	* TCCTCAAT	160 CAAACCCTTTT	* GGTTTGAAA	180 GTCA		180
TrMDHd2 TrMDHd3	:	TTGGAAC TTGGAAC	TGCCCAAAC TGCCCAAAC	AGGGAGGCCAC1 AGGGAGG¶CAC1	TCCTCAAT	'CAAACCCTTT'I 'CAAACCCTTTT	GGTTTGAAA GGTTTGAAA	AGTCA AGTCA		178 172
			*	200 TAAGACCTTCT	*	220	* ምርጥርጥስ አር 7	240	:	240
TrMDHd1 TrMDHd2	:	ATTCCCA	GGTTAATTI	TAAGACCTTCT(TAAGACCTTCT(TAAGACCTTCT(CTGGTCTCA	AGGCCATGTCA	TCTCTAAGA	ATGCG	:	238 232
TrMDHd3	:	ATTCCCA	GGIIAAIII	TAAGACCIICIO		M10000111010,	; <u> </u>		•	
TrMDHd1		АСТСТСА	*	260 CTTTGGCAACG	* AAACTAGTO	280 CTGCTCTGCGT	* GCAACTTT	300 IGCAC	:	300
TrMDHd2 TrMDHd3	:	AGTCTGA	רידידים אירידיים	CTTTGGCAACG CTTTGGCAACG	AAACTAGTO	CTGCTCTGCGT	GCAACTTT:	rgcac	:	298 292
TIMBIAS	•	11010101								
TrMDHd1	:	CCAAAGO	* CTCAAAAGG	320 AAAACCAAAACA	* TCAACCGC	340 AATTTGCATCC	* CAGGCATC	360 CTACA	:	360
TrMDHd2 TrMDHd3	:	CCAAAGC	TCAAAAGG	AAAACCAAAACA AAAACCĞAAACA	TCAACCGC	AATTTGCATCC:	CAGGCATC:	CTACA	:	358 352
		_						400		
TrMDHdl	:	ĀAGTGG	* CGGTTCTTG	380 GTGCTGCAGGAG	* GAATTGGT	400 CAGCCACTGGC	* ACTTCTCAT	420 TAAGA	:	420
TrMDHd2 TrMDHd3	:	AAGTGG(AAGTGG(CGGTTCTTG CGGTTCT[]G	GTGCTGCAGGAG GTGCTGCAGGAG	GAATTGGT GAATTGGT	CAGCCACTGGC. CAGCCACTÏGC.	ACTTCTCAT ACTTCTCAT	TAAGA TAAGA	:	418 412
			a.	440	*	460	*	480		
TrMDHdl	:	TGTCGC	CTTTGGTTT	CCGACCTGCATC	TTTATGAT	ATCGCGAATGT	TAAGGGAGT	TGCTG	:	480 478
TrMDHd2 TrMDHd3	:	TGTCGC	CTTTGGTTT	CCGACCTGCATC	TTTATGA	ATTGCGAATGT	TAAGGGAGT	TGCTG	:	472
			*	500	*	520	*	540		
TrMDHd1 TrMDHd2		CTGATA	TCAGTCATT	'GCAACACTCCT' 'GCAACACTCCT'	CAAAGGTI	TTGGATTTCAC	AGGTGCTTC	TGAGT	:	
TrMDHd3	:	CTGATA	TCAGĈCATT	'GCAACACTCCT'	rcaaaggtt	TTGGATTTCAC	AGGTGCTTC	TGAGC	:	532
			*	560	*	580	*		F	54
TrMDHd1 TrMDHd2	:	TGGCAA	ATTGTTTG-	AAGGTGTGGAT(AAGGTGTGGAT	TAGTTGTT	ATACCTGCTGC	TGTTCCCAC	G :	5	93 90
TrMDHd3		TAGCAA	ATTGTTTGA	MAGGIGTGGAT	31.1.G1.1.G1.1	AIACCIGCIGG	, real rectal		ر	

159/241

TrMDHe	:	TTNTNTTT	* \TTTTATGT	20 TTTTTNCCTCC	* FACATATA!	40 ACTCTTNACTTN	* GCATACACT	60 GTG	:	60
TrMDHe	:	TCTCTCAA	* CTATTATTA	80 GTCCTTAGAAA'	* TGGAAGCA(100 CATGCAGCTGGA	* .GCCAATCAG	120 BAGG	:	120
TrMDHe	:	ATTGCAAG	* AATCTCTGC	140 TCATCTTCAAC	* CTCCAAAT	160 TTCCAGGAAGGA	* \GGTGATGT]	180 GCA	:	180
TrMDHe	:	ATTAGCAA	* AGCTAACTO	200 CAGAGCAAAAG	* GTGGGGCG	220 CCGGGATTCAA	* AGTAGCAAT(240 CTTG	:	240
TrMDHe	:	GGGGCTGC	* TGGTGGAA	260 TTGGTCAATCCC	* TTTCTTTG	280 CTGTTGAAGAT	* CAATCCATT(300 GGTT	: '	300
TrMDHe	:	TCAGTTCT	* TCATCTTT	320 ATGATGTTGTCA	* ACACTCCT	340 GGTGTCACTGC	* FGATGTTAG	360 ICAC	:	360
TrMDHe	:	ATTGACAC	* CGGTGCTG	380 IGGTTCGTGGC1	* TTCTAGGG	400 GCAGGCACAACT	* TGAGAATGC	420 ACTT	:	420
TrMDHe	:	ACAGGCAT	* GGACTTGG	440 TCGTTATACCTO	* GCTGGTGTG	460 GCCGAGGAAACC	* TGGAATGAC	480 AAGG	:	480
TrMDHe	:	GATGACTI	* :ATTTAAGA	500 TAAATGCTGGAA	* ATTGTGAGG	520 SACTCTTAGCGA	* AGGAATTGC	540 CAAG	:	540
TrMDHe	:	AGCTGTC	* CTAATGCAA	560 TTGTCAACTTG	* ATTAGCAA	580 FCCAGTGAATTC	* CACTGTGCC	600 AATT	:	600
TrMDHe	:	: GCTGCTG	* AGGTTTTCA	620 AGAAAGCCGGT	* ACATATGA'	640 ICCAAAGCGACI	* TTTAGGGGT	660 TACA	:	660
TrMDHe	;	: ACCCTCG	* ATGTTGTGA	680 AGGGCAAATACC	* TTTGTGGC	700 AGAAGTACTTGG	* FTGTTGATCO	720 CAAGA		720
TrMDHe	!	: GAGGTTG	* ATGTTCCAG	740 STGGTAGGAGGG	* CACGCAGG	760 AGTCACAATATI	* PACCTCTTT	780 FGTCA		780
TrMDHe	:	: CAGGTTA	* AGCCTCCC!	800 AGTAGCTTCACC	* GCAGAAGA	820 AACCGAATACC	* rgacaaanco	840 SCATT		840
TrMDHe	2	: CAAAANG	* GCGGAACA	860 CAAGTTGTTGAG	* GCAAAGGC	880 TGGGGCTGGTT	* CGGCAACAC	900 NTNAT		900
TrMDHe	•	: ATGGCCT	* ATGCAGCT	920 GCCAAGTTTGCT	* CAACGCATG	940 CCTCCGTGGCT	* TGAAAGGAG	960 AAGCC		960

FIGURE 67

160/241

* 1040 * 1060 * 1080 TrMDHe : AAGGTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATATCAACTTGGTCCCCTTAATGAG : 1080

* 1100 * 1120 * 1140

TrMDHe : TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAAAGAGTTAGCAGGAAGCATCCAGAAGGGA : 1140

* 1160 * 1180 * 1200 TrMDHe : GTAGAATTCATCAAAAAAAAAAAAAGATAAGGAAAAATTAGTTTTGTATTGNCTCTTTCT : 1200

* 1220 *
TrMDHe : ATATCTATAAAGAACTTGTGTAATAATTCC : 1230

		7	k	20	*	40	ж	60		
rMDHe	:	MEAHAAGAN			VAISKANC	RAKGGAPGFKVA	ILGAAGGI	GQS	:	60
			*	80	*	100	*	120		
rrMDHe	:	LSLLLKINP			SHIDTGAV	VRGFLGQAQLEN	ALTGMDLV		:	120
			* 1	. 40	*	160	*	180		
TrMDHe	:	AGVPRKPGM			AKSCPNAI	VNLISNPVNSTV	PIAAEVFI	CKAG	:	180
			* 2	00	*	220	*	240		
TrMDHe	:	TYDPKRLLG			PREVDVP	/VGGHAGVTILPI	LSQVKPPS	SSFT	:	240
			* 2	:60	*	280	*	300		
TrMDHe	:	AEETEYLTX			LAAAYAAAI	KFANACLRGLKGI	EAGIVECA	FVDS	:	300
			* 3	320	*	340	*			
тжМОНе	:	OVTELPFFA			NEYERIGL	EKAKKELAGSIQ	KGVEFIKK	KXR :	: 3	359

			0 *		40	*	60		
rrMDHe1	:	TTNTNTTTATTTTATGTTT	TTTNCCTCCTA	CATATAAC'	TCTTNACTTNG	CATACAC'	rotg	:	60
TrMDHe2	:						-GNG	:	3
TrMDHe3	:						-GTG	:	3
TrMDHe4	:							:	-
TrMDHe5	:							:	-
TrMDHe6	:							:	-
TrMDHe7	:							:	-
TrMDHe8	:							:	-
TrMDHe9	:							:	-
TrMDHe10	:							:	-
			30 +		00	*	120		
TrMDHe1	:	TCTCT-AATTATTATTAGT	CCTTEGAAAT	GAAGCACA	TGCAGCTGGT	*CCAATCA	.GAGG	:	119
TrMDHe2	:	TCTCTCAATTATTATTAGT	CCTTAGAAAT	GAAGCACA	TGCAGCTGGTC	SCCAATCA	GAGG	:	63
TrMDHe3	:	TCTCTCAATTATTATTAG	CCTTAGAAAT	ggaagc@ca	TGCAGCTGGA	GCCAATCA	GAGG	:	63
TrMDHe4	:	KVAG	CCTTAÑAAAT	GAAGCACA	TGCAGCTGGA	GCC-ATC-	GAGG	:	44
TrMDHe5	:		GAGAAAT(GGAAGCACA	TGCAGCTGGA	SCCAATCA	GAGG	:	38
TrMDHe6	:			- @@AN	TGCAGCTGG	GCCANTN	GAGG	:	26
TrMDHe7	:						~	:	-
TrMDHe8	:							:	-
TrMDHe9	:							:	-
TrMDHe10	:							:	-
		* 1	40		L60	*	180		
TrMDHe1	:	ATTGCAAGAATCTCTGCT	CATCTTCAĞCC'	TCCAAATTT	CCAGGAAGGA	GGTGATG1	"TGCA	:	179
TrMDHe2	:	ATTGCAAGAATCTCTGCT	CATCTTCAACC	TCCAAATTI	CCAGGAAGGA	GGTGATG:	l'TGCA	:	123
TrMDHe3	:	ATTGCAAGAATCTCTGCT	CATCTTCAACC	TCCAAATT	rccaggaagga	GGTGATG'.	l"I'GCA	:	123
TrMDHe4	:	ATTGCAAGAATCTCTGCT	CATCTTC-@CC	TCCAAATT	rccaggaagga	AGTGATG:	rggca	:	103
TrMDHe5	:	ATTGCAAGAATCTCTGCT	CATCTTCAACC	TCCAAATT'	rccaggaagga	GGTGATG'.	rigca	:	98
TrMDHe6	:	ATTGC-AGAATCTCTGCT	CATCTT - ÑACC	TCC-AATT	rccaggaagga	GGTGATG'	ITGCA	:	83
TrMDHe7	:							:	_
TrMDHe8	:							:	-
TrMDHe9	:							:	_
TrMDHe10	:							:	-
				_			240		
		* 2	00		220	**		_	239
TrMDHe1	:	ATTAGCAAAGCTAACTGC	AGAGCAAAAGG	TGGGGCGC	CGGGATTCAAA	GTAGCAA		•	183
TrMDHe2	:	ATTAGCAAAGCTAACTGC	AGAGCAAAAGG	TGGGGCGC	CGGGATTCAAA	GTAGCAA		:	183
TrMDHe3	:	ATTAGCAAAGCTAACTGC	AGAGCGAAAGC	TGGGGCGC	CGGGATTCAA	GTAGCAA	TCTTG	:	163
TrMDHe4	:	ATTAGCAAAGCTAACTGC	AGAGCAAAAGC	TGGGGCGC	CGGGATTCAA	GTAGCAA		:	158
TrMDHe5	:	ATTAGCAAAGCTAACTGC	AGAGCAAAAGC	TGGGGCGC	CGGGATTCAA	GTAGCAA	TCTTG	:	143
TrMDHe6	:	ATTAGCAAAGCTAACTGC	CAGAGCAAAAGC	TGGGGCGC	CGGGATTCAA	GTAGCAA	ICIIG	:	143
TrMDHe7	:							:	-
TrMDHe8	:							:	_
TrMDHe9	:							:	_
TrMDHe10	:							:	-

		* 260 * 280 * 300		
TrMDHe1		200 200	: 2	99
	•	GGGGCTGCTGGTAGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT	-	43
TrMDHe2 TrMDHe3	:	GGGGCTGCTGGTAGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT		43
	:	GGGGCTGCTGGTAGATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT	-	23
TrMDHe4	:	GGGGCTGCTGGTAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT		18
TrMDHe5	:	GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT	-	203
TrMDHe6	:	GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT		,05
TrMDHe7	:		:	_
TrMDHe8	:		:	_
TrMDHe9	:		•	_
TrMDHe10	:		:	-
		* 320 * 340 * 3	60	
		* 320 * 340 * 3 TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC		359
TrMDHe1	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC	-	303
TrMDHe2	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTACGATCAC	-	303
TrMDHe3	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC	-	283
TrMDHe4	:	TCGGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC		
TrMDHe5	:	TCGGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC		278
TrMDHe6	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC	: :	263
TrMDHe7	:		:	
TrMDHe8	:		:	-
TrMDHe9	:		:	-
TrMDHe10	:		:	-
		* 380 * 400 * 5	20	
		* 380 * 400 * 4 ATTGACACCGGTGCTGTGGTTCGTGGCTTCTAGGGCAGGCA		419
TrMDHe1	:		-	363
TrMDHe2	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTTAGGGCAGAAAC11GAGAATGCAC11	-	363
TrMDHe3	:	ATTGATACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCA	-	343
TrMDHe4	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCA	-	338
TrMDHe5	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCA		
TrMDHe6	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCA	:	323
TrMDHe7	:	GTTTCAACTTGAÄAATGCACTT	:	22
TrMDHe8	:	;	:	-
TrMDHe9	:	:	:	-
TrMDHe10	:		:	_
		* 440 * 460 *	480	ļ
TrMDHe1	:		:	479
TrMDHe2	:		:	423
TrMDHe3	:	ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	423
TrMDHe4	:	ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	403
TrMDHe5	:	ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	398
TrMDHe6	:	ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	383
TrMDHe7		ACAGGCATGGACTTGGTCGÑTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	82
TrMDHe8	•		:	_
TrMDHe9	:		:	_
	. :		:	_
TrMDHe10	•	• • • • • • • • • • • • • • • • • • • •	_	
			540	
TrMDHe1		: GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG	:	539
TrMDHe2		• GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG	:	483
TrMDHe3		• GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG	:	483
TrMDHe4		• GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG	:	463
TrMDHe5		• GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG	:	458
TrMDHe6		• GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG	:	443
TrMDHe7		: GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG	:	142
TrMDHe8			•	-
TrMDHe9				_
TrMDHe10	`	,		_
TTIMETO	-	•		

		* 560 * 580 * 600		
TrMDHe1		AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT:	5	99
	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT:	5	43
TrMDHe3	•	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT:	5	43
	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT:	9	523
TrMDHe5	•	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT:	5	518
	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT:	5	503
TrMDHe6	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT :	2	202
TrMDHe7	:	AGCIGICCIAAIGCAAIIGICAACIIGATIACAAICCAGIGATA		_
TrMDHe8	:			_
TrMDHe9	:			_
TrMDHe10	፥			
		* 620 * 640 * 660		
TrMDHe1		GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTANGGGTAACA:		659
TrMDHe1	•	GCTGCTGAGGTTTTCAAGAAAGCCGGTACAT		574
TrMDHe3	•	GCTGCTGAGGTCTTCAAGAAAGCCGGTACATAT		576
TrMDHe3	:	GCTGCTGAGGTCTTCAAGAAAGCCGGTACATATGATCCAAAACGACTTTTAGGAGTTACA		583
	:	GCTGGTGAGGTCTTCAAGAAAGCCGGNACATATGATCCAAAACNACTTTTAAGGGTTACA		578
TrMDHe5	:	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTAG		555
TrMDHe6	:	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATTCAAAGCGACTTTTAGGGGTAACA		262
TrMDHe7	:	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATCATTCCTTTTTAGG-GCTACA		28
TrMDHe8	:			_
TrMDHe9	:			_
TrMDHe10	:			
		* 680 * 700 * 720		
TrMDHe1	_	ACCCTCGATGNTGT	:	673
	:	ACCCICGATENTET	:	_
TrMDHe2	:		:	
TrMDHe3	:	ACCCTCGATG	:	593
TrMDHe4	:	ACCCTNGATGTTGNGAGGGCAAATACTTTTGTGGCANAAG-NCTTGGNGTTGANCCCAAA	:	637
TrMDHe5	:	ACCCTNGATGTTGNGAGGGCAAATAC#TTTGTGGCAYAAG MCTTGAAGTTGTAG	:	_
TrMDHe6	:	ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTTGATCCAAGA		322
TrMDHe7	:	ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTTGATCCAAGA	:	88
TrMDHe8	:	ACCCICGAIGIIGIGAGGGCAAAIACCIIIGICCCACIIGIIGI		_
TrMDHe9	:		:	_
TrMDHe10	:			
		* 740 * 760 * 780		
TrMDHe1	•		:	-
TrMDHe2			:	-
TrMDHe3			:	-
TrMDHe4	:		:	-
TrMDHe5		NAGGGTNATNTTCCANTGGTAGGAGGCCCCCNGGANT-ACAANATTACC-CTTTTTT	:	693
TrMDHe6	:		:	-
TrMDHe7	:	GAGGTTGATGTTCCAGNGGTAGGATGGCACGCANGAGT-ACAATATTACCTCTTTTGTCA	:	381
TrMDHe8	:	GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTTGTCA	:	148
TrMDHe9	;		:	-
TrMDHe10	;		:	-
		* 800 * 820 * 840	_	
TrMDHe1			:	_
TrMDHe2			:	-
TrMDHe3		:	:	-
TrMDHe4			:	-
TrMDHe5		:	:	-
TrMDHe6		:	:	4.4.6
TrMDHe7		CAGGTTAAGCCTNCCAGTANCTT-ACCGNAGAANAACCGAATACCTGACANANCGNATT	:	440
TrMDHe8		CAGGITAAGCCTCCCAGTAGCTTCACTGCAGAAGAAACCGAATACCTGACAAATCGCATT	:	208
TrMDHe9			:	-
TrMDHe10)	:	:	-

			*	860	*	880	*	900	
TrMDHe1	:							:	-
TrMDHe2	:							:	-
TrMDHe3	:							:	-
TrMDHe4	:							:	-
TrMDHe5	:							:	_
TrMDHe6	:			CAAGTGGTTGAGG				:	473
TrMDHe7	:	CAAAANGC	JCGGAACA(AAGTIGGTTGAGG BAAGTTGTTGAGG		CCCCCTCCTTC	CCCAACAC	PANTA:	268
TrMDHe8 TrMDHe9	:	CAAAA	5 KGGAACAL	GTTGTTGAGG	CAAAGGCI	GGGGCTGGTTC	GGCAACAC'	TANTN	42
TrMDHe10	:					GGGGCTGGTTC			38
Tribhero	•								
			*	920	*	940	*	960	
TrMDHe1	:							:	-
TrMDHe2	:							:	-
TrMDHe3	:							:	-
TrMDHe4	:							:	_
TrMDHe5	:							:	
TrMDHe6	:							:	_
TrMDHe7 TrMDHe8	:	ATCCCMT	ATCCACCT	GCCAAGTTTGCT	ACCCATG	CTCCGTGGCT	rgaaaggag	AAGCC :	328
TrMDHe9		ATGGCGT	ATGCAGCT	GCCAAGTTTGCT	ACGCATG	CCTCCGTGGCT	TGAAAGGAG	AAGCC:	
TrMDHe10	•	ATGGCCT	ATGCAGCT	GCC-AGTTTGCT	AACGCATG	CCTCCGTGGCT	rgaaaggag	AAGCC :	97
11.10.10.10	٠					-	2.5.20		
			*	980	*	1000	*	1020	
TrMDHel	:								-
TrMDHe2	:							· :	-
TrMDHe3	:								. <u>-</u>
TrMDHe4	:								_
TrMDHe5	:								_
TrMDHe6 TrMDHe7	:								<u> </u>
TrMDHe8		GGGATAG	TGGAGTGT	GCTTTTGTTGAT	TCTCAGGT	TACGGAACTTC	CTTTCTTTC	CAGCC	388
TrMDHe9	:	GGGATAG	TGGAGTGT	GCTTTTGTTGAT	TCTCAGGT	TACGGAACTTC	CTTTCTTTG	CAGCC	: 162
TrMDHe10	:	GGGATAG	TGGAGTGT	GCTTTTGTTGAT	TCTCAGGT	TACGGAACTTC	CTTTCTTTC	CAGCC	: 157
			_			1000		1080	
			*	1040	*	1060		1080	
TrMDHe1	:							·	·
TrMDHe2 TrMDHe3	:								: -
TrMDHe4	•								: -
TrMDHe5									: -
TrMDHe6	:								: -
TrMDHe7	:								: -
TrMDHe8	:	AAGGTT	CGTCTTGGT	rcgcggtggagca	GAAGAGAT	ATACCAACTTC	GTCCCCTT	AATGAG	: 448
TrMDHe9	:	AAGGTTO	CGTCTTGG	rcgcggtggagca	GAAGAGAT	ATATCAACTTO	GTCCCCTT	AATGAG	: 222
TrMDHe10	:	AAGGTTC	CGTCTTGG	TCGCGGTGGAGCA	GAAGAGAT	'ATATCAACI''IG	GTCCCC1.1.	AATGAG	: 217
		•							
			*	1100	*	1120	*	1140	
TrMDHe1									: -
TrMDHe2					. 				: -
TrMDHe3	,								: -
TrMDHe4									: -
TrMDHe5	:								: -
TrMDHe6	:								: -
TrMDHe7	:	·						7 7 C C C 7	
TrMDHe8	:	TATGAG	$AGGATTGG_{i}$	GTTGGAAAAAGC	JAAGAATGA	AGTTAGCGGGA	AGCATCCAG	AAGGGA AAGGGA	: 508 : 282
TrMDHe9		TATGAG	AGGATTGG.	ÄTTÄGAAAAAGC(ATTAGAAAAAGC(JAAGAAAGA	AGTTAGCAGGA	AGCATCCAG.	AAGGGA	: 282 : 277
TrMDHe10)	TATGAG	AGGATTGG	ATTAGAAAAAGC(JAAGAAAG/	AGT TAGCAGGA	AGCAT CCAG		. 2//

			*	1160	*	1180	*	1200	
TrMDHe1	:							:	-
TrMDHe2	:							:	_
TrMDHe3	:							:	-
TrMDHe4	:							:	-
TrMDHe5	:							:	_
TrMDHe6	:							:	-
TrMDHe7	:							:	
TrMDHe8	:	GTAGAATT	CATCAGA	AAATAAGTCAGAT	AAGG	AAAAATTAGTT	TTGTATTGNCTCT	ance :	568
TrMDHe9	:							:	306
TrMDHe10	:	GTAGAATT	CATCAAA	AAAAAN				:	299
			*	1220	*				
TrMDHe1	:				:	-			
TrMDHe2	:				:	-			
TrMDHe3	:				:	-			
TrMDHe4	:				:	-			
TrMDHe5	:				:	: -			
TrMDHe6	:				:	-			
TrMDHe7	:				:				
TrMDHe8	:	ATATCTAT	TAAAGAAC	TTGTGTAATAATT	CC:	: 598			
TrMDHe9	:				:	-			•
TYMDUA10					:	<u>-</u>			

167/241

ጥrMDH£	:	GNNTACNG	* CTATCNACC	20 CTTCTTTCTTAT	* TACAATAAT	40 NATAGATAAA	* ITCATCTGCT	06 AAA	:	60
	•									
™×MDU£		ጥጥልጥሮርልር	* ሮሮልልልሞሞሮል	80 GATGCAAATCA	* ACGAATCGC	100 AAGAATCTCC	* GCCACCTAA	120 ATC	:	120
TIPLIT	•	111100110								
		~~~~~~~~~~	*	140 AATGAACATGG	*	160 "TTTCACAAGT"	* TTCCATTCC	180 'GTG		180
TYMDHI	:	CICCCAAT	TTCAAGAIG	AAIGAACAIGG	IGALICIIC	LITORCHAGI	1100411000	.010	•	
			*	200	*	220	*	240		240
TrMDHf	:	CAAAAGGT	GGAGCACCI	GGATTCAAAGT	TGCAATTTT	TAGGTGCTGCT	GGTGGCATAC	GIC	•	240
			*	260	*	280	*	300		
TrMDHf	:	AACCTCTT	TCAATGTTC	ATGAAGATGAA	TCCTTTGG?	TTNAGTTCTT	CATCTTTATC	BATG	:	300
			*	320	*	340	*	360		
TrMDHf	:	TTGTTAAT	ACTCCTGG:	rgttacttctga	TATTAGTC	ATATGGATACT	GCTGCTGTT(	FTTC	:	360
			*	380	*	400	*	420		
TrMDHf	:	GAGGGTTT	TTGGGGCA	AAATCAGCTTGA	.GGATGCAC	TTACAGGTATG	GATTTGGTA	ATCA	:	420
			*	440	*	460	*	480		
TrMDHf	:	TTCCTGCC	CGGTGTTCC	CCGTAAACCTGG	;AATGACAA	GAGATGATCTC	TTCAATATA	AATG	:	480
			*	500	*	520	*	540		
TrMDHf	:	CCGGGAT	CGTTAAAAC.	ACTCTGTGAAGO	CAATTGCAA		TAAGGCGATT	GTCA	:	540
•			ı	560	*	580	*	600		
TrMDHf	:	ACGTGAT	ragtaatcc	GGTTAACTCCAC	CTGTCCCCA		\GTTTTCAAA		:	600
						640	•	660		
TrMDHf	;	CCGGTAC	* TTATGATCC	620 CAAGAGACTTT	* rgggagtga	640 CAATGCTTGA	rgtggttcgg		:	660
						,		700		
TrMDHf	: :	: ATACGTT	* TGTGGCTGA	680 AGTTCTTGGTC	* ITGATCCAA	700 \GGGATGTGGA	* IGTCCCAGTI	720 GTCG	:	720
TrMDHf	:	: GAGGACA	* TGCCGGAAT	740 CACCATTTAC	* CTCTGCTTI	760 CTCAGGTTAA	* ACCACATTCC	780 TCTT		780
ரு√MDधf	:	<ul> <li>тсхссас</li> </ul>	* "AAADDAAA"	800 TGAGTACTTGA	* CAGATCGC	820 ATACAAAACGG	* TGGAACTGAA	840 GTTG		840
TTLINIT	•									
CO-ANGENET T	=	. സസംവരദേശം	* 'CA	860 BAGCTGGCTCT	: 866					
LIMINUI	•	· TIGWGGC	· caracac + GC	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,						

## FIGURE 70

		*		20	*	40	* ````````````````````````````````````	60 TGO		60
rmDHf	:	MEPNSDANQE	RIARISGHL	NPPNFKMNEHG	DSSLISFR	CRAKGGAPGFKV	AIDGAAGG		•	-
		•	•	80		100	*	120		
rrMDHf	:	PLSMLMKMN	PLVXATHTA	DVVNTPGVTSD	ISHMDTAA	VVRGFLGQNQLE	DALTGMDL	VII	:	120
							*	100		
TrMDHf	:			140 INAGIVKTLCEA	* IAKRCPKA	160 AIVNVISNPVNST		180 KRA	:	180
							_	- 40		
TrMDHf	:		*	200 RANTFVAEVLGL	* .DPRDVDVI	220 PVVGGHAGITILE	* PLLSQVKPF	240 ISSF	:	240
TrMDHf	:			260 EVVEAKAGAGS	: 268					

			*	20	*	40	*	60		
TrMDHf1	:	GNNTACN	GCTATCNAC(	CTTCTTTCTTA	TACAATAA'	TNATAGATAAAT	TCATCTGCT	AAA :		60 -
TrMDHf3	:							:		-
			*	80	*	100	*	120		
TrMDHf1	:	TTATGGA	GCCAAATTC	AGATGCAAATCA	ACGAATCG	CAAGAATCTCCG	GCCACCTAA	ATC	. 1	20
TrMDHf2	:								:	_
	-									
			*	140	*	160	*	180		
TrMDHf1	:	CTCCCAA	TTTCAAGAT		TGATTCTT	CTTTGACAAGTT	TCCATTGCC	CGTG	: 1	.80
TrMDHf2	:								: · :	_
11.101113	•									
			*	200	*	220	*	240		
TrMDHf1	:	CAAAAGG	TGGAGCACC		FTGCAATTI	TAGGTGCTGCTC	GTGGCATA(	GTC	: 2	40
TrMDHf2	:						GTGNCATA(	₹G.TÎŹ	:	12
IIIIIII	•									
			*	260	*	280	*	300		
TrMDHf1	:	AACCTCT	TTCAATGTT	GATGAAGATGA	ATCCGTTGC	TTT-AGTTCTTC	CATCTTTAT	GATG		299
TrMDHf2	:	ACCTCT	TT-NATGTI	GATGAAGATGA	ATCCTATGO	STTT <mark>-</mark> AGTTCTT( STTTNNGTTCTT)	CATCTTTAT(	GATG GATG	:	70 29
ITMDULS	•						Maria			
			*	320	*	340	*	360		
TrMDHf1	:	TTGTTA	ATACTCCTGG	GTGTTACTTCTG.	ATATTAGT	CACATGGATACT	ggtgctgtt	GTTC		359
TrMDHf2 TrMDHf3	:	TTGTTA	ATACTCCTGG	TGTTACTTCTG	ATATTAGT( ATATTAGT	CATATGGATACT( -ATATGGATACT(	GCTGCTGTT GCTGCTGTT	GTTC GTTC	: :	130 86
ITMDALS	•		TIACICCICC	310 111011010						
			*	380	*	400	*	420		
TrMDHf1	:	GAGGAT	TTTGGGGC	AAAATCAGCTTG	AGGATGCA	CTTACAGGTATG	GATTTGGTA	ATCA		419
TrMDHf2		GAGGGT'	FTTTGGGGC <i>I</i> FTTTGGGGC	AAAATCAGCTTG AAAATCAGCTTG	AGGATGCA	CTTACAGGTATG CTTACAGGTATG	GATTTGGTA GATTTGGTA	ATCA ATCA		190 146
TTMDHLS	•	GAGGGI	1 11100000	THE THE TENT	11001110011					
			*	440	*	460	*	480		
TrMDHf1	. :	TTCCTG	CIGGTGTTC	CCCGTAAACCTG	GAATGACA	AGAGATGATCTC	TTCAATATA	AATG	-	479
TrMDHf2		TTCCTG	CCGGTGTTC( CCGGTGTTC)	CCCGTAAACCTC CCCGTAAACCTC	GAATGACA GAATGACA	AGAGATGATCTC AGAGATGATCTC	TTCAATATA TTCAATATA	AATG		250 206
TIPIDITES	•	110010	000010110							
			. *	500	*	520	*	540		
TrMDHfl	. :	CCGGGA	TCGTTAAAA	CACTCTGTGAAG	CAATTGCG	AAGCGATGTCCT	AAGGCGATT	GTCA	-	539
TrMDHf2		CCGGGA	TCGTTAAAA	CACTCTGTGAAG CACTCTGTGAAG	CAATTGCA CAATTGCA	AAGCGATGTCCT AAGCGATGTCCT	'AAGGCGA'I''I 'AAGGCGGT'I	GTCA		310 266
TIMDULS	, :	- COUCE	TCOLIMAN	0110101010111	7					
			*	560	*	580	*	600		
TrMDHf1	L :	ACGTGA	TTAGTAATC	CGGTTAACTCCA	ACTGTCC				:	572
TrMDHf2		ACGTGA	TTAGTAATC	CGGTTAACTCC	ACTGTCCCC ACTGTCCCC	ATTGCGGCTGAA ATTGCGGCTGAA	.GTTTTCAA <i>!</i> .GTTTTCAA <i>!</i>	AGAG AAGAG	:	370 326
TrMDHf3	•	ACGTGA	LIAGIAAIC	COGLIAACICCA	30101000	717 1000001012			•	

			*	620	*	640		000		_
rrMDHfl rrMDHf2 rrMDHf3	:	CCGGTACT' CCGGTACT'	TATGATCC( TATGATCC(	CAAGAGACTTTT CAAGAGACTTTT	GGGAGTGA GGGAGTGA	CAATGCTTGATG' CAATGCTTGATG'	IGGTTCGG IGGTTCGG	GCCA GCCA		430 386
TrMDHf1 TrMDHf2 TrMDHf3	:	ATACGTTT ATACGTTT	* GTGGCTGA GTGGCTGA	680 AGTTCTTGGTCT AGTTCTTGGTCT	* TGATCCAA TGATCCAA	700 GGGATGTGGATG GGGATGTGGATG	* TCCCAGTT TCCCAGTT	720 GTCG GTCG	•	- 490 446
TrMDHf1 TrMDHf2 TrMDHf3	: :	GAGGACAT GAGGACAT	* CGCCGGAAT	740 CACCATTTACC CACCATTTACC	* TCTGCTTT	760 CTCAGGTTAAAC	* CACATTCC	780 TCTT	: :	- 550 506
TrMDHf1 TrMDHf2 TrMDHf3	: :	TCACGACA TCACGACA	* AAAGGAAAT AAAGGAAAT	800 TGAGTACTTG TGAGTACTTGAC	* CAGATCGCA	820 TACAAAACGGTG	* GGAACTGA	840   AGTTG	:	- 576 566
TrMDHf1 TrMDHf2	: :	TTGAGGC	*  CAAAGCTGC	860 	: - : - : 592					

			*	20	*	40	*	60		
rMDhg	:	GTAGGCAGC	ATCTAACA	GCACAATGAACA	TGGAAATO	TTTGCTTTG(	SAAATTATGG	ACAA	:	60
TrMDhg	:	TACGGTCCI	* TAAAAAAT	80 CTGTTCTTGTTI	* TATTTTG1	100 PACTTTTTG	* L'TTTGGAAGA'	120 TCGT	:	120
[rMDhg	:	TAGATACAT	* rgtgtggtc	140 TTCTCAAAGTT	* SATAAGGA!	160 ACCAGTCACTO	* GTATTGGTCA	180 CTGG	:	180
CrMDhg	:	TGCTGCAGO	* BACAAATTG	200 GNTATGCTCTT	* SNTCCAATO	220 GATTGCAAGA	* GGGATGATGC	240 TAGG	:	240
TrMDhg	:	CCCAAATC	* AACCTGGAA	260 ATTCTTCATATGO	* CTNGATAT	280 TGAACCAGGA	* TTAGAGGCCC	300 TTAA	:	300
TrMDhg	:	AGGGGTGA	* AGATGGAA(	320 CTGATTGATGGT	* GCTTTCCC	340 ACTTCTTAGA	* .GGTGTTGTTG	360 CTAC	:	360
TrMDhg	:	TACGGATG'	* TTGTTGAA(	380 ECATGCAAGGAT	* GTTAACAT	400 TGCTGTTATG	* CTTGGTGGAT	420 CCCC	:	420
TrMDhg	:	AAGGAAGG:	* AAGGAATG(	440 GAAAGAAAAGAT	* GTAATGTC	460 TAAGAATGTT	* TCAATTTACF	480 AGGC		480
TrMDhg	:	TCAAGCTT	* CAGCTTTG	500 GAGGAGCATGCT	* GCTGCAGA	520 TTGTAAAGTG	* CTAGTGGTAG	540 CCAA		540
TrMDba	:	TCCAGCAA	* ACACAAAT	560 GCTCTAATATTG	* AAAGAATT	580 TGCTCCATCA	* AATCCCTGAGA	AAA!	:	599

TrMDhg	:	* MCGLLKVDKEPVTVL	20 VTGAAGQIX	* YALXPMIARGMN	40 ILGPNQPGII	* .HMXDIEPGL:	60 EALKGV	:	60
TrMDhg	:	* KMELIDGAFPLLRGV	80 VATTDVVEA	* CKDVNIAVMLGO	100 SSPRKEGME	* RKDVMSKNVS	120 IYKAQA	:	120
TrMDhq	:	* SALEEHAAADCKVLV	140 VANPANTNA	* ALILKEFAPSIP	EK : 157				

			*	20	*	40		*	60		
rrMDHg1 : rrMDHg2 :	. (	GTAGGCA <u>I</u> C GNNGO	A <mark></mark> TAACAG ATCTAACAG	CACAATG -ACAATG	AACATGGA AACATGGA	AAATGTTT AAATGTTT	GCTTTGGAA GCTTTGGAA	ATTATGGAC ATTATGGAC	CAATA :		60 57
TrMDHg1 TrMDHg2	:	CGGTCCTTA	80 DTOTAAAAAA DTOTAAAAAA	TTCTTGT	* TTTATTT TTATTT	100 FGTACTTT FGTACTTT	* TTTGTTTTC TTTGTTTTC	120 GAAGATCG GAAGATCG	TTAGA :	_	122 119
TrMDHg1 TrMDHg2	:	* TACATGTGT TACATGTGT	140 TGGTCTTCTC	CAAAGTTO CAAAGTTO	* BATAAGGA BATAAGGA	160 ACCAGTCA ACCAGTCA	* .CTGTATTGC	180 TCACTGGT TCACTGGT	GCTGC		184 181
TrMDHg1 TrMDHg2	:	* AGGACAAA AGGACAAA	200 FTGGNTATGO FTGGTTATGO	* CTCTTGNI CTCTTGII	rNCAATGA'	<b>20</b> TTGCNAMA TTGCAAGA	* AGGGATGAT( AGGGATGAT(	240 GCTANGNCC GCTAGGCCC	AAATC AAATC	:	246 243
TrMDHg1 TrMDHg2	:	Å ÄACCTGÄÄ ÄACCTGÄÄ	260 ATTGTTGAT ATTCTTCAT	* ATGCTNGI ATGCTÆGI	280 ATNTTG ATATTGAA		* FAGAGGCCC	300 TTAAAGGGG			276 305
TrMDHg1 TrMDHg2	:		20  GATTGATGG	* TGCTTTC	340 CCACTTCT	TAGAGGT(		60 ACTACGGA'I	* CGTTGT	:	- 367
TrMDHg1 TrMDHg2	:	380 TGAAGCAT	GCAAGGATG	* TTAACAT	400 TGCTGTTA	* \TGCTTGG	420 TGGATCCCC	AAGGAAGGA	* AGGAA	:	- 429
TrMDHg1 TrMDHg2	:	440 TGGAAAGA	* AAAGATGTA		60 AGAATGTI	* TCAATTT	480  ACAAGGCTC	* AAGCTTCAC	CTTTG	:	- 491
TrMDHg1 TrMDHg2	:	500 GAGGAGCA	* ATGCTGCTGC	520 AGATTGT		* ragtggta	540 GCCAATCCA	.GCAAACAC	5 AAATGC	:	- 553
TrMDHg1 TrMDHg2		60 TCTAATAT	* TTGAAAGAAT	580	CATCAATC	* CCTGAGAA	: - AA : 594				

#### 174/241

TrMDHh	:	* GNNTACNGCTATC	20 NACCCTTCTTTC	* TTATACAAT	40 AATNATAGATA	* AAATTCATCTG	60 CTAAA :	:	60
TrMDHh	:	* TTATGGAGCCAAA	80 TTCAGATGCAAA	* TCAACGAAT	100 CGCAAGAATC	* TCCGGCCACCT	120 AAATC :	:	120
TrMDHh	:	* CTCCCAATTTCAA	140 GATGAATGAACA	* ATGGTGATTC	160 TTCTTTGACA	* AGTTTCCATTG	180 CCGTG	:	180
TrMDHh	:	* CAAAAGGTGGAGC	200 ACCTGGATTCA	* \AGTTGCAAT	220 TTTAGGTGCT	* GCTGGTGGCAT	240 AGGTC	:	240
TrMDHh	:	* AACCTCTTTCAAT	260 GTTGATGAAGA	* rgaatccttt	280 GGTTTNAGTT	* CTTCATCTTT#	300 TGATG	:	300
TrMDHh	:	* TTGTTAATACTCC	320 CTGGTGTTACTT	* CTGATATTAG	340 TCATATGGAT	* 'ACTGCTGCTG'	360 TTGTTC	:	360
TrMDHh	:	* GAGGGTTTTTGGG	380 GCAAAATCAGC	* TTGAGGATGC	400 ACTTACAGGT	* 'ATGGATTTGG'	420 TAATCA	:	420
TrMDHh	:	* TTCCTGCCGGTG	440 TTCCCCGTAAAC	* CTGGAATGAC	460 CAAGAGATGAT	* CTCTTCAATA	480 FAAATG	:	480
TrMDHh	:	* CCGGGATCGTTA	500 AAACACTCTGTG	* AAGCAATTG(	520 CAAAGCGATG	* CCTAAGGCGA'	540 ITGTCA	:	540
TrMDHh	:	* ACGTGATTAGTA	560 ATCCGGTTAACT	* CCACTGTCC	580 CCATTGCGGC	* rgaagttttca	600 BABAGAG	:	600
TrMDHh	. :	* CCGGTACTTATG	620 ATCCCAAGAGAC	* TTTTGGGAG	640 FGACAATGCT	* TGATGTGGTTC	660 GGGCCA	:	660
TrMDHh	L :	* : ATACGTTTGTGG	680 CTGAAGTTCTTG	* GTCTTGATC	700 CAAGGGATGT	* GGATGTCCCAG	720 TTGTCG	:	720
TrMDHh	L	* : GAGGACATGCCG	740 GAATCACCATT	* TTACCTCTGC	760 TTTCTCAGGT	* TAAACCACATT	780 CCTCTT		780
TrMDHh	ı.	* : TCACGACAAAGG	800 BAAATTGAGTACT	* FTGACAGATC		* CGGTGGAACTG	840 SAAGTTG		840
TrMDHh	ı	* : TTGAGGCCAAAG	860 CTGGAGCTGGC	rct : 866					

# FIGURE 76

#### 175/241

WO 2004/089066

		*		20 ³	*	40	*	60		
rMDHh	:	MEPNSDANQR	IARISGHL	NPPNFKMNEHGI	DSSLTSFH	CRAKGGAPGFKV	AILGAAGG	IGQ :		60
		*		80		100		120		
r'rMDH'h	:	PLSMLMKMNP	LVXVLHLY	DVVNTPGVTSD	ISHMDTAA	VVRGFLGQNQLE	DALTGMDL	VII :	: 1	.20
	•	<b></b>								
		•								
		*	. 1	40	*	160	*	180		
rrMDHh		DAGVDRKDGM	ד <b>וא</b> קיזממאדיי	NAGTVKTLCEA	IAKRCPKA	IVNVISNPVNST	VPIAAEVF	KRA	: 1	.80
TIMMI	•	PAGVITURE OF	1110000111							
		*	. 2	00	*	220	*	240		
rrMDHh	_	משעה מאנונים.	ב. בתאור האידינטי	ANTEVARVIGI	TYTYTHE	PVVGGHAGITILP	LLSQVKPH	ISSF	: 2	240
LEMDUII	:	GIIDERRIDG	A THIND A AL	CHILL AID ADOP			-			
		•	•	•						
		4	. 2	260 .						
		mmverevi mi			: 268					
	•		フベエンがいひてエン	A A TICTOTOO	. 200					

TrMDHh1 TrMDHh2 TrMDHh3	:	GNNTACNG	* GCTATCN	20 ACCCTTCTTTC	* TTATACAATA	40 ATNATAGATA	* AATTCATCTG(	60 CTAAA :		60 - -
TrMDHh1 TrMDHh2 TrMDHh3	: :	TTATGGAC	.* GCCAAAT	80 TCAGATGCAAA	* ATCAACGAATO	100 CGCAAGAATCI	* CCGGCCACCT	120 AATC :	: 1 :	L20 - -
TrMDHh1 TrMDHh2 TrMDHh3	: :	CTCCCAA'	* TTTCAAG	140 ATGAATGAACA	* ATGGTGATTC	160 FTCTTTGACA	* \GTTTCCATTG	180 CCGTG :	: í	180 - -
TrMDHh1 TrMDHh2 TrMDHh3	:	CAAAAGG	* TGGAGCA	200 CCTGGATTCA	* AAGTTĞCAAT'	220 TTTAGGTGCT(	* GCTGGTGGCAT GTGÑCAT	240 AGGTC AGGTÑ	: : :	240 12 -
TrMDHh1 TrMDHh2 TrMDHh3	:	AACCTCT AECCTCT	* TTCAATC	260 ETTGATGAAGA ETTGATGAAGA	TGAATCCT	GGTTT-AGTT	* CTTCATCTTTA CTTCATCTTTA CTTÄÄÄÄCTTTA	TGATG	:	299 70 29
TrMDHh1 TrMDHh2 TrMDHh3	: :	TTGTTAA	TACTCC	rggtgttactt	CTGATATTAG	TCATATGGAT	* ACTGGTGCTGT ACTGCTGCTGT ACTGCTGCTGT	TGTTC:		359 130 86
TrMDHh1 TrMDHh2 TrMDHh3	:	GAGGGTT	TTTGGG	GCAAAATCAGC	TTGAGGATGC	ACTTACAGGT	* ATGGATTTGGT ATGGATTTGGT	'AATCA	:	419 190 146
TrMDHh1 TrMDHh2 TrMDHh3	:	TTCCTGC	CGGTGT'	TCCCCGTAAAC	CTGGAATGAC	CAAGAGATGAT	* 'CTCTTCAATA' 'CTCTTCAATA' 'CTCTTCAATA'	raaatg	: :	479 250 206
TrMDHh1 TrMDHh2 TrMDHh3	. ;	CCGGGAT	rcgtta a	AACACTCTGTC	GAAGCAATTG	CAAAGCGATG	* CCTAAGGCGA CCTAAGGCGA CCTAAGGCGG	ITGTCA	-	539 310 266
TrMDHh1 TrMDHh2 TrMDHh3	:	ACGTGA	гтастаа	560 TCCGGTTAAC TCCGGTTAAC TCCGGTTAAC	TCCACTGTCC	CCATTGCGGC'	* FGAAGTTTTCA	600 AAAGAG AAAGAG	:	

			*	620	*	640	*	660		
TrMDHh1 TrMDHh2 TrMDHh3	:	CCGGTACT CCGGTACT	TATGATCC( TATGATCC(	CAAGAGACTTTT CAAGAGACTTTT	GGGAGTGA GGGAGTGA	CAATGCTTGATG CAATGCTTGATG	rggttcgg( rggttcgg(	GCCA GCCA	-	430 386
TrMDHh1 TrMDHh2 TrMDHh3	:	ATACGTTT ATACGTTT	* GTGGCTGA GTGGCTGA	680 AGTTCTTGGTCT AGTTCTTGGTCT	* TGATCCAA TGATCCAA	700 GGGATGTGGATG GGGATGTGGATG	* TCCCAGTT TCCCAGTT	720 GTCG GTCG	-	- 490 446
TrMDHhl TrMDHh2 TrMDHh3	:	GAGGACAT GAGGACAT	* GCCGGAAT GCCGGAAT	740 CACCATTTTACC	* CTCTGCTTT CTCTGCTTT	760 CTCAGGTTAAAC CTCAGGTTAAAC	* CACATTCC	780  TCTT TCTT	:	- 550 506
TrMDHh1 TrMDHh2 TrMDHh3	:	TCACGACA TCACGACA	* AAGGAAAT AAGGAAAT	800 TGAGTACTTG- TGAGTACTTGAG	* CAGATCGC	820 ATACAAAACGGTO	* GGAACTGAA	840	: :	- 576 566
TrMDHh1 TrMDHh2 TrMDHh3	: :	TTGAGGC	* CAAAGCTGG	860 SAGCTGGCTCT	: - : - : 592					

# 178/241

		*	20	*	40	*	60		
rmDHi	:	GNAATCCTCTTTG	NCTCCCCTACCC	TCCTTTTT	TTCCTTCCTT(	CTTACACCTTC	TCTTA	:	60
rrMDHi	:	* TCAACTTTCCACC	80 TCTGAACAAAAC	* TTCAATCTT	100 TTCTCATTTT	* CTTATACCCTT	120 TTACA	:	120
rrMDHi	:	* AACTTCTTCATAA	140 AGTGTTAGGTTT	* TTTTTTTATT	160 'ACTCTTTTCA	* AGAACCACAA!	180 AAACAG	:	180
TrMDHi	:	* TGTTTCTTGAATT	200 CTTTGGAATTTI	* TTTTTTCCT	220 GCAACCATGG	* CCTTGGCACA(	240 CTTAAA	:	240
TrMDHi	:	* CAACCCCACTTGC	260 TCAAAAACTCAA	* ACTTCACTCA	280 ATCACAACTCI	* CATTTCTCTC	300 FAGGAC	:	300
TrMDHi	:	* TCTCCCTAGGCAA	320 ATATCACTGTACT	* FTTTGCACC	340 ACTTCACAGAA	* ACTCAACATGG	360 CAGAAT	:	360
TrMDHi	:	* TACTTGTTCTGT	380 rgcaccaaatca	* AGTGCAGGCT	400 rccagctgtac	* CAATCACAGGA	420 TCCCAA	:	420
TrMDHi	:	* GAATAAGCCTGA	440 TTGCTATGGTGT	* CTTCTGCCT	460 FACCTATGAT	* TTGAAGGCTGA	480 AGAGGA	:	480
TrMDHi	:	* GACAAAATCCTG	500 GAAGAAATTAAT	* CAACATTGC	520 AGTCTCAGGT	* GCTGCTGGAAT	540 GATTTC	:	540
TrMDHi	:	* CAATCATCTACT	560 TTTCAAGCTTGC	* ATCTGGTGA	580 AGTTTTTGGC	* CCAAATCAACC	600 TATTGC	:	600
ттмоні		* GCTGAAATTATT	620 AGGATCAGAAAG	* GTCCTTCCA	640 AGCTCTTGAA	GGTG : 647			

# FIGURE 79

rrMDHi	:	* MALAHLNNPTCSKTQLH	20 SSQLSFLSRTLI	* PRQYHCTFA	40 PLHRTQHGRITC	* CSVAPNQVÇ	60 QAPA	:	60
rrMDHi	:	* VQSQDPKNKPDCYGVFC	80 LTYDLKAEEETI		100 AVSGAAGMISN	* HLLFKLAS(	120 SEVF	:	120
тrMDHi			140 QALEG : 142						

			*	20		*	40		*		60		
rMDHil :		GNAATCCT	CTTTGN	CTCCCCT	ACCCTC	TTTTTT	TTCCTT	CTTCT	raca <mark>-</mark> c ragacc	TTCTCT TTCTCT	TAT	:	60 19
rrMDHi1 FrMDHi2	: [	CAACTTTC -AACTTTC	* CACCT( NACCT(	80 TGAACAA TGAAC	AACTTC AA <mark>-</mark> TT-	* TATCTTT AATCTTT	100 TCTCAT TCT-AT	PTTCTT.	* ATACCC ATACCC	12 CTTTTAC	AAA	: : :	121 76
IrMDHi1 IrMDHi2	:	* CTTCTTCA CTTCTTCA	TAAAG TAAAG	140 GTTAU¶T GTTĞGGT	<mark>TTTT</mark> TTTTTT	* TTATTAC TTATTAC	160 TCTTTT	CAAGAA CAAGAA	* CACA/	180 AAAACAG AAAACAG	TGT	: :	180 137
TrMDHi1 TrMDHi2	:	* TTCTTGAA TTCTTGAA	TTCTT	200 IGPAATTT IGGAA <mark>-</mark> TT	* TTTTTTT TTTTTT	TCCTGC#	220 ACCATG ACCATG	GCCTTG GCMTTG	* GCACA GCACA	240 TTAAA( TTAAA(	CAAT CAAC	:	241 196
TrMDHi1 TrMDHi2	:	* CCCACTTO	7 7 7 7 7 7	260 AAACTCAA AAACTCAA	* CTTCAC	TCATCAC	280 CAACTCT CAĞCTCT	* CATTTIC	TGTCT.	300 AGGACT AGGACT	CTCC	:	302 257
TrMDHi1 TrMDHi2	:	* CTAGGCAI CTAGGCAI	TATCA	20 CTGTACTT CTGTACTT	TTTGCAC	34 CCACTTCA CCACTTCA	ACAGAAC	* CTCAACA CTCAACA	ATGGCA ATGGCA	360 GAATTA GAATTA	CTTG CTTG	:	363 318
TrMDHi1 TrMDHi2	:	* TTCTGTTC	38 GCACCA GCACCA	AATCAAC	rgcagg	40 CTCCAGC CTCCAGC	TGTACAZ	* ATCACAC	GATCC	<b>420</b> CAAGAA CAAGAA	TAAG TAAG	:	424 379
TrMDHi1 TrMDHi2	:	* CCTGATT	440 GCTATO	СТСТСТТ	CTICCCTI	460 TACCTAT TACCTAT	GATTTG	* AAGGCT( AAGGCT(	GAAGAG	80 GAGACA GAGACA	TAAA TAAA	:	485 440
TrMDHi1 TrMDHi2	:	* CCTGGAA CCTGGAA	<b>500</b> GAAATI GAAATI	'AATCAAC 'AATCAAC	* ATTGCA ATTGCA	GTCTCAG	GTGCTG GTGCTG	* CTGGAA' CTGGAA'	54 TGATTI TGATTI	CCAATO	ATCT ATCT	:	546 501
TrMDHi1 TrMDHi2	:	* ACTTTTC ACTTTTC	560 AAGCT AAGCT	GCATCTG	* GTGAAG GTGAAG	580 TTTTTGG	ETCCAAA ECCCAAA	* TCAACC' TCAACC'	600 TATTGO TATTGO	GCTGA-	*  ATTA	:	602 562
TrMDHil	:	TTAGGAT	620 CAGAA		CCAAGC		AGGTG :	- 599					

		*		20	*	40	*	60		
rMDHj	:	GCAAAGCNCT	CNCNGACO	TGGTGTGGAGC	GAGCAGCT	TTGCTAGACA	TAAATGGGCA	GAT	:	60
rrMDHj	:	* TTTTGCGGAG		80 AAGCTCTAAATG		100 TCTCGCAATO	* GTCAAAGTTAI	120 AGT	:	120
гrМDНj	:	* TGTGGGAAAC	CCTTGCA	140 ATACAAATGCAT	* TTAATATGO	160 CTTGAAGAATO	* GCTCCAAATAT	180 TTCC	:	180
ГrMDHj	:	* TGCAAAAAAT	TTTTCATG	200 CTTTAACCCGT	* FTAGATGAG	220 BAACAGAGCA	* AAATGTCAGC	240 TAGC	:	240
TrMDHj	:	CCTCAAGGCA	, AGGTGTCT	260 TCTACGATAAA	* GTGTCGAA	280 FATGACGATA	* TGGGGAAACC	300 ACTC	:	300
TrMDHj	:	AACTACTCAC	* GGTCCCCG	320 ATTTCTTAAAT	* GCCAGAAT(	340 CGATGGTTTG	* CCTGTCAAAG	360 AAGT	:	360
TrMDHj	:	GATTAAGGA	* TCAAAAGT	380 GGTTAGAGGAA	* GAGTTCAC	400 CGAAAAAGTT	* CAAAAGAGAG	420 GTGG	:	420
TrMDHj	:	CGTGCTTAT"	* TCAAAAGT	440 GGGGAAGATCG	* TCTGCTGC	460 ATCAACTTCT	* GTGTCGATAG	480 TTGA	:	480
TrMDHj	:	TGCCATACG.	* ATCTTTG#	500 YTCACTCCTACT	* CCGGAGGG	520 TGATTGGTTI	* TCTACTGGTG	540 TGTA	:	540
TrMDHj	:	TACAGCTGG	* AAATCCTI	560 PATGGAATAGCT	'G : 569					

rrMDHj	:	* QSXXXPGVERAALLDIN	20 GQIFAEQGKALN	* IAVASRNVI ·	40 KVIVVGNPCNTN	* ALICLKNAP	MIP	:	60
rrMDHj	:	* AKNFHALTRLDENRAKC	80 QLALKAGVFYDI	* CVSNMTIWO	100 GNHSTTQVPDFLI		120 KEV	:	120
rrMDHj	:		140 RGGVLIQKWGRS	* SSAASTSV	160 SIVDAIRSLITP		180 GVY	:	180
Ͳ·ϒϺϽឣ·ϳ		TAGNPYGTA: 189							

		*	20	*	40	*	60		
TrMDHk		GNGTAGAACCCGT		CCTCCGGTCTC	CCCGCTTGC	CCGTCGCCGT	CAATT	:	60
TIMDEK	•	GNGIAGAACCCGI	GAAGCCIIIIC	.010000101					
			•						
		*	80	*	100	*	120		
		GCTGCTTGTGTCG				ልልሮሮሮልልሞሞልሮ		:	120
TrMDHK	:	GCTGCTTGTGTCG	TUGUUT CUAGU.	rccrccrc	CACIGIGCO	MCCOMIL XIIO		•	
				*	160	*	180		
		*	140						180
TrMDHk	:	AAAAAAATGGCGA	ACTTGTTTGCAA	ACACAACTCC.	rccacacaag.	ACCITITCAGI	11000	•	100
							240		
		*	200	*	220	*	240		040
TrMDHk	:	TCTTCCTCGTCG	ACAAGACCAACT"	TCCCTAAGAT	GTTCCGCCGC	CACCCCATCCA	CCAAA	:	240
		*	260	*	280	*	300		
TrMDHk	:	AAATCCTACAAA	ATCACTCTTCTT	CCGGGTGATG	GCATAGGTCC	TGAAGTCGTTT	CCGTC	:	300
	_								
		*	320	*	340	*	360		
m~MD⊞b		GCTAAAGACGTT		GGATCCATCC	ATGGGATTAA	ACTTGAGTTTC	AAGAG	:	360
TIMDUK	•	GCIAAAOACGII	01101001010-	•••••					
		*	380	*	400	*	420		
		AAGCTTTTGGGT		י. ארו א חינו ביודי א ביודים:		ימכירממדממדי		:	420
TrMDHk	:	AAGCTTTTGGGT	GGIGCIGCICII	GAIGCIACIG	GAGIICCIII			•	
				44.	460	*	480		
		*	440	, 		 			480
TrMDHk	:	TCTGTTGCTAAG	CAATCTGATGCT	GTTCTTCTTG	GIGCIATIGO	AGGGIAIAAA.	LGGGAI	•	400
							-40		
		*	500	*	520	*	540		- 40
TrMDHk	:	AAAAATGAGAAA	CAGCTGAAGCC	\GAAACTGGA1	"TGCTTCAGC"	CACGAGAAGGG	JTCAA	:	540
		*							
CT 3 CT TT1-			OMOROR . EES	<b>.</b>					

TrMDHk	:	* MATCLQTQLLHTRPF	20 QFRSSSSTRI	* PTSLRCSAAT	40 PSTKKSYKITI	* LLPGDGIGPE	60 VVSVAK	:	60
TrMDHk	:	DVLLLTGSIHGIKLE	80 FQEKLLGGA	* ALDATGVPLI	100 PDDTLSVAKQSI	* DAVLLGAIGG	120 YKWDKN	:	120
ጥቍለነገዝራ		* *	140	: 144					

			*	20	*	40	*	60		
[rPEPCa	:	GNNACATI	rnccgaatgc	TGCTGAACTAGG	GAGTGAT.	CCCTTGGAGC	CTATGTCAT	CTCT	:	60
TrPEPCa	:	ATGGCCT	* CAAGTGCAAG	80 GCGATGTCCTTGC	* CAGTAGAG	100 CTTTTACAGAA	* GGATGCACG	120 ICTT	:	120
TrPEPCa	:	ACAGTTT	* GTGGAGAATI	140 TAGGAAGAGCATO	* STCCGGGT	160 GGAACGCTTCG	* GGTGGTTCC	180 ICTA	:	180
TrPEPCa	:	TTTGAAA	* CTGTGCAAG!	200 ACCTGAGAGGAG	* CTGGTGCA	220 GTTATCAGAAA	* .ACTTTTATC.	240 AATC	:	240
TrPEPCa	:	GATTGGT.	* ACCGCCAAC	260 ACATCATTAAGA	* ACCATAAC	280 GGACACCAAGA	* \GGTTATGGT	300 CGGT	:	300
TrPEPCa	:	TATTCTG	* ATTCTGGTA	320 AAGATGCCGGGC	* GCTTTACT	340 GCTGCTTGGG	* \ACTTTACAA	360 AGCT	:	360
TrPEPCa	:	CAAGAGG	* ATGTAGTGG	380 CTGCTTGCAATA	* AGTACGAI	400 'ACTAAGGTTA	* CTTTGTTCCA	420 .CGGC	:	420
TrPEPCa	:	CGCGGAG	* GGAGTATTG	440 GACGTGGCGGAG	* GCCCAACA	460 ATATCTGGCTA	* TTCAGTCCCA	480 GCCA	:	480
TrPEPCa	:	CCTGGCT	* CTGTGATGG	500 GAACCCTTCGGI	* CAACTGAC	520 ECAGGGAGAGA'	* TGGTGCAGGC	540 CGAG	:	540
TrPEPCa	:	TTTGGGI	* TTGCCACAGA	560 .CAGCAGTTAGAC	* CAACTTGA	580 AATATACACAA	* CAGCTGTGCT	600 TACTT	:	600
TrPEPCa	:	: GCTACAC	* CGTCGTCCAC	620 CCACTCCCACCTC	* CGAGAAGA	640 AAAATGGCGTA	* ATCTAATGG!	060 AAGAC		660
ጥኍኮፑኮርລ		· ኔጥለጥሮኔ	* ^AAATCAGTT	680 CGTCAGTCCTAC	* CGCAGTGT	700 AGTCTATGAAA	* ATCCAGN :	713		

		*	20	*	40	*	60		
rrPEPCa	:	XTXPNAAELGSDSLGA	AYVISMASSA	ASDVLAVELLÇ	OKDARLTVCG	ELGRACPGGTLI	RVVPL	:	60
		*	80	*	100	*	120		
[rPEPCa	:	FETVQDLRGAGAVIR	KLLSIDWYR(	QHIIKNHNGHÇ	)EVMVGYSDS	GKDAGRFTAAW:	ELYKA	:	120
		*	140	*	160	*	180		
TrPEPCa	:	QEDVVAACNKYDTKV	TLFHGRGGS:	IGRGGGPTYL <i>l</i>	AIQSQPPGSV	MGTLRSTEQGE	MVQAE	:	180
		*	200	*	220	*			
T~DEDC≃		ECT. DOTAVEOT. ETYT	TAVITATER	PPLPPREEKWI	RNLMEDXSKI	SCOSYRSVVYE	NP : 2	237	7

		*		20	*	40	*	60		
TrPEPCal :	•	GNNACATTNC	CGAATGC	rgctgaactage	GAGTGATT	CCCTTGGAGCCT	ATGTCATC	TCT	:	60
TrPEPCa2 :	:								:	_
IlFErcas .	•									
						100		120		
TrPEPCa1		* ATGGCCTCAA	GTGCAAG	80 CGATCTCCTTGC		100 TTTT-CAGAAGO	ATGCACG	120	: :	119
TrPEPCa2	:	AIGGCCICAL			GMAC	TTTTACAGAAG	GATGCACGT	CTT	:	27
TrPEPCa3	:				AGC	TTTTACAGAMG(	GATGCACGI	CTT	:	26
		*		140	*	160	*	180		
TrPEPCa1	:	<b>GCIGGTANT</b>	GAGAGTT	CGGAAGAGCATC	FTCCTGGTG	GAACGITGCGG	GTEGTECCT	CTA	:	179
TrPEPCa2	:	ACAGTTTGTC	GAGAATT.	AGGAAGAGCAT(	TCCGGGTG	GAACGCTTCGG( GAACGCTTCGG(	GTGGTTCCT	rCTA	:	87 86
TrPEPCa3	:	ACAGTTTGTC	GAGAATT.	AGGAAGAGCAT	31000010	GAACGCTTCGG	31001100	CLA	•	00
		-		200	*	220	*	240	_	239
TrPEPCal	:	TTTGAAACTC	GTGAAGGA GTGCAAGA	CCTGAGAGGAGG CCTGAGAGGAGG	TGGTECAC	TTATCÜĞÜAAA TTATCAGAAAA	CTTTTATC	AATC	-	147
TrPEPCa2 TrPEPCa3	:	TTTGAAACTC	TGCAAGA TGCAAGA	CCTGAGAGGAG	CTGGTGCAC	TTATCAGAAAA	CTTTTATC	AATC	:	146
			<b>L</b> .	260	•	280	*	300		
TrPEPCa1		GAETGGTAC	CGTGAACA	260 CATCATTAAGA	ACCAGAATO	GACALICAAGAG	GTTATGGT		:	299
TrPEPCa2	:	GATTGGTAC	CGCCAACA	CATCATTAAGA	ACCATAACO	GGACACCAAGAG	GTTATGGT	CGGT	:	207
TrPEPCa3	:	GATTGGTAC	CGCCAACA	CATCATTAAGA	ACCATAACO	GGACACCAAGAG	GTTATGGT	CGGT	:	206
			*	320	*	340	*	360		
TrPEPCa1	:	TATTCTGAT	TCGGGTAA	AGATGCTGGCC	GCTTQACT	GCTGCTTGGGAA	CTTTACAA	AGCT	:	359 267
TrPEPCa2	:	TATTCTGAT	${ m TCTGGTA}^{ m F}$	AGATGCCGGGC	GCTTTACT(	GCTGCTTGGGAA GCTGCTTGGGAA	CTTTACAA CTTTACAA	AGCT	:	266
TrPEPCa3	•	IAIICIGAI	TCIGGIA	HOAT OCCOOC	001111101	30130110311				
								400		
mDEDG-1		CACCACCAT	*	380 TECTTECANTE	*	400 ATTAAAGTTAC	* GTGTTTCA	420		419
TrPEPCa1 TrPEPCa2	:	CAAGAGGAT	GTAGTGG(	CTGCTTGCAATA	AGTACGAT.	ACTAAGGTTACI	TTGTTCCA	CGGC	:	327
TrPEPCa3	:	CAAGAGGAT	GTAGTGG	CTGCTTGCAATA	AGTACGAT	ACTAAGGTTACT	TTGTTCCA	.CGGC	:	326
							•			
			*	440	*	460	*	480		
TrPEPCa1	:	CGTGGAGGG	AGTATTG	GTCGAGGTGGTG	GCCCACA	TATCTGGCTATT	CAGTCCCA	<u>A</u> CCA	:	479
TrPEPCa2	:	CGCGGAGGG	AGTATTG	GACGTGGCGGAG	GCCCAACA	TATCTGGCTATT	CAGTCCCA	GCCA	:	387 386
TrPEPCa3	:	CGCGGAGGG	AGTATTG	GACGTGGCGGAG	GCCCAACA	TATCTGGCTATT	CAGICCCA	CCCA	•	300
			*	500	*	520	*	540	_	E20
TrPEPCal	:	CCTGGGTCT	GTGATGG CTGATGG	GAACACTTCGG1	rcaactgac	CAGGGAGAAT CAGGGAGAGAT	GTAGAGGC GTGCAGGC	CAAG CGAG	:	539 447
TrPEPCa2	:	CCTGGCTCT	GTGATGG	GAACCCTTCGG	CAACTGAG	CAGGGAGAGAT	GTGCAGGC	CCGAG	:	446
22222	•									
			*	F60		580	*	600		
ጥ~ኮቪኮሮ≃ ነ		тттссстт	CCACAGA	560 TAGCEGTTAGA	CAACTTGAN	N				576
TrDEDCa2		TTTGGGTTC	CCACAGA	CAGCAGTTAGA	CAACTTGAA	ATATACACAAC.	AGCTGTGC:	PACTT	:	507
TrPEPCa3	:	TTTGGGTTC	CCACAGA	CAGCAGTTAGA	CAACTTGAA	ATATACACAAC.	AGCTGTGC'	FACTT	:	506

			*	620	*	640	*	660		
TrPEPCal TrPEPCa2 TrPEPCa3	:	GCTACAC GCTACAC	GTCGTCC	CACCACTCCCA CACCACTCCCA	CCTCGAGAAG CCTCGAGAAG	AAAAATGGCG' AAAAATGGCG'	PAATCTAATG PAATCTAATG	GAAGAC GAAGAC	:	567 566
			*	680	*	700	*			
TrPEPCal TrPEPCa2	:	ATN	AAATCA	TTGTCAGTCC	TACCGCAGTO	TAGTCTATGA	AAATCCAGN	: 570 : 619		

			*	20	*	40	*	60		
rpepcb :	:	GNAAGGGA	CAAGCTCTA	TCGTACTCGTGA	GCGGTCTC	GCTATCTCT.	ragctcatgg(	CTAT	:	60
rpepcb	:	TCTGAAAT	* CCTGAAGA	80 AAGCCACATTCAC	* CGATGTTC	100 SATGAGTTCT	* IGGAACCTCT	120 TGAA	:	120
[rPEPCb	:	CTATGCTA	* CAGATCACI	140 rctgtgcttgtg	* STGATCGT(	160 GCGATTGCCG	* ATGGAAGCCT	180 TCTT	:	180
TrPEPCb	:	GATTTCTT	* GAGGCAAGI	200 ITTCCACTTTTG	* GACTGTCA	220 CTGGTAAGAC	* TTGATATAAG	240 GCAA	:	240
TrPEPCb	:	GAGTCAGA	* TCGTCACA	260 CGGACGTGATGG	* ATGCCATT	280 ACCAAACATT	* TGGAAATTGG	300 ATCC	:	300
TrPEPCb	:	TACCAAGA	* .CTGGTCTG.	320 AAGAAAAAAGAC	* AGGAATGG	340 CTTTTGTCTG	* AGTTGGTTGG	360 CAAA	:	360
TrPEPCb	:	AGGCCGCT	* TTTTGGAC	380 CTGACCTACCTC	* AAACCGAT	400 GAAATTAGAG	* BAAGTTTTAGA	420 AGACA	:	<b>420</b>
TrPEPCb	:	TTTCATG	* CATAGCAG	440 AACTTCCATCAG	* ACAACTTI	460 GGAGCCTAT!	* ATCATTTCGAT	480 IGGCA	:	480
TrPEPCb	:	ACTGCCC	* CGTCTGATG	500 TGCTAGCGGTTG	* SAACTTCTI	520 CAACGTGAA	* rgcaaaatcai	540 AGAAT		540
TrPEPCb		CCGTTAA	* EAGTTGTTO	560 CCGTTGTTTGAGA	* AACTTGCT	580 GATCTCGAG	* rctgctcctg	CTG :	5	98

rrPEPCb	:	* 20 XRDKLYRTRERSRYLLAHGY	* SEIPEEATFTD	40 VDEFLEPLELCYRS	* LCACGDRAI	60 ADGSLL	:	60
TrPEPCb	:	* 80 DFLRQVSTFGLSLVRLDIRQ	* ESDRHTDVMDA	100 ITKHLEIGSYQDWS	* EEKRQEWLL	120 SELVGK	:	120
TrPEPCb	:	* 140 RPLFGPDLPQTDEIREVLET	* FHVIAELPSDN	160 FGAYIISMATAPSD	* VLAVELLQR	180 ECKIKN	:	180
ო≁চ∉চ∩ე		* PLRVVPI,FEKLADLESAPA	: 199			•		

			*	20	*	40	* 60		
rpepcb1 rpepcb2	:	GNAAGGGA( GAAAGGGA(	CAAGCTCTA' CAAGCTCTA'	TCGTACTCGTGA TCGTACTCGTGA	GCGGTCTC GCGGTCTC	GCTATCTCTTA( GCTATCTCTTA(	GCTCATGGCTAT GCTCATGGCTAT	:	60 60
rrPEPCb1 FrPEPCb2	:	TCTGAAAT TCTGAAAT	* CCTGAAGA CCTGAAGA	80 AGCCACATTCAC AGCCACATTCAC	CGATGTTG	100 ATGAGTTCTTG ATGAGTTCTTG	* 120 GAACCTCTTGAA GAACCTCTTGAA	:	120 120
TrPEPCb1 TrPEPCb2	:	CTATGCTA	CAGATCACT	140 CTGTGCTTGTGG CTGTGCTTGTGG	* FTGATCGTG FTGATCGTG	160 CGATTGCCGAT CGATTGCCGAT	* 180 GGAAGCCTTCTT GGAAGCCTTCTT	:	180 180
TrPEPCb1 TrPEPCb2	:	GATTTCTT GATTTCTT	* GAGGCAAGT GAGGCAAGT	200 TTCCACTTTTGO TTCCACTTTTGO	* SACTGTCAC SACTGTCAC	220 CTGGTAAGACTT CTGGTAAGACTT	* 240 GATATAAGGCAA GATATAAGGCAA	:	240 240
TrPEPCb1 TrPEPCb2	:	GAGTCAGA GAGTCAGA	* TCGTCACAC TCGTCACAC	260 CGGACGTGATGGA CGGACGTGATGGA	* ATGCCATTA ATGCCATTA	280 ACCAAACATTTG ACCAAACATTTG	* 300 GAAATTGGATCO	:	300 300
TrPEPCb1 TrPEPCb2	:	TACCAAGA TACCAAGA	* CTGGTCTGA CTGGTCTGA	320 AGAAAAAAGAC AAGAAAAAAGAC	* AGGAATGG AGGAATGG	340 CTTTTGTCTGAC	* 360 TTGGTTGGCAA TTGGTTGGCAA	A :	360 360
TrPEPCb1 TrPEPCb2	:	AGGCCGCT AGGCCGCT	* TTTTTGGAC(	380 CTGACCTACCTC CTGACCTACCTC	* AAACCGAT AAACCGAT	<b>400</b> GAAATTAGAGAA GAAATTAGAGAA	* 42 AGTTTTAGAGAC AGTTTTAGAGAC	Α :	: 420 : 420
TrPEPCb1 TrPEPCb2		TTTCATG1	* CATAGCAG CATAGCAG	440 AACTTCCATCAG AACTTCCATCAG	* ACAACTTT ACAACTTT	460 GGAGCCTATATO GGAGCCTATATO	* 48 CATTTCGATGGC	Α	: 480 : 480
TrPEPCb1 TrPEPCb2		ACTGCCC	* CGTCTGATG CGTCTGATG	500 TGCTAGCGGTTG	* SAACTTCTT	520 CAACGTGAATG CAACGTGAATG	* 54 CAAAATCAAGAA CAAAATCAAGAA	$\mathbf{T}$	: 540 : 540
TrPEPCb1		CCGTTAA	* GAGTTGTTC	560 CGTTGTTTGAGA CGTTGTTTGAGA	* \AACTTGCT \AACTTGCT	580 GATCTCGAGTC GATCTCGN	* TGCTCCTGCTG		598 584

		*	•	20	*	40	*	60		
TrPEPCc	:	GTCACATGAC	AAACNAT	ATCTCCCTTTC	CTAACTCC	GTGATCAAGG	CGTTAGTTAC	STTA	:	60
TrPEPCc	:	* CACAAATTGO		80 STTTCGTTGTAC	* FTTCCCGT	100 CAATCCATAG	* TATCTTGGA	120 GGAA	:	120
TrPEPCc			· FTTTCCAC	140 CCTAGGTCGTCA	* CGAGATTT	160 CCTCTTCACT	* 'ATTTTTCTT'	180 TTTC	:	180
TrPEPCc	:		* CTCAACAC	200 CTTTTTCTAGCT	* ACTTACTA(	220 GTACTGTGTA	* \CACAAATTT	240 TATT	:	240
TrPEPCc	:		* FACTCCT(	260 CGCAACATTGAA	* AAAATGGC'	280 TTCAATTGATC	* SCTCAATTGA	300 GACT	:	300
TrPEPCc	:		* AAGGAAA	320 GTTTCTGATGAT	* 'GATAAACT'	340 TGTCGAGTATO	* BATGCTTTGT	360 TATT	:	360
TrPEPCc	: :	GGATCGATT	* CCTTGAC	380 ATTCTTCAAGAI	* TTGCATGG	400 AGAAGATATC	* AGACAAACTG	420 FTTCA	:	420
TrPEPCo	: :	: AGATTGTTA	* TGAGTTA	440 TCGGCAGAGTAI	* CGAAGGGGA	460 GCTTAAGCCG	* GAGAAATTGG	480 AGGA		480
TrPEPCo	: :	: ACTTGGGAA	* TATGCTT	500 ACTGGTCTTGAT	* rgctggaga	520 ATTCTATTGTT	* ATAGCAAAAT	540 CATI	•	540
T∼DEDC	,	• ጥጥሮጥሮልጥልባ	* የርረጥጥልልጥ	560 TTGGCAAACTT	* =GCAGAGN	: 575				

#### 193/241

		*	20	*	40	*	60		
TrPEPCc	:	MATPRNIEKMASIDAQ	LRLLAPR	KVSDDDKLVEY	DALLLDRFLD:	ILQDLHGEDIF	QTVQD	:	60

* 80 * 100 * TrPEPCc : CYELSAEYEGELKPEKLEELGNMLTGLDAGDSIVIAKSFSHMLNLANLAE : 110

			20	*	40	*	60		
TrPEPCc1 TrPEPCc2	:	GTCACATGACEÑA	TODOTOTATAEO. CNATATOTOTATA	TTCTCTAAC TTCTCTAAC	TCCGTGATCAA TCCGTGATCAA	AGGCGTTAGT AGGCGTTAGT	PAGTTA PAGTTA	:	60 54
TrPEPCc1 TrPEPCc2	:	* CACAAATTGCTGT CACAAATTGCTGT	80 TAGGTTTCGTTG TAGGTTTCGTTG	* TACTTTCCC TACTTTCCC	100 GTGCAATCCAT GTGCAATCCAT	* PAGTATCTTG PAGTATCTTG	120 GAGGAA GAGGAA	:	120 114
TrPEPCc1 TrPEPCc2	:	* CAAACTAGATTTT CAAACTAGATTTT	140 CCACCTAGGTCG CCACCTAGGT∏G	* TCACGAGAT TCACGAGAT	160 TTTCCTCTTCA TTTCCTCTTCA	* ACTATTTTTC ACTATTTTTC	180 TTTTTC TTTTTC	:	180 174
TrPEPCc1 TrPEPCc2	:	* ATATAATAACTCA ATATAATAA∭TCA	200 ACACTTTTCTA ACACTTTTCTA	* GCTACTTAC GCTACTTAC	220 TAGTACTGTGT TAGTACTGTGT	* TAACACAAAT TAACACAAAT	240 TTTATT TTTATT	:	240 234
TrPEPCc1 TrPEPCc2	:	* CATTATGGCTACT CATTATGGCTACT						:	300 294
TrPEPCc1 TrPEPCc2	:	* ACTAGCACCAAGO ACTAGCACCAAGO	320 AAAGTTTCTGAT AAAGTTTCTGAT	* GATGATAAA GATGATAAA	340 CTTGTCGAGTA CTTGTCGAGTA	* ATGATGCTTT ATGATGCTTT	360 GTTATT GTTATT	-	360 354
TrPEPCc1 TrPEPCc2	:		380 TGACATTCTTCAA TGACATTCTTCAA	* GATTTGCAT GATTTGCAT	400 'GGAGAAGATA' 'GGAGAAGATA'	* FCAGACAAAC FCAGACAAAC	420 TGTTCA TGTTCA	-	420 414
TrPEPCcl TrPEPCc2	:	* AGATTGTTATGAC AGATTGTTATGAC						-	480 474
TrPEPCcl TrPEPCc2	:	* ACTTGGGAATATC						:	540 534
TrPEPCc1 TrPEPCc2	:	* TTCTCATATGCT TTÑ			N : 575				

# 195/241

			*	20	*	40	*	60		
TrPEPCd	:	AGAAGATC'	CATGTTTC	SAGTTGTCTATG	rggcgctgc	CAACGACGAGCT	CCGTGTTA	GAGC	:	60
			*	80	*	100	*	120		
TrPEPCd	:	TGAAGAGC'	rtcatagat	CCTCAAAGAAA	JATGCAAA!	ACATTATATTGA	GTTTTGGA	AACA	:	120
			*	140	*	160	*	180		
TrPEPCd	:	GATTCCTC	CAAACGAGO	CCATATCGTGTT	ATTCTTGG/	AGGTGTGAGGGA	CAAACTGT	AATA	:	180
			*	200	*	220	*	240		
TrPEPCd	:	TACACGTG	AACGTGCT	CGACAGTTATTÁ	GCAAATGG!	AACCTCTGACAT	CCTTGAAG	AGAC	:	240
			*	260	*	280	*	300		
TrPEPCd	:	AACCTTCA	CGAATGTTC	SAGCAGTTTCTG(	GAGCCTCT		TAGGTCAC'		:	300
			*	320	*	340	*	360		
TrPEPCd	:	TGCATGTG	GTGACCGA:	CAATAGCAGAC	GGAAGCCT'		'GCGACAAG'		:	360
			*	380	*	400	*	420		
TrPEPCd	:	TACATTTG	GACTTTCAC	CTTGTAAGACTC	GACATCCG'				:	420
			*	440	*	460	*	480		
TrPEPCd	:	CGTTATGG		ACAAAACACTTG	GAGATTGG				:	480
			*	500	•	520	•	540		
TrPEPCd	:	ACGCAGGC		CTCTTGTCTGAG	CTTAGTGG		CTTCGGCC		:	540
			*	560		F00	_	<b>600</b>		
TrPEPCd	:	TCTTCCTA		SAAATTGCCGAT(	GTTTTAGA'	580 TACCTTNCACGT	* NATTTCAN	600 AACT	:	600
									7	
			•	620		640		c c o		
TrPEPCd	:	TNCCTCAN	ATAGCTTT(	GTGCCTATATC	ATCTCAAT	640 GGCAACCTCCCC	ATCTGATG	660 TGCT	:	660
			-						-	
			•	600		700		<b>300</b>		
TrPEPCd	:	AGCTGTCG	 AGCTTTTA	680 CAACGTGAATGT	^ CATGTGAA	700 GCAGCCGTTAAN	* CTTGTTGAI	720 CACT		720
									•	
				740		760		<b>500</b>		
TrPEPCd	:	GTTTGAAA	AGCTCGCCI	740 NGTCTTGAGTCT		760 TGCGGNAGCGCG	ւրԽւնանակար ×	780 TAGA	•	780
	-								-	
			*	000	_	000		040		
TrPEPCd	:	TTGGGNCA		800 NTAATGGAAAGC	^ AGAAGTፕላህ	820 TGATAGGTACTO	ANACTNGG	840 GAAA		840
	•								•	- 10
TrDEPCd		AGATGCTG	* GCCGNN :	854						
	-			- <del>-</del>						

# FIGURE 95

		*	20	*	40	*	60	
TrPEPCd	:	EDLMFELSMWRCN	DELRVRAEELHR	SSKKDAKHY:	IEFWKQIPPN	EPYRVILGGVR	OKLYN :	60
TrPEPCd	:	* TRERARQLLANGT	80 SDILEETTFTNV	* EQFLEPLEL	100 CYRSLCACGD	* PRSIADGSLLDF:	120 LRQVS :	: 120
TrPEPCd	:	* TFGLSLVRLDIRÇ	140 ESDRHTDVMDAI	* TKHLEIGSY	160 REWSEERRQE	* WLLSEĻSGKRP	180 LFGHD :	180
TrPEPCd	:	* LPKTEEIADVLDI	200 XHXISXLXSXSF	* 'GAYIISMAT	220 SPSDVLAVEL	* LQRECHVKQPL	240 XVVPL :	: 240
TrPEPCd		* FEKLAXLESAPAA	260 XAREXI DWXXTX	* XMESRSXDR	280 YSXXGKDAGX	: 284		

		*	20	*	40	*	60		
TrPEPCe	:	GTTCACTGTCTCTCTG	NCCAATTTTCCT	CCCTTGTC	CTTCTTTTTCTT	CTTCTTCCT	CGTA	:	60
				*		.4.			
TrPEPCe		· 매근까까 C까근 CC C C C C C C C C C C C C C C C	80 		100	*	120		100
ITPEPCE	•	TCTTACTGCCTCATTA	CACGGGIGAGAA	GGAGTGAA	ATTGCTCCAATG	3CAACAAAC	AAAA	:	120
		*	140	*	160	*	180		
TrPEPCe	:	TGGAAAAAATGGCATC	'AATTGATGCACA	GCTTAGAC		<b>GCAAAAGTT</b>		:	180
		*	200	*	220	*	240		
TrPEPCe	:	AAGATGATAAACTTAT	TGAGTATGATGC	TTTGTTGT	TTGGATCGGTTT	CTTGATATC	CTTC	:	240
		*	260	*	280	*	300		
TrPEPCe	:	AGGATTTACATGGAGA						:	300
							0000	-	
		-							
		*	320	*	340	*	360		
TrPEPCe	:	AGTATGAAAGAAAGCA	ATGATCCTAAGAA	ACTTGAAC	GAGCTCGGAAAT'	<b>TTGATAACA</b>	AGTT	:	360
			380	•	400	•	420		
TrPEPCe		TAGATGCAGGAGATTC	•	יייים אביייריריי	=	יי רידיים א רידידים			420
1111100	٠	Inoniociochonii	MIIOIIOI	IAMGICC.	IIICOCACAIG	CITARCITO	GCCA	•	420
		* .	440	*	460	*	480		
TrPEPCe	:	ACTTAGCTGAAGAGGT	TCAGATTGCTCA	ATCGTCGA	AGGAACAAGTTG	AAGAAAGGA	GATT .	:	480
mDEDG-		*	500	*	520	*	540		
TrPEPCe	=	TTAGGGATGAGAGCA	ATGCAACTACCGA	AATCAGACA	ATCGAAGAAACT	CTTAAGAGA	CTTG	:	540
		*	560	*	580	*	600		
TrPEPCe	:	TGTTTAATATGAAGAA	ATCTCCTCAGG	AGTTNTT	-	AACCNNACC		:	600
m		*	620	*	640	*	660		
TrPEPCe	:	ATTTGGTTCTTACTG	CTCATCCCACTC	AGTCCGTT	CGANGNCCNCTG	CTTCCCNNN	IGCCT	:	660
					•				
		*	680	*					
m		CONTA COCCONTA COCCONTA			600				

TrPEPCe	:	* MATNKMEKMASIDAQLRO	20 QLVPAKVSEDDK	* LIEYDALI	40 LLDRFLDILQDLI	* IGEDLKDSV	60 QEV	:	60
<b>IrPEPC</b> e	:	* YELSAEYERKHDPKKLE	80 ELGNLITSLDAG	* SDSIVVAK	100 SFSHMLNLANLA	* EEVQIAHRI	120 RRNK	:	120
TrPEPCe	:	* LKKGDFRDESNATTESD	140 IEETLKRLVFNN	* MKKSPQEV	160 XDALKNXTVDLV	* LTAHPTQS	180 VRXX	:	180
mDEDG0		* ************************************	. 196						

# 199/241

		* 20		40	*	60		
TrCSa	:	GNNNCNCNACCATTACATT	AATNACACTTTC	CNCTTTCGCC	TTGTTCTTTC	TCTTCTCAA	:	60
		* 80		400				
TrCSa	:	* 80		100 GGATCCGAAA	* TCATTCATTC	120 TACGCGTCT!	:	120
		* 140	o· *	160	*	180		
TrCSa	:	TCTCTCTTCTCTGCGTTTC	AAACCCTAGTTG	TTTTGTTGAT	TGATCTAAAT	GGCGTTCTT	:	180
TrCSa		* 200 TCGAAGCGTTTCTGCGCTT		220	*	240		240
IICSa	•	TCGAAGCGTTTCTGCGCTT.	ICAAAACTACGA	reregietee	GTCAACAACC	TAGTCTTGC	:	240
		* 260	n *	280	*	300		
TrCSa	:	TAATTCAGTTAGATGGCTC					:	300
		* 320	-	340	*	360		
TrCSa	:	GAAGGAGCTAGTTCCAGAG	TATCAGGAACGT	GTTAAGAAGT	TGAAGAAAGA	CCATGGAAG	:	360
			_					
TrCSa	:	* 386 TGTTGAATTGGGAAAAATC		400 GTACTTGGTG	* SDADTAAD	420 הארכבריים בי		420
							-	
		* 44	0 *	460	*	480		
TrCSa	:	TTTAGTGTGGCTAGGCTCAG	GCTGTTGACCCA	AGATGAGGGAA	TTCGCTTTAG	GGGCATGAC	:	480
TrCSa		* 500 AATTCCTGACTGCCAGAAA	_	520	*	540		~ 4 0
iicsa	•	AATTCCTGACTGCCAGAAA	ACACTICCAGG1	IGCITITECTG	GIGGGGAGCC	.111GCCCGA	•	540
		* 56	0 *	580	*	600		
TrCSa	:	GGCTATACTGTGGCTTCTA			AAGAGCAAGI		:	600
maa		* 62		640	*	660		
Tresa	:	AGCTCACGAATTGCGAAGT	CGTGCAAAATC	CCAGAGTATG	C'I"I'ACAAGGC	CAATTGATGC	:	660
		* 68	0 *	700		720		
TrCSa	:	ACTGCCTGTTTCTGCTCAT			GTGTAATGGO		:	720
		* 74	-	760	*	780		
TrCSa	:	GGAGAGTGAGTTTACAAAG	GCATACGAGAG1	rgggatacata	AGTCAAGGT	ATTGGGAGCC	:	780
TrCSa	:	* 80 AACTTATGAGGATAGCTTG		820 CCTTTGCCTG	* GAATTGCTGG	840 CCTATATTTA	:	840
		5 5 <b></b> -					-	
		* 86	0 *	880	*	900		
TrCSa	:	TCGACGGATATACAAGGAT	GGAAAAATCATA				•	900

# FIGURE 99

		* 920 * 940 * 960		
CrCSa	:	AAACTATGCTCACATGTTAGGATTTGATGATCCAGAAACGCTGGAGTTTATGAGGCTGTA	:	960
[rCSa	:	* 980 * 1000 * 1020 TATTTCTATCCATAGTGATCATGAAGGNGGCAACGTTAGTTCTCACACAGCTCACCTAGT	:	1020
[rCSa	:	* 1040 * 1060 * 1080 TGCTAGTTCACTATCAGATCCTTATCTTGCATTCGCAGCTGCTCTGAATGGTTTAGCTGG	:	1080
IrCSa	:	* 1100 * 1120 * 1140 CCCACTGCATGGTTTAGCCAATCAGGAAGTTCTACGATGGATCAGAAACATAGTTAAGGA	:	1140
IrCSa	:	* 1160 * 1180 * 1200 GTTTGGAACTCCAAACATAAGTACAGAACAATTGAGCGACTACATTCATAAAACATTGAA	:	1200
TrCSa	:	* 1220 * 1240 * 1260 CAGTGGCCAGGTTGTGCCTGGATATGGACATGGAGTTTTGCGCAATACAGACCCAAGATA	:	1260
TrCSa	:	* 1280 * 1300 CACTTGCCAGAGGGAGTTTGCATTGAAGCATTTGCCTAATGATCCAN: 1307		

		* 20 * 40 * 60		
rcsa	:	MAFFRSVSALSKLRSRVGQQPSLANSVRWLQTPSSSNTDLYSEMKELVPEYQERVKKLKK	:	60
rrCSa	:	* 80 * 100 * 120 DHGSVELGKITADMVLGGMRGMTALVWLGSAVDPDEGIRFRGMTIPDCQKTLPGAFPGGE	:	120
frCSa	:	* 140 * 160 * 180 PLPEAILWLLLTGKVPSKEQVDSLAHELRSRAKIPEYAYKAIDALPVSAHPMTQFSTGVM	:	180
ľrCSa	:	* 200 * 220 * 240 ALQVESEFTKAYESGIHKSRYWEPTYEDSLNLIARLPGIAAYIYRRIYKDGKIIPLDDSL	:	240
<b>I</b> rCSa	:	* 260 * 280 * 300 DYGANYAHMLGFDDPETLEFMRLYISIHSDHEGNVSSHTAHLVASSLSDPYLAFAAALNG	:	300
<b>IrCSa</b>	:	* 320 * 340 * 360 LAGPLHGLANQEVLRWIRNIVKEFGTPNISTEQLSDYIHKTLNSGQVVPGYGHGVLRNTD	:	360
TrCSa	:	* PRYTCOREFALKHLPNDP : 378		

	*	20	*	40	*	60
TrCSa1 :	GNNNCNCNACCATTA	CGTTAATTACA	TTTCHNCTTT		TCTCTTCTCAA	: 60
TrCSa2 :		CATTEGTNATIN	ČTTTĪĆĪCTTT	CGCCTTGTTCTT	TCTCTTCT-AA	: 45
TrCSa3 :						: -
TrCSa4 :						: -
TrCSa5 :						
TrCSa6 :						· -
TrCSa7 :						
						•
•						
	*	80	*	100	*	120
TrCSa1 :	TATAAAGACCAATTO	CAATTCCCAATT	CTTTTGGATCC	GAAATCATTCAT	TCTACCCTTCT	: 120
TrCSa2 :	TATAAAGACC-ATT	CAATTCCCAATT	CTTTTGGATCC	GAAATCATTCAT	TCTACGCTTCT	: 104
TrCSa3 :		TACCGNAAZ	CTHINGHTNO	-TACTTTTCA	CONCTNEGNET	: 40
TrCSa4 :		<del></del>			GTNCCCGAAA	: 10
TrCSa5 :	~					: -
TrCSa6 :		<del>-</del>				: -
TrCSa7 :		<del>-</del>				: -
	*	140	*	160	*	180
TrCSa1 :	TCTCTCTTCTCTGC					: 180
TrCSa2 :	TCTCTCTTCTCTGC					: 164
TrCSa3 :	TCTTNCTTCTCTGC					: 100
TrCSa4 :	TNITTCGTTTCTAC	-TTT-INACCCT	-GTTGTTTÑGT	TGATTGATCTA	AATGGCGTTCTT	: 67
TrCSa5 :						: -
TrCSa6 :	~					: .
TrCSa7 :						: .
	4	200		224		244
MwGG n 1	*	200	*	220	*	240
TrCSal :	* TCGAAGCGTTTCTG	CGCTTTCAAAAC		GTGGGTCAACA		: 240
TrCSa2 :	TCGAAGCGTTTCTG	CGCTTTCAAAAC CGCTTTCAAAAC	TACGATCTCGT	TGTGGGTCAACA TGTGGGTCAACA	ACCTAGTCTTGC	: 246
TrCSa2 : TrCSa3 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG	CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC	TACGATCTCGT TACGATCTCGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA	ACCTAGTCTTGC ACCTAGTCT(GC	: 246 : 224 : 166
TrCSa2 : TrCSa3 : TrCSa4 :	TCGAAGCGTTTCTG	CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC	TACGATCTCGT TACGATCTCGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA	ACCTAGTCTTGC ACCTAGTCT(GC	: 246
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG	CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC	TACGATCTCGT TACGATCTCGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA	ACCTAGTCTTGC ACCTAGTCT(GC	: 246 : 224 : 166
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG	CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC	TACGATCTCGT TACGATCTCGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA	ACCTAGTCTTGC ACCTAGTCT(GC	: 246 : 224 : 166
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG	CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC	TACGATCTCGT TACGATCTCGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA	ACCTAGTCTTGC ACCTAGTCT(GC	: 246 : 224 : 166
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG	CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC	TACGATCTCGT TACGATCTCGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA	ACCTAGTCTTGC ACCTAGTCT(GC	: 246 : 224 : 166
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG	CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC	TACGATCTCGT TACGATCTCGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA	ACCTAGTCTTGC ACCTAGTCT(GC	: 246 : 224 : 166 : 12'
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG	CGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAAC	TACGATCTCGT TACGATCTCGT TACGATCTCGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC	: 246 : 224 : 166 : 12' :
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 : TrCSa1 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT	CGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTCCAAACTCGGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TAGGGTCAACA	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC  * TTATTCTGAGAT	: 246 : 224 : 166 : 12' : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 : TrCSa1 : TrCSa2 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT	CGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGGCTCCAAACTCGGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TAGGGGTCAACA TAGGGTCAACA 280 TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC  * TTATTCTGAGAT	: 240 : 224 : 166 : 12* : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa6 : TrCSa7 : TrCSa1 : TrCSa2 : TrCSa3 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT	CGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGGCTCCAAACTCGGCTCCAAACTCGGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT	TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TAGGGGTCAACA, TAGGGGTCAACA, TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC  * TTATTCTGAGAT TTATTCTGAGAT	: 240 : 224 : 160 : 12' : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa2 : TrCSa3 : TrCSa4 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT	CGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGGCTCCAAACTCGGCTCCAAACTCGGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT	TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TAGGGGTCAACA, TAGGGGTCAACA, TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC  * TTATTCTGAGAT TTATTCTGAGAT	: 240 : 224 : 166 : 12* : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa2 : TrCSa3 : TrCSa4 : TrCSa4 : TrCSa5 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT	CGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGGCTCCAAACTCGGCTCCAAACTCGGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT	TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TAGGGGTCAACA, TAGGGGTCAACA, TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC  * TTATTCTGAGAT TTATTCTGAGAT	: 240 : 224 : 160 : 12' : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa2 : TrCSa3 : TrCSa4 : TrCSa4 : TrCSa6 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT	CGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGGCTCCAAACTCGGCTCCAAACTCGGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT	TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TAGGGGTCAACA, TAGGGGTCAACA, TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC  * TTATTCTGAGAT TTATTCTGAGAT	: 240 : 224 : 160 : 12' : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa2 : TrCSa3 : TrCSa4 : TrCSa4 : TrCSa5 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT	CGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGGCTCCAAACTCGGCTCCAAACTCGGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT	TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TAGGGGTCAACA, TAGGGGTCAACA, TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC  * TTATTCTGAGAT TTATTCTGAGAT	: 240 : 224 : 160 : 12' : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa2 : TrCSa3 : TrCSa4 : TrCSa4 : TrCSa6 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT	CGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGGCTCCAAACTCGGCTCCAAACTCGGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT	TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TGTGGGTCAACA, TAGGGGTCAACA, TAGGGGTCAACA, TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC  * TTATTCTGAGAT TTATTCTGAGAT	: 240 : 224 : 160 : 12' : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa2 : TrCSa3 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa6 : TrCSa7 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT	CGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGCTTTCAAAACCGGCTCCAAACTCGGCTCCAAACTCGGCTCCAAACTCGGCTCCAAACTCGGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC  * TTATTCTGAGAT TTATTCTGAGAT TTATTCTGAGAT TTATTCTGAGAT	: 240 : 224 : 160 : 12' : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa6 : TrCSa7 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT	CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC CGCTTTCAAAAC CGCTCCAAACTC GGCTCCAAACTC GGCTCCAAACTC GGCTCCAAACTC CGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC  * TTATTCTGAGAT TTATTCTGAGAT TTATTCTGAGAT TTATTCTGAGAT ACTTCTGAGAT ACTTCTGAGAT ACTTCTGAGAT ACTTCTGAGAT ACTTCTGAGAT ACTTCTGAGAT	: 240 : 224 : 160 : 12' : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa3 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa6 : TrCSa7 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT	260  260  GGCTTTCAAAAC  GGCTTTCAAAAC  GGCTTTCAAAAC  GGCTCCAAACTC	TACGATCTCGT TACGATCTCGT  TACGATCTCGT  TACGATCTCGT  CAAGCTCCAGT CAAGCTCCAGT CAAGCTCCAGT CAAGCTCCAGT CAAGCTCCAGT	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTTGAGAT TTATTCTGAGAT TTATTCTGAGAT TTATTCTGAGAT ACTTCTGAGAT AGACCATGGAAG AGACCATGGAAG	: 240 : 224 : 160 : 12' : 300 : 284 : 220 : 18 : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa3 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa6 : TrCSa7 :  TrCSa7 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT GAAGGAGCTAGTTC GAAGGAGCTAGTTC GAAGGAGCTAGTTC	260  260  GCTTTCAAAAC  GCTTTCAAAAC  GCTTTCAAAAC  GCTTTCAAAAC  GCTCCAAACTC  GGCTCCAAACTC  GGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT CAAGCTCCAGT AACGTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACACGTGTTAACGAACG	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGAGAT TTATTCTGAGAT TTATTCTGAGAT TTATTCTGAGAT AGACCATGGAAG AGACCATGGAAG AGACCATGGAAG	: 240 : 224 : 160 : 12' : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa6 : TrCSa7 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  *  TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT GAAGGAGCTAGTTC GAAGGAGCTAGTTC GAAGGAGCTAGTTC	260  260  GCTTTCAAAAC  GCTTTCAAAAC  GCTTTCAAAAC  GCTTTCAAAAC  GCTCCAAACTC  GGCTCCAAACTC  GGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT CAAGCTCCAGT AACGTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACACGTGTTAACGAACG	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGAGAT TTATTCTGAGAT TTATTCTGAGAT TTATTCTGAGAT AGACCATGGAAG AGACCATGGAAG AGACCATGGAAG	: 240 : 224 : 160 : 12' : 300 : 284 : 220 : 18 : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa3 : TrCSa4 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa3 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa6 : TrCSa7 :  TrCSa7 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT GAAGGAGCTAGTTC GAAGGAGCTAGTTC GAAGGAGCTAGTTC	260  260  GCTTTCAAAAC  GCTTTCAAAAC  GCTTTCAAAAC  GCTTTCAAAAC  GCTCCAAACTC  GGCTCCAAACTC  GGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT CAAGCTCCAGT AACGTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACACGTGTTAACGAACG	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGAGAT TTATTCTGAGAT TTATTCTGAGAT TTATTCTGAGAT AGACCATGGAAG AGACCATGGAAG AGACCATGGAAG	: 240 : 224 : 160 : 12' : : : : : : : : : : : : : : : : : : :
TrCSa2 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa1 : TrCSa2 : TrCSa3 : TrCSa4 : TrCSa5 : TrCSa6 : TrCSa7 :  TrCSa6 : TrCSa7 :	TCGAAGCGTTTCTG TCGAAGCGTTTCTG TCGAAGCGTTTCTG  * TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT TAATTCAGTTAGAT GAAGGAGCTAGTTC GAAGGAGCTAGTTC GAAGGAGCTAGTTC	260  260  GCTTTCAAAAC  GCTTTCAAAAC  GCTTTCAAAAC  GCTTTCAAAAC  GCTCCAAACTC  GGCTCCAAACTC  GGCTCCAAACTC	TACGATCTCGT TACGATCTCGT TACGATCTCGT  * CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT CCAAGCTCCAGT CAAGCTCCAGT AACGTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACCGTGTTAACGAACACGTGTTAACGAACG	TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGTGGGTCAACA TGACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT TAACACTGATCT	ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGC ACCTAGTCTTGAGAT TTATTCTGAGAT TTATTCTGAGAT TTATTCTGAGAT AGACCATGGAAG AGACCATGGAAG AGACCATGGAAG	: 240 : 224 : 160 : 12' : : : : : : : : : : : : : : : : : : :

	*	380	*	400	*	420	
TrCSa1 :	TGTTGAATTG				GAATGAGAGGAA		: 420
TrCSa2 :					GAATGAGAGGAA		404
TrCSa3 :					GAATGAGAGGAA		340
TrCSa4 :					GAATGAGAGGA		: 307
TrCSa5 :					GAATGAGAGGAA		: 51
TrCSa6 :					GNAGAGGA		: 16
TrCSa7 :							
iicsar .						•	•
	*	440	*	460	*	480	
TrCSal :	TTTAGTGTGG	CTAGGCTCAG	CTGTTGACCC	AGATGAGGGAA	TTCGCTTTAGGC	GGCATGAC	: 480
TrCSa2:					TTCGCTTTAGG		: 464
TrCSa3 :	TTTAGTGTGG	CTAGGCTCAG	CTGTTGACCC	AGATGAGGGA	TTCGCTTTAGG	GCATGAC	: 400
TrCSa4 :					TTCGCTTTAGG		: 367
TrCSa5 :	TTTAGTGTGG	CTAGGCTCAC	CTGTTGACCC	AGATGAGGGA	TTCGCTTTAGG	GGCATGAC	: 111
TrCSa6 :	TTTAGTGTGG	CT-GGCT-NC	CTGTTGACCC	AGATGAGGGAA	TTCGCTTTAGG	GGCATGAC	: 74
TrCSa7 :							: -
		500	, +	520	*	540	
TrCSa1 :	AATTCCTCAC				GTGGGGAGCCT'		: 540
TrCSa1:					GTGGGGAGCCT'		: 524
TrCSa2 :					GTGGGGAGCCT'		: 460
TrCSa4 :	AATICCIGAC	TGCCAGAAA TGCCAGAAA	ACACT TECAGG ACACTTĞCAGG	TGCTTTTÄCT(	egggggagnc't'	TTGNCCNA	: 427
TrCSa4 :	AAI ICCIGAC	TECCAÇAAA	CACTIGCAGG		GTGGGGAGCCT	TTGCCCGA	: 171
TrCSa6 :	AATICCIGAC	TECCCACATA	CACTICCAGG	TCCTETTCCT(	GTGGGGAGCCT GTGGGGAGCCT	TTGCCCGA	: 133
	AATTCCTGAC	LGCCAGEAA	ACACIICCAGG	16011110010	3G1GGGGAGCC1	TIGCCCGA	. 133
TrCSa7 :							•
	*	56		580	*	600	
TrCSal :					AAGAGCAAGTA		: 600
TrCSa2 :					AAAGAGCAAGTA		: 584
TrCSa3 :					AAAGAGCAAGTA	GATTCATT	: 520
TrCSa4 :			TTGACCGGNN-				: 456
TrCSa5 :					AAAGAGCAAGTA		: 231
TrCSa6 :	GGCTATACTO	GTGGCTTCTA	ITGACCGGAAA	GGTACCAAGT.	AAAGAGCAAGTA	GATTCATT	: 193
TrCSa7 :							: -
	4	* 62	n *	640	*	660	
TrCSa1 :					GCTTACAAGGCA		: 660
TrCSa2	AGCN						: 588
TrCSa3		ATTGCGAAGT	CGTGCAAAAAT	CCCAGAGTAT	GCTTACAAGGCA	ATTGATGC	: 580
TrCSa4							: -
TrCSa5	AGCTCACGA	ATTGCGAAGT	CGTGCAAAAAT	CCCAGAGTAT	GCTTACAAGGCA	ATTGATGC	: 291
TrCSa6	AGCTCACGA	ATTGCGAAGT	CGTGCAAAAAT	CCCAGAGTAT	GCTTACAAGGCA	ATTGATGC	: 253
TrCSa7							: -
				. <del>-</del>		<b></b>	
m	a amagamam	* 68		700	*	720	: 692
TrCSa1		TTCTGCTCAT	CCAATGACACA	W41V			. 092
TrCSa2					COMONA A TOPOS	CTCCACCT	: 640
TrCSa3	7 CMCCCCCC	mmamaamaam					
m		TTCTGCTCAT	CCAATGACACA	ATTIAGIACI	GGIGIAAIGGCC	CICCAGGI	. 040
TrCSa4							: -
TrCSa5	ACTGCCTGT	TTCTGCTCAT	CCAATGACACA	ATTTAGTACT	GGTGTAATGGCC	CCTCCAGGT	: - : 351
	ACTGCCTGT	TTCTGCTCAT	CCAATGACACA	ATTTAGTACT		CCTCCAGGT	: -

		*	740	*	760	*	780
TrCSa1 :				·			: -
TrCSa2 :							: -
TrCSa3 :	GGAGAGT	GAGTTTAC	AAAGGCATATGAC	AGTGGGAT	'ACATN		: 681
TrCSa4 :							<u></u> : , -
TrCSa5 :			AAAGGCATACGAC				
TrCSa6 :	GGAGAGT	GAGTTTAC	AAAGGCATACGAC				
TrCSa7 :			CNTCAC	BAGTGGGA-	NCNT-AGT-AA	GG-ATTGGG	AGCC : 34
						_	
maa1		*	800	*	820	*	840
TrCSal:							: -
TrCSa2 :							
TrCSa3 :							
TrCSa4 :	2 2 6 7 7 7	CA CCA MAC	CTTGAATTTAAT			CECCOTATA	471 : 471
TrCSa5 :			CTTGAATTTAAT CTTGAATTTAAT				
TrCSa6 :			CTTGAATTTAAT. CTTGAATTTAAT:				
TrCSa7 :	-ACTIAT	GAGGAT-G	CIIGAALITAAL	IGCICGII.	IGCCIGGAAIIC	CIGCLAIP	32
		*	860	*	880	*	900
TrCSa1 :							<b> : -</b>
TrCSa2 :							: -
TrCSa3 :							: -
TrCSa4 :							: -
TrCSa5 :	TCGACGG	ATATACAA	GGATGGAAAAT	CATACCAT	TGGATGATTCTT	TGGATTATO	GTGC : 531
TrCSa6 :			GGATGGAAAAT				
TrCSa7 :			GGATGGAAAAAT				
		والمنتبذ والمنابذ والمنابذ والمنابذ					
		*	920	*	940	*	960
TrCSa1 :							: -
TrCSa2 :							' : -
TrCSa3 :							: -
TrCSa4 :							<del></del> :
TrCSa5 :			GTTAGGATTTGA				
TrCSa6 :			GTTAGGATTTGA				
TrCSa7 :	AAACTAT	GCTCACAT	GTTAGGATTTGA	TGATCCAG	AAACGCTGGAG'	I'T'TATGAGG	CTGTA: 212
							•
		*	980	*	1000	*	1020
TrCSal :							
TrCSa2							
TrCSa3							: -
TrCSa4							: -
	TATTTCT	'ATN					: 601
TrCSa6	TATTTCT	PATCCATAC	TGATCATGAAGG	N			
TrCSa7	TATTTCT	PATCCATAG	TGATCATGAAGG	TGGCAACG	TTAGTTCTCAC	ACAGCTCAC	CTAGT : 272
					_		
		*	1040	*	1060	*	1080
TrCSal							: -
TrCSa2							: -
Trcsa3	:						: -
TrCSa5	•						•
TrCSa6	•		CAGATCCTTATCT				•
TrCSa7	IIGCIIAG'	r rcac'ra'i'(	AGATCCTTATCT	IGCATTC	CAGCIGCICIG	AAIGGIIIA	GCTGG : 332

			*	7100	ж	1120	*	1140	
TrCSa1	:							:	-
TrCSa2	:							:	-
TrCSa3	:								
TrCSa4	:							•	-
TrCSa5	:							:	-
TrCSa6	:							•	-
TrCSa7	:	CCCACTO	CATGGT	TTAGCCAATCA	GGAAGTTCTA	ACGATGGATCA	GAAACATAG	TTAAGGA:	392
			*	1160	*	1180	*	1200	
TrCSa1	:							:	_
TrCSa2	:							:	_
TrCSa3	:							:	_
TrCSa4	:								
TrCSa5	:							:	_
TrCSa6	:							:	_
TrCSa7	:	GTTTGG/	ACTCCA	AACATAAGTAC	AGAACAATT	GAGCGACTACA'	TTCATAAAA	CATTGAA :	452
22004.	•	0							
			*	1220	*	1240	*	1260	
TrCSa1									_
TrCSa2								:	_
TrCSa3	:							:	
TrCSa4	:								
TrCSa5	:								
TrCSa6	:								
TrCSa7	:	CACTCC	CAGGTT	GTGCCTGGATA	тссасатес	A GTTTTTGCGCA	ATACAGACC	CAAGATA	512
iicba,	•	CHOIGG		010001007117	110011011100	101111000011	111110110110	·	
			*	1280	*	1300			
Trees1								-	
TICOGI	•								
TrCSa2				·					
TrCSa3	•						•	-	
	:							-	
TrCSa5	:							•	
TrCSa6	:						<b>.</b>	-	
TrCSa7	:		CCAGAGG	GAGTTTGCATT	KG/AVA(G/G/AVIIIIIIII	GCCTAATGATC	CAN : 559	,	

## 206/241

			*	20	*	40	*	60		
TrCSb	:	CNTTTCNTT	TCCACAGO	CATCCTAATCCT	AATCCTAAT	CCTAATCCTAI	TACTAATTA	CTA	:	60
			*	80	*	100	*	120		100
TrCSb	:	ATTACTAAT	TTACTAGT?	ACTAATTAGTAA	TACCGATCO	CCTTTTTCTCGE	ACCCATTCA	TTC	:	120
			*	140	*	160	*	180		100
TrCSb	:	AAGNAGAA	GAAGGAAA <i>l</i>	DADDTAAAAADAA	ACAAACAA	ACATCTTACAA(	CAATGTCAAC	GAC	:	180
			*	200	*	220	*	240		240
TrCSb	:	AACTACTAC	CAACCGAC	GAATCCAAGCTG	CACGACGC.	IGCACGGAACCC	FITTGGCCAC	CCI	•	240
<b></b>		aman a ama	*	260 CCTTCCTCCACA	*	280	* \	300	:	300
Tresb	:	CTCAGCTC	ACTIGCTI	CCTTCCTCCACA	MCCICCGC	CGCGCTCCTCC	AICCIAIICA	3CC1	•	500
mCCb			*	320 ATCTCCCCACCG	* !ጥረጥል ልጥረጥ!	340	⋆ ͲϹΔϹϹϾͲͲϾ·	360 TTGA		360
TrCSb	•	TICTICTE	CC1CCGGG.	AICICCCCACCC	orcimio.	Cramicol Micro			•	
ሞፖሮዊክ		<b>TGNNCGTN</b>	* CCGGGAAG	380 AAGTATACCATI	* ''GAGGTCTC'	400 TCCTGATGGCA	* CCGTTAAAG	420 CCAA	:	420
11030	•	IGMCOIN	ccocomo							
TrCSb	:	TGATTTCA	* AGAAGATA	440 TCAACTGGGAAG	* BAATGATAA	460 GGGACTCAAAC	* TTTATGATC	480 CTGG	:	480
11002										
TrCSb	:	ATATTTAA	* ACACTGCT	500 CCTGTGCGATC	* \ACAATTTC	520 TTATATTGATG	* GTGATGAGG	540 GAAT	:	540
TrCSb	:	CCTTAGAT	* 'ATAGAGGA	560 TACCCCATTGA	* GAGTTGGC	580 CGAGAAAAGCA	* .CCTTTCCGG	600 AAGT	:	600
TrCSb	:	GGCATATO	* TCATATTG	620 TATGGAAATTT	* GCCTTCTGC	640 AAATCAGTTAC	* AAGAATGGG	660 AATT	:	660
TrCSb	:	TGCTATAT	* CTCAGCAT	680 TCAGCCTTACC	* TCAAGGAGT	·700 TTTGGATCTCA	* .TACAATCAA	720 TGCC	:	720
TrCSb	:	TCAAGATO	* ECACATCCI	740 TATGGGCGTCCT.	* AGTGAATGC	760 CAATAAGCGCTC	* TGTCTGTTT	780 TTCA		780
						000		040		
TrCSb	:	TCCTGACG	* CAAATCC1	800 TGCTCTCAGAGG	TCTTGACAT	820 CTACAACTCAA	AGCAAGTGA	840 GAGA		840
				860	*	880	*	900		
		~~~~~~~	~	860 73 mm3 mmCC3 3 3	። መስመአአመአአሪ		። ደረጎን አጥጥን አጥር	_		900

FIGURE 102

			*	920	*	940	*	960		
TrCSb	:	AATGGCAG	BAAGGCCA	.CCTGTGCTTCCA	TCCAACA	AACTATCTTAC	ACAGAGAAC'	TTCCT	:	960
			*	980	*	1000	*	1020		
TrCSb	:	ATACATGC	TTGATTCT	'CTAGGCAATCGG'	TCATATA	AACCCAACCCTC	CAGCTAACT	CGTGC	:	1020
			*	1040	*	1060	*	1080		
TrCSb	:	ACTAGACA?	CATCTTC	CATCCTGCATGCA	GAACATG.	AAATGAATTGC:	rctacatet	GCTGT	:	1080
			*	1100	*	1120	*	1140		
TrCSb	:	ACGACACC'	TTGCATC	AGCGGCGTCGAT	GTATACA	CTGCTATTGCT	GGAGGTGTT	GGAGC	:	1140
			*	1160	*	1180	*	1200		
TrCSb	:	TCTGTATG	GACCTCT	CATGGTGGAGCT	AATGAGG	CGGTCCTTAAA	ATGCTGAGT	GAAAT	:	1200
			*	1220	*	1240				
TrCSb	:	TGGAAGTG	TCGATAA	CATTCCAGAGTTC	ATTGAAG	GTGTTAANN:	1244			

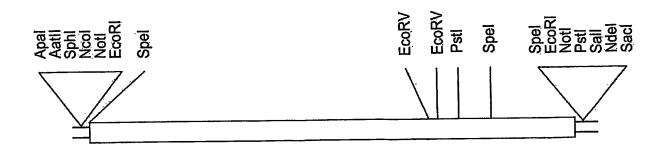
			*	20	*	40	*	60		
rrCSb	:	MSTTTTTT	esklhdaa	RNRLATLSAHLI	LPSSTTSA	ALLHPIHLSSSS	GISPPSNVI	(GTL	:	60
			*	80	*	100	*	120		
rrCSb	:	TVVDERTGE	CKYTIEVSF	DGTVKANDFKK	ISTGKNDKO	GLKLYDPGYLNT	APVRSTIS:	(IDG	:	120
			*	140	*	160	*	180		
rcsb	:	DEGILRYRO	YPIEELAE	KSTFPEVAYLI	LYGNLPSAI	NQLQEWEFAISQ:	HSALPQGVI	PDFI	:	180
			*	200	*	220	*	240		
TrCSb	:	QSMPQDAH	PMGVLVNA	SALSVFHPDAN	PALRGLDI	YNSKQVRDKQIA	RIIGKITT:	AAAI	:	240
		•	*	260	*	280	*	300		
TrCSb	:	TNLRMAGRI	 PPVLPSNKI		SLGNRSYK	PNPQLTRALDII	FILHAEHE		:	300
	-					-				
				200		240	*			
			*	320	*	340			2 E	_
TrCSb	:	TSAVRHLAS	SSGVDVYT	AIAGGVGALYGP	LHGGANEA	VLKMLSEIGSVD	NTERFE	vx :	35	8

		*	20	*	40	*	60
TrCSb1 :	CMTTTCMT	TTCCACACC			CCTAATCCTAT		
TrCSb1 :	CIVITICIVI	LICCACAGO	AICCIAMICCI		CCIANICCIAL	INCHAIL LAC	
TrCSb2 :							
TrCSb4:							
TrCSb4:							
TrCSb6:							
TrCSb7:							
		*	80	*	100	* 12	20
TrCSb1 :	ATTACTAA	ТТАСТАСТА		TACCGATCO	CTTTTTCTCGA		
TrCSb2 :							
TrCSb3 :							
TrCSb4:							: -
TrCSb5 :							: -
TrCSb6:							: -
TrCSb7:							: -
IICOD, .							
		*	140	*	160		30
TrCSb1 :	AATT C 學AA	GAAGGAAAA	ACAAAAT-CAC	ACAAACAAA	ACATCTTACAAC	AATGTCAACG	AC : 179
TrCSb2 :	GNAGNA	GAAGGAAA	MC-AAATCCAC	AAAC-AAA	AC <mark>-</mark> TCTTACAAC ACATCTTACAAC	AATGTCAACÕ	AC : 55
TrCSb3 :	GNNGNA	.GAAGGAAA	ACAAAATNCAC	AAACAAAA	ACATCTTACAAC	AATGTCAACC	AC : 58
TrCSb4 :	@NAA	AGAGGAAA	AC-AAATNC	AČAĀĀČ-AZ	ACATCTTAC-AC	AATGTC-ACG	AC : 50
TrCSb5 :		NAAGGAAA			AC-TCTTAC-AC		
TrCSb6		(d):					 ; -
TrCSb7							: -
110007							-
		*	200	*	220		40
TrCSb1 :	AACTACTA	CAACCGAC	GAATCCAAGCTC	CACGACGC'	TGCACGGAACCG	TTTGGCTACC	CT : 239
TrCSb2					TGCACGGAACCG		
TrCSb3 :	AACTACTA	CAACCGAC	GAATCCAAGCTC	CACGACGC	TGCACGGAACCG	TTTGGCCACC	CT : 118
TrCSb4	AACTACTA	CAACCGAC	GAATCCAAGCTC	CACGACGC'	TGCACGGAACCG	TTTAGCCACC	CT : 110
TrCSb5	AACTACTA	CAACCGAC	GAATCCAAGCTC	CACGACGC	TGCACGGAACCG	TTTGGCTACC	CT : 105
TrCSb6							: -
TrCSb7	:						: -
		*	260	*	280		00
TrCSb1	CTCAGCTC	CACTTGCTT	CCTTCCTCCACA	AAACTCCGC	IIGCGCTIICTCCA	ATCCTATCCAC	CT: 299
TrCSb2					ĞGCGCTĞCTCC <i>i</i>		
TrCSb3					CGCGCTCCTCC		
TrCSb4	CTCAGCTC	CACTTGCTT	CCTTCCTCCAC	AACCTCCGC	CGCGCTCCTCC	ATCCTATTCAC	CT : 170
TrCSb5	: CTCAGCTC	CACTTGCTT	CCTTCCTCCAC	AAACTCCGC	TGCGCTTCTCC	ATCCTATCCAC	CT : 165
TrCSb6	:						: -
TrCSb7	:						: -
		*	320	*	340		60
TrCSb1	: TTCTTCT	rcctcziggg	ATCTCCCCACC	STCTAATGT	CAAAGGAACAC'	CACCGTTGTT	GA : 359
TrCSb2					CAAAGGAACAC'		
TrCSb3	: TTCCCCCT	FCCTCCGGG	ATCTCCCCACC	GTCTAATGT	'CAAAGGAACAC'	CACCGTTGTT	GA: 238
TrCSb4	: TTCTTCT	FCCTCCGGG	ATCTCCCCACC	GTCTAATGT	'CAAAGGAACAC'	CACCGTTGTI	GA : 230
TrCSb5	: TTCTTCTT	rcctciiggg	ATCTCCCCACC	GTCTAATGT	'CAAAGGAACAC'	FCACCGTTGTT	GA : 225
TrCSb6	:						: -
TrCSb7	:						: -

		*	•	380	· *	400	*	420	
TrCSb1	: 1	GAACGTACC	GGGAAGA	AAGTATACCAT	TGAGGTCT	CTCCTGATGGC	ACCGTTAAA	GCCAA:	419
TrCSb2	. 1	GAACGTACC	GGGAAG	TACEATATE	TGAGGTCT	CACCTGATGGC	ACCGTTAAA	GCCAA :	295
TrCSb3		CAACCTACC	GGGAAG	Ταθάατατρα	TGAGGTCT	CACCTGATGGC	ACCGTTAAA	GCCAA:	298
TrCSb4						CTCCTGATGGC			290
TrCSb4						CTCCTGATGGC			285
TrCSb6		GAACGIACC	CCCALAG	AMGIAIACCAI	IGMGCICI				
TrCSb7	• -					- 			
TICSDI	: -							•	•
			•	440	•	460	*	480	
mach1			1 A A C A T A C		~ 	AGGGGCTCAAA	CTTTATCAT		: 479
TrCSb1		IGAIIICAAG	ALAGATA	TCAACIGGGAA		AGGGÄCTCAAA		CCTCC .	: 355
TrCSb2						AGGGACTCAAA AGGGACTCAAA			: 358
TrCSb3		rgarirreaac	SAAGATA	TCAACTGGGAA	AGAATGATA	AGGGACTCAAA AGGGACTCAAA		CCIGG	: 350
TrCSb4	: }	rga i i rcaac	JAAGATA	TCGACTGGGAA	AGAATGATA	AGGGACICAAA AGGGACICAAA	CITIAIGAI	CCIGG	: 350
TrCSb5	:	rgattricaac	JAAGATA	TCAACTGGGAA	AGAATGATA	agggĞctcaa <i>f</i>	CTTTATGAT	CCIGG	: 345
TrCSb6	: -						Par		: -
TrCSb7	: •								: 1
			. .	500		520	*	540	
TrCSb1		א מא מיים מיים א			ገለ እ ር ለ እ ጥጥጥ	CTTATATTGAT			: 539
TrCSb1		ALALLIAAA		CCTGTGCGAT	כאאכאאדדד מאאראאדדד	CTTATATTGAT	CGTCATGAC	GGAAT	: 415
	•	AIAIIIAAA		CCIGIGCGAI	CHACHALLI	CTTATATTGAT	CCTCATCAC	CCAAT	: 418
TrCSb3	: 1	ATATTTAAA		CCTGTGCGAT		CITATATIGAT	CCTCATCAC	CCAAT	: 410
TrCSb4	: !	A.I.Y.I.,I.,I.YAY(CACTGCT	CCTGTGCGAT	CAACAATTT	CTTATATTGAT		CCAAT	
TrCSb5	: !	ATATTTAAA	CACTGCT	CCTGTGCGAT	CAACAA1"1"I	CTTATATTGA	GGTGATGAC	LAADDE	: 405
TrCSb6	:								: -
TrCSb7	:								: -
			•	F.C.O.	•	ERO	*	600	
mClob 1	. 1		*	560	* ************************************	580	* ~*	600	. 599
TrCSb1	: }	CCTTAGATA	* TAGAGGA	TACCCCATTG	AAGAGTTGC	CCGAGAAAAG	CACCTTTCCC	GAAGT	: 599 · 475
TrCSb2	:	CCTTAGATA	TAGAGGA	TACCCCATTG.	AAGAGTTGC AGGAGTTGC	CCGAGAAAAG CCGAGAAAAG	CACCTTTCCC CACCTTTCCC	GAAGT GAAGT	: 475
TrCSb2 TrCSb3	:	CCTTAGATA' CCTTAGATA'	TAGAGGA TAGAGGA	TACCCCATTG TACCCCATTG TACCCCATTG	AAGAGTTGC AGGAGTTGC AGGAGTTGC	CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG	CACCTTTCC(CACCTTTCC(CACCTTTCC(GAAGT GAAGT GAAGT	: 475 : 478
TrCSb2 TrCSb3 TrCSb4	:	CCTTAGATA' CCTTAGATA' CCTTAGATA'	TAGAGGA TAGAGGA TAGAGGA	TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG	AAGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC	CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC	GAAGT GAAGT GAAGT GAAGT	: 475 : 478 : 470
TrCSb2 TrCSb3 TrCSb4 TrCSb5	:	CCTTAGATA' CCTTAGATA' CCTTAGATA'	TAGAGGA TAGAGGA TAGAGGA TAGAGGA	TACCCCATTG. TACCCCATTG. TACCCCATTG. TACCCCATTG. TACCCCATTG.	AÄGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC AÄGAGTTGC	CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC	GAAGT GAAGT GAAGT GAAGT GAAGT	: 475 : 478 : 470 : 465
TrCSb2 TrCSb3 TrCSb4 TrCSb5 TrCSb6	:	CCTTAGATA' CCTTAGATA' CCTTAGATA'	TAGAGGA TAGAGGA TAGAGGA TAGAGGA	TACCCCATTG. TACCCCATTG. TACCCCATTG. TACCCCATTG. TACCCCATTG.	AÄGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC AÄGAGTTGC	CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC	GAAGT GAAGT GAAGT GAAGT GAAGT	: 475 : 478 : 470
TrCSb2 TrCSb3 TrCSb4 TrCSb5	:	CCTTAGATA' CCTTAGATA' CCTTAGATA'	TAGAGGA TAGAGGA TAGAGGA TAGAGGA	TACCCCATTG. TACCCCATTG. TACCCCATTG. TACCCCATTG. TACCCCATTG.	AÄGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC AÄGAGTTGC	CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC	GAAGT GAAGT GAAGT GAAGT GAAGT	: 475 : 478 : 470 : 465
TrCSb2 TrCSb3 TrCSb4 TrCSb5 TrCSb6	:	CCTTAGATA' CCTTAGATA' CCTTAGATA'	TAGAGGA TAGAGGA TAGAGGA TAGAGGA	TACCCCATTG. TACCCCATTG. TACCCCATTG. TACCCCATTG. TACCCCATTG.	AÄGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC AÄGAGTTGC	CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC	GAAGT GAAGT GAAGT GAAGT GAAGT	: 475 : 478 : 470 : 465
TrCSb2 TrCSb3 TrCSb4 TrCSb5 TrCSb6	:	CCTTAGATA' CCTTAGATA' CCTTAGATA'	TAGAGGA TAGAGGA TAGAGGA TAGAGGA	TACCCATTG TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG	AÄGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC AÄGAGTTGC	CCGAGAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC	GAAGT GAAGT GAAGT GAAGT GAAGT	: 475 : 478 : 470 : 465
TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7	: :	CCTTAGATA CCTTAGATA CCTTAGATA CCTTAGATA	TAGAGGA TAGAGGA TAGAGGA TAGAGGA TAGAGG	TACCCCATTG. TACCCCATTG. TACCCCATTG. TACCCCATTG. TACCCCATTG.	AAGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC AAGGAGTTGC AAGGAGTTGC	CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC	egaagt egaagt egaagt egaagt egaagt egaagt	: 475 : 478 : 470 : 465 : 49 : -
TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7	: :	CCTTAGATA CCTTAGATA CCTTAGATA CCTTAGATAA	TAGAGGA TAGAGGA TAGAGGA TAGAGGG TAGAGGG	TACCCATTG TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG	AAGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC AAGGAGTTGC	CCGAGAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CGAGAAAAG	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC	egaagt egaagt egaagt egaagt egaagt egaagt	: 475 : 478 : 470 : 465 : 49 : -
TrCsb2 TrCsb4 TrCsb5 TrCsb6 TrCsb7 TrCsb1 TrCsb2	:::::::::::::::::::::::::::::::::::::::	CCTTAGATA CCTTAGATA CCTTAGATA CCTTAGATA A GCTTAGATA A GGCATATCT GGCATATCT	TAGAGGA TAGAGGA TAGAGGA TAGAGGG TAGAGGG * CATATTO	TACCCATTG TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG	AAGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC *	CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CGAGAAAAG	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTAT * ACAAGAATG	egaagt egaagt egaagt egaagt egaagt egaagt 660	: 475 : 478 : 470 : 465 : 49 : -
TrCsb2 TrCsb4 TrCsb5 TrCsb6 TrCsb7 TrCsb1 TrCsb2 TrCsb3		CCTTAGATA CCTTAGATA CCTTAGATA CCTTAGATA A A A A A A A A A A A A A A A A	TAGAGGA TAGAGGA TAGAGGGA TAGAGGG * * CATATTC	TACCCATTG TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG 620 ETATGGAAATT ETATGGAAATT	AAGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC AGGAGTTGC * TGCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	CCGAGAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CGAGAAAAG 640	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTATC * ACAAGAATGC ACAAGAATGC	GGAAGT GGAAGT GGAAGT GGAAGT GGAAGT GGAAGT GGAAGT	: 475 : 478 : 470 : 465 : 49 : -
TrCsb2 TrCsb4 TrCsb5 TrCsb6 TrCsb7 TrCsb1 TrCsb2 TrCsb3 TrCsb4		CCTTAGATA CCTTAGATA CCTTAGATA CCTTAGATA A GGCATATCT GGCATATCT GGCATATCT GGCATATCT	TAGAGGA TAGAGGA TAGAGGGA TAGAGGG * CATATTC CATATTC	TACCCATTG TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG TACCCCATTG 620 GTATGGAAATT GTATGGAAATT GTATGGAAATT	AAGAGTTGC AGGAGTTGG AGGAGTTGG AAGGAGTTGG AAGGAGTTGG * TGCCTTCTC TGCCTTCTC	CCGAGAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CGAGAAAAG 640 GCAAATCAGTT GCAAATCAGTT	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTATC * ACAAGAATGC ACAAGAATGC ACAAGAATGC	egaagt egaagt egaagt egaagt egaagt 660 egaatt egaatt egaatt egaatt	: 475 : 478 : 470 : 465 : 49 : -
TrCsb2 TrCsb4 TrCsb5 TrCsb6 TrCsb7 TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb4		CCTTAGATA CCTTAGATA CCTTAGATA CCTTAGATA A GGCATATCT GGCATATCT GGCATATCT GGCATATCT GGCATATCT	TAGAGGA TAGAGGA TAGAGGG TAGAGGG * CATATTC CATATTC	TACCCCATTG TATTGGAAATT TATTGGAAATT	AAGAGTTGC AGGAGTTGG AGGAGTTGG AAGGAGTTGG AAGGAGTTGG * TGCCTTCTC TGCCTTCTC TGCCTTCTC	CCGAGAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CGAGAAAAG GCAAATCAGTT GCAAATCAGTT GCAAATCAGTT	CACCTTTCCC CACCTTTCCC CACCTTTCCC CACCTTTATC * ACAAGAATG ACAAGAATG ACAAGAATG ACAAGAATG	egaagt egaagt egaagt egaagt egaagt egaagt 660 egaatt egaatt egaatt	: 475 : 478 : 470 : 465 : 49 : -
TrCsb2 TrCsb4 TrCsb5 TrCsb6 TrCsb7 TrCsb1 TrCsb2 TrCsb3 TrCsb3 TrCsb4 TrCsb5 TrCsb5		CCTTAGATA CCTTAGATA CCTTAGATA CCTTAGATA A GGCATATCT GGCATATCT GGCATATCT GGCATATCT GGCATATCT	TAGAGGA TAGAGGA TAGAGGG TAGAGGG * CATATTC CATATTC	TACCCCATTG TATTGGAAATT TATTGGAAATT	AAGAGTTGC AGGAGTTGG AGGAGTTGG AAGGAGTTGG AAGGAGTTGG * TGCCTTCTC TGCCTTCTC TGCCTTCTC	CCGAGAAAG CCGAGAAAAG CCGAGAAAAG CCGAGAAAAG CGAGAAAAG 640 GCAAATCAGTT GCAAATCAGTT	CACCTTTCCC CACCTTTCCCC CACCTTTCCCC CACCTTTTATC * ACAAGAATGC ACAAGAATGCACAAGAATGCACAAGAATGCAAGAATGCAAGAATGCAAGAATGCAAGAATGCACAAGAATGCACAAGAATGCACAAGAATGCAACAAGAATGCAAAGAATGCAAGAAATGCAAAAATGCAAAGAAAATGCAAGAAATGCAAAAAAAA	egaagt egaagt egaagt egaagt egaagt egaagt 660 egaatt egaatt egaatt egaatt egaatt	: 475 : 478 : 470 : 465 : 49 : - : 609 : 535 : 538 : 530 : 525 : 108
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TrCSb2	:							:	_
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TrCSb4									_
TrCSb5	:	TCAAGNN							592
TrCSb6	•			ATGGGÄGTCCTA					228
	:	TCAMGATGCA		ATOCOMOTO A	GIGAAIGC	RATAAGCGCICI		TICA:	
TrCSb7	:	TCAAGATGC	ACA TCCT	atgggcgt@cti;	GTRAATGC	T@TAAGAGCTAT	31016111	IICA :	130
		•	t.	800	*	820	*	840	
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TrCSb2	:								-
TrCSb3	:							· :	-
TrCSb4	:							:	
TrCSb5	•							:	_
TrCSb6	:	TCCTGACGC	TOOTAAE	GCTCTJAGAGGT	СТТСАПАТ	TTACGACTCAAA	GGAAGTGA	GAGA	288
TrCSb7	:	TCCTCAFICC	AAT CCT	GCTCTCAGAGGT	CTTCACAT	CTACAACTCAAA	GCAAGTGA	GAGA	190
TTC2D1	•	TCCTGWAGC	MARICCI	GCICICAGAGGI	CIIGNOVI	CIACAACICAAA	OCEMIO I GE		170
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			*	860	*	880	*	900	
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TrCSb6	:	CAAACAAAT	AGCACGO	SATTATTGGAAAG	ATTATAAC	AATTGCTGCTGC	AGTTTATO	CTTAC :	348
TrCSb7		CAAACAAAT	AGITCICGO	ATTATTGGAAAG	ΑΤΆΓΑΡΑ	'A ATTGCTGCTGC	TATTATT	TTTAG:	: 250
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TrCSb6	:	AATGGCAGG	AAGGCC	ACCTGTGCTTCCA	ATCCAACCA	ACTATCTTACAC	TGAGAAC'	TTCCT :	: 408
TrCSb7	:	ATTGGGAGG	AAGGCC	ACCTGTËCTTCC <i>F</i>	ATCCAACÃA	ACTÏTCTTACAC	'AGAGAAC'	TTCCT	: 310
			*	980	*	1000	*	1020	
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TrCSb3	•								
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TrCSb5		20202				7 0007 7 00000	COMPACE	coree	: 468
TrCSb6	:	ATACATGCT	IGATTC	TTAGGCAATCG	5TCATATA	AACCCAACCCTC	AGCTAACT	CGIGC	400
TrCSb7	:	TTACATGCT	TGATTC'	rctiiggcaatcg(JTCATATA	AACCTAATCCTC	TCTAACT	CGTGC	: 370
			*	1040	*	1060	*	1080	
TrCSb1	:								: -
TrCSb2	:								: -
TrCSb3	:								-
TrCSb4									: -
TrCSb5	:								: -
Treshe	•	ACTAGACAT	TATCTT	CATCCTGCATGC	AGAACATG	AAATGAATTGCT	CTACATCT	GCTGT	: 528
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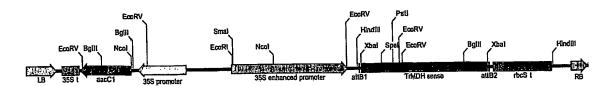
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TrCSb5	:								-
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TrCSb7	:	ACGCCA	CCTTGCA	TCAAGÏGGÏGT	CGATGTATA	CACTGCTATTG	CTGGAGGTGT	TGGAGC:	490
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			*	1160	*	1180	*	1200	
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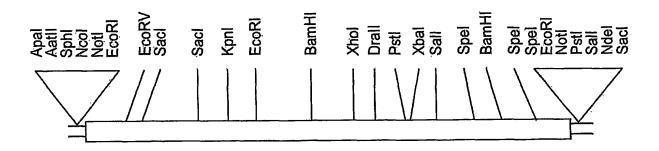
TrMDH

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101	TTCTCCTTCC	AATTCCCATT	ACCATTCATT	CCCAGAGGTC	GAGATGGCAG
151	CATCAGCAGC	AGCTACTTTT	ACTATTGGAA	CTGCCCAAAC	AGGGAGGCCA
201	CTTCCTCAAT	CAAACCCTTT	TGGTTTGAAA	GTCAATTCCC	AGGTTAATTT
251	TAAGACCTTC	TCTGGTCTCA	AGGCCATGTC	ATCTCTAAGA	TGCGAGTCTG
301	AATCATCTTT	CTTTGGCAAC	GAAACTAGTG	CTGCTCTGCG	TGCAACTTTT
351	GCACCCAAAG	CTCAAAAGGA	AAACCAAAAC	ATCAACCGCA	ATTTGCATCC
401	TCAGGCATCC	TACAAAGTGG	CGGTTCTTGG	TGCTGCAGGA	GGAATTGGTC
451	AGCCACTGGC	ACTTCTCATT	AAGATGTCGC	CTTTGGTTTC	CGACCTGCAT
501	CTTTATGATA	TCGCGAATGT	TAAGGGAGTT	GCTGCTGATA	TCAGTCATTG
551	CAACACTCCT	TCAAAGGTTT	TGGATTTCAC	AGGTGCTTCT	GAGTTGGCAA
601	ATTGTTTGAA	AGGTGTGGAT	GTAGTTGTTA	TACCTGCTGG	TGTTCCCAGA
651	AAACCTGGCA	TGACTCGTGA	TGACCTTTTC	AACATCAATG	CCGGTATAGT
701	CAGGGACTTG	GTCACCGCTG	TTGCAGATAA	TTGCCCTGGT	GCTTTTATTC
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801	CTGAAACAAA	AGGGTGTTTA	TGATCCTAAA	AAGCTCTTTG	GTGTTACTAC
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951	ATTCTTCCTC	TTCTGTCAAA	GACAAGACCC	TCAGCAAATT	TCACTGATGA
1001	AGAAATTGAG	GCGCTAACTG	TCAGGATTCA	AAATGCTGGA	ACTGAAGTTG
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1401	CTCTAGCGTC	CATGCGAGAG	AATGTCAATG	GGTGATTTCT	TGGGTTATGG
1451	ATTTATTTGA	GCATGAATAC	TACTTAGAGG	ACTTAGATTG	CAGATTTATG
1501	TAGCATCATT	TACTGCTTCC	AGAACTTATG	TTTAAATTT	TCCATAGTAT
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1	MAASAAATFT	IGTAQTGRPL	PQSNPFGLKV	NSQVNFKTFS	GLKAMSSLRC
51	ESESSFFGNE	TSAALRATFA	PKAQKENQNI	NRNLHPQASY	KVAVLGAAGG
101	IGQPLALLIK	MSPLVSDLHL	YDIANVKGVA	ADISHCNTPS	KVLDFTGASE
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pPZP221:TrMDH sense



TrPEPC

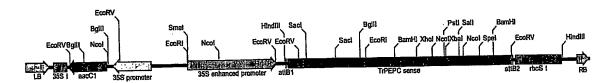
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101 TCGTATCTTA CTGCCTCATT ACAGGGGGA GAAGAGGAG ATTGCTCAA 151 TGGCAACAAA CAAAATGGAA AAAATGGAT CATTGATGC ACAGCTTAGA 201 CAATTAGTAC CAGCAAAAGT TAGTGAAGAT CATTGATGC ACAGCTTAGA 251 TGCTTTGTTG TTGGATCGGT TTCTTGATAT CCTTCAGGAT TTACATGAGG 251 GAAGACAAGC ATGATCCTAA GAAACTTGAA GAGCTTCT TGCGGAGTAT 351 GAAGAAAGC ATGATCCTAA GAAACTTGAA GAGCTCGGAA ATTTGATAC 401 AAGTTTAGATT GGCGACATTA CAAAATGGT TTGCAGAGGAA ATTTGATAC 401 AAGTTTAGATT GGCCACTTA CAAAATGGT TTACATGAGG 501 AGGAACAAGT TGAAGAAAAG CTCTTAAGAG ACTTGTGTTT TAATACAC 401 AAGTTCACCA GAAAGAAA CTCTTAAGAGA CTTGTGTTT TAATAGAAC 601 AATCTCCTCA GGAAGTTTTT GAAGAAAAG TCTTTAAGAG ACTTGTGTTT AATATGAAGA 601 AATCTCCTCA GGAAGATTTT GAAGAAGAG CTTTAACAGA CTTTTAAGAG CTTGATGTTC 701 GCAGGAAGAG GTAAGGAAC CTCTTAAGAGA CTTGTATTT 601 GCATGATGA TAAGCAAGAG CTCTTAAGAGA CTTGTATTT 702 CTCTGATGA TAAGCAAGAG CTCTAAGAGA CTCTTCAAGAGA CTTGATATTG 703 CTCCTGATGA TAAGCAAGAG CTCTAAGAGA CTCTCAAAAA 803 GCTGCATTCC GTACCGATGA AATCAAGAGG CTCCCAGAG GAGATTCAA 804 GCTGCATTCC GTACCGATGA AATCAAGAGG CTCCCAGAG GAGATTCAA 805 TGAGCATGAG CTCCCAAGAG CTCCCAAGAG AACACTCA 806 TGCCCATTCC GTACCGATGA AATCAAGAGG CTCCCAAGA AAGACAACA 807 TCCCCTAAAT TCTTCGCCGTT GTTGATACTG CTCCAGAGA AACACACC 808 TGAGAGGATA TCTCCCAGAGA TCCCCAGAGAAACAAT TGGAAGATC 901 TCCCTAAATT TCTTCGCCGT GTTGATACTG GTTGAAGAA CATTAGAGAG 1001 GAGGAGCTA TCCCCCATAA TCCCCCCAGAGAAACAAT TCCAGGAGT 1001 GAGGAGATC TATCTTTTGA ACTCCCAGGAA TTCCAGGAGA TTCCAGGAGA 1001 ATGAAGAAC TCTTTTTGA ACTCCCAGGAA TTCCAGGAGA TTCCAGGAGA 1001 ATGAAGAAC TCTTTTTGA ACTCCCAGGAA TTCCAGGAAA TTCCATGAGA 1001 GAGGAGCTA TCGGTGATGGT ATCCCAGGAGA TTCCAAGAGAA 1001 ATGAAGAAC TCTTTTGTAC ACTGCCAGAAAAAAAA TCCCTTCAA TTCATGCTAC 1001 CAAAACACTA CATAGAGTT TGGAAGAAAAAAA TTCCTTTGAA TAACCGAGA 1001 ATGAAGAAC TCTTTTGTGCT AAGGCACAAG TTCCACAGAAAAAAAAAA						
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251 TGCTTTGTTG TTGGATGGT TTCTTGATAT CCTTCAGAT TTACATGGAG 301 AGGATCTGAA AGATCTGTT CAGAAAGTGT ATGACATTTC TGCGAGATAT 515 GAAACAAGC ATGATCCTAA GAAACTTGAT GAGCACTTC TGCGGAGATAT 516 AGGATCAGAC ATGATCCTAA GAAACTTGAT GAGCACGTACT 401 AGGTTAGATT GCCAGAGAGAT CAATTGTTGT TGCTAAGTCC TTTTCGCACA 401 AGGTTAGATT GCCAGAGAGAA CATTGATGTT TCAGATTGC TCAGCTCTGA 401 AGGTACAGCT TGAAGAAGAG CATTTTAGGAGAG TTCAGATTGC TCAGCTCGA 501 AGGAACAAGT TGAAGAAGAG ACTTTAAGAG 501 AGTCTCCTCA GGAAGATAT CTCTAAGAGAG TTCAGATTGC TCATCTTCC TCAGCTGTA 651 GTTCTTACTG CTCATCCTAC TCAGCTGTA AGAACCAGAC CTGTTGATTTG 651 GTTCTTACTG CTCATCCTAC TCAGCTGTA AGAACCAGAC CTGTTCAAAA 701 GCAGGAAGAG TTATATCTCA ATTGTATACTG 651 GTCCTGATGA TAAGCAGAGG CTCGACGAGA CTCTCCAGAG 801 GCTGCATTCC GTACCGATG ATCATCCTAC 751 CCCCTGATGA TAAGCAGAGG CTCGACGAAG CCCTCCAAGA 801 GCTGCATTCC GTACCGATG ATCATCCTC 901 TCCCTAAATT TCTTCGCCGT GTTGATACTG CGAAACAATT TGGAAGGGTG 901 TCCCTAAATT TCTTCGCCGT GTTGATACTG CGAAACAATT TGGAAGGGTG 1001 ATGATTGCT ACTAGCTAG ATCATCCTCT 1001 GGGGGGTGAT CGTGAAGGAA ATCCCAGAGAT TACCACAGAG 1001 ATGAACACTA ACTAGCAGAA ATCCCAGAGAT TACCAGGAAT 1001 GGGGGGTGAT CGTGAATGGTA ATCCCAGAGAT TACCAGGAAT 1001 GGGGGGTGAT CTTAGCTGA ATGATGCTT CAAACACACTA CACCACAGA 1101 ATTGAAGAGTC TTATGTTGA ACTGCTCATT TGGAACACACTA CATGAGGATT 1201 CAAACACACTA CATGAGAGTT TGGAAAAAAA TTCCATGAGA ATGATGAGTT 1211 GCGTGATTCC CTTTGGTGATG TTCACCAGGAA TTCCATGAGA ATGATGAGTT 1221 CAAACACACTA CTCTTAGCTC ATGCTATT TGGAACACACTA CTCTTAGCTC ATGCTATT CTCTTAGGAT TCTTTGAGAC CTCTTTGAACT CTCTTAGACT ATGCTACT CAACACACAC CTCTTGAACT CTCTTAGACT CACACGGAC TGAATTCGT CAAACACACTA CTCTTAGCTC CAACACACAC TGAAATTCCT CAACACACAC TGAAATTCCT CAACACACAC TGAAATTCCT CAACACACAC TGAACACACT CACACAGAC TTCACAGAGA AACACACAGAA 1601 ATGGCTTTTG TCTGAGTGT TCTTGAGATT TCCATGAGT CAACACACAC CAACACACACA CACCAC						
301 AGARTCTGA AGARTCTGAT CAGAAGTGT TAGAGAGTAT						
351 GAAGAAAGC ATGATCCTAA GAACTTGAA GACCTGGAA ATTTGATAAC 401 AAGTTTAACTT GGCCAACTTA CATTGTTGT TGCTAAGCTC TTTTTCGCACA 451 TGCTTAACTT GGCCAACTTA GCTGAAGAGG TTCAGATTGC TCATCGTCGA 511 AGGATCAACT TGAAGAAAGG AGATTTTAGG GATGAGACACTAC 512 GAATCAGAC ATGCAAGAAA CTCTTAAGAGA ACTTTGAGATAC 513 CAAACCACTAC GGAAGATTTT GATGGCACACTAC 514 CATCGACAGAA CTCTAAGAGA ACTTTGAGAGA 615 ATCTCCTCA GGAAGTTTTT GATGGCTTCA AGACCAGAC CGTTGATTTG 616 GTTCTTACCTG GTAAGGAACT GTTTAACGA ACACCAGAC CGTTGATTTG 617 CTCCGATGA ATGCAAGAAG CTCGACGAGA CTCCACGAGA 618 GCTGCATTCC GTACCGAGA CTCGACGAGA CTCCACGAGA 619 GCTGCATTCC GTACCGAGA ATTCAAGAGG ACCCCTCCAA ACCCACACAGA 610 GCTGCATTCC GTACCGAGAG ATTCATCAGAGG 611 TCCCTAAATT TCTCCCCGT GTTGATACTCA ATGCACAATT TGGAGGGGTG 611 TCCCTAAATT TCTCCCCGT GTTGATACTCA CACCACACACACACACACACAGAG 612 TCCCTAAATT TCTCCCCGT GTTGATACTC 613 AGGAACGTG TTCCCCTATAA TCCTCCTCT ATTCAGTTTT CTTCATGGAT 614 TTGAAGACCT ACTAGAGAGA TTCACAGAGA 615 ATGTTGCTT ACTAGCTAGA ATGATGGCTG CAAACTACTA GTAACGAGGT 616 ATGTAGACACT CATTGAGATA ATCCCAGACAT TTCACAGATT 617 ATTGAAGACC TACTGAGATA ATCCCAGACAT TTCCCATGAGT 6101 ATTGAAGACACT ACTTGATGATA TTCACAGGAA TTCCCAGAGAAC 6101 ATTGAAACACTA CATTGAGAGTT TTCACAGGAA TTCCCAGAACAT TTCCAAGAGAAC 6101 ATTGAAACACTA CATTGAGAGTT TTCACAGGAAC TTCCCAGACAC 61101 ATTGAAGACACTA CATTGAGAGTT TTCACAGGAAC TTCCCAGACAC 612 CTCTCTTGTG TTCTTTAGCTC TAGGCAACACT CACAGGAAC 61301 GCTCCCTATA CTCTTAGGTC ATGCTATT TGGAAGTACT CTCTAGACT 61301 GTCCCCTATA CTCTTAGACT ATGCTGACAC 61301 CTCTCTTGTG TCTCTAGACT ATGCTGACAC 61301 CTCTCTTGTG TCTTGAGTC ATGCTGATT TGGAACTACCT CAGAGACAC 61301 CTCTCTCTGG CTTCTTGGTG TCTTGAGAC TTCTTGAACT ATGCTACACA 61301 CTCCCCCATTT TCTGAGATC TCTTAGACT TCTAGACT ATGCTACACA 61301 TAAGGCAGAG GTCAGATTCT CCAAGATTG TCTAGAACT ATGCTACACA 61301 TAAGGCAGAG GTCAGATCT TCTTGGACG TTCTTGAACT ATGCTACACA 61301 TAAGGCAGAG GTCAGATTC TCAGAATTG TCTCAGATTC TCAGAATTG TCTAGAACACACACACACACACACACACACACACACACAC						
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651 ARTCTCCTCA GGAGGTTTTT GATGGTTGA AGAACCAGAC CGTTGATTTG 651 GTCTTACTG CTCATCCTAC TCAGTCGGTT GTTAGTCGAAA 701 GCATGGAAGG GTAAGGAACT GTTTATCTCA ATTGTATGCT AGACATCA 751 CTCCTGATGA TAAGCAAGAG CTCGACGAAG CTCTCCAGAG GAGATTCAA 801 GCTGCATTCC GTACCGATGA ATCAAGAGG CTCTCCAGAG GAGACTACA 801 TCCCTAAATT TCTTCGCGT GTTGATACTC CGAAACAATT TGGAAGGGTT 901 TCCCTAAATT TCTTCGCCGT GTTGATACTC CGTTGAAGAA 751 AGAGACGTG TTCCCTATAA TGCTCCTCTT ATTCAGTTTT CTTCATGGAT 1001 GGGGGTGAT CGTGATGAA ATCAAGAGG GACCCTCCTAA 1001 GGGGGTGAT CGTGATGGTA ATCCGAGGAT GAACAATTT TCTTCATGGAT 1001 ATGTTTGCTT ACTAGCTAGA ATGATGGCT CAAATTTGTA TTTATTCCTG 1101 ATTGAAGATC TTAGTTTGA ATGCTGTTAT TGGGGTTGCA ATGATGACGT 1201 CAAAACACTA CATAGAGAAC TTCACAGGAA TTCCCAGAAA GATGAGACT 1211 CAGTGTATAC CTCATAGATT TGGAGATACA CTCTTGAAC 1251 CGTGTTATAC TTGGTGTATT TGGAGAAAAAA TTCCCAGGAA 1351 CATTCACCAA TTGATGAG TTCTTGAAC CTCTTGAAC 1351 CATTCACCAA TTGATGAG TTCTTGAAC CTCTTGAAC 1451 TTCTTGAGG 1451 TTCTTGAGG CAAGTTCCA TCGTGACGCG 1451 TTACTTCAGG CAAGTTCCA CTCTTGAAC TATGCTACAGA 1551 CATTTGAGAA TTCGAGATCAT CCACAGGAC CTCTTTCGTA 1451 TTCTTGAGG CAAGTTCCA CTCTTGAACT ATGCTACAGA 1551 CATTTGAGAAA TTCGAGTCCT CCACAGAAC CTCTTTGAAC AGCCTTCTTGA 1451 TACCCCCGTT CTTGAGTCA CCACAGACG CTCTATGCAC AGCCTCTTCTGA 1551 CATTTGAGAAA TTCGAGTCCT CCACAGAAC CTCTTTGACC AGCCTCTTCTGA 1551 CATTTGAGAAA TTCGAGTCCT CCACAGAAC GCCCTTCTTGAAC 1551 TACCCCCGTCT CAAGATCCT CCACAGAAC CTCTTTGACC AGCCCAGAAC 1551 TACCCCCGTCT CAACAGACA CTTTTGGAC CTCTTGAACT ATGCCACAAA 1551 TACCCCCGTCT CAACAGACA CTTTTGGAC CTCTTGAACT ACCCAAAA 1551 TACCTCAAC CTCTGAGTTG TCTGAGACT TCTCAAGAAAC 1551 TACCCCAGTAA CTCTGAGACA CTTTTGAAC CTCTTGAACT 1751 TGCCCCGTT CAACAGACA CTTTTGAAC CTCTTGAACT 1751 TACCCCCGTCT CAACAGACA CTTTTGAAC CTCTTTTACACGT GAACATCTC 1751 TACAGAACTC CAACAGAAC CTCTTCAACG GACACATT TCAGGACAC 1751 TACAGAACTC CAACAGAAC CTCTTCAACG GACACATT TCTCAACAC 1751 TACAGAACTC CAACACACA CAACAACAAC GACACATT TCTCAACCAC 1751 TACAGACCCC CAACACAACA CTTTCCCCCC TTCAGACCAC ACCACACAAC ACCACACACAAC ACCACACACAAC ACCACC						
551 GTTCTACTG CTCATCCTAC TCAGTCGGTT CGTAGGTCGT TGCTTCAAAA 701 GCATGGAAGG GTAAGGAACT GTTTATCTCA ATTGTATGCT AAAGACATCA 751 CTCCTGATGA TAAGCAAGAG CTCGACGAAG CTCTCCAAGA GAGAGATTCAA 861 GCTGCATTCC GTACCGATGA AATCAAGAGG ACACCTCCAA CACCACAAGA 851 TGAGATGAGA GCAGGGATGA GTTACTACCT CGAAGAACATT TGGAAGGGTT 861 TCCCTAAAATT TCTCTCGCCGT GTTGATACTG CGATGAAGAA CACCACCAAGA 851 TGAGGACGTG TCCCTATAA TGCTCCTCTT ATTCAGTTTT CTTCATGGAG 951 AACGAACGTG TCCCTATAA TGCTCCTCTT ATTCAGTTTT CTTCATGGAG 1001 GGGGGGTGAT CGTGATGGTAA ATCCAGAGGT GACTCCTGAA GTAACGAGAG 1051 ATGTTTGCTT ACTAGCTAGA ATGATGGCTG CAAATTTGTA TTATCCCAG 1101 ATTGAAGATC TATAGTTTTGA ACTGTCTATT TGGCCTTGAA TTATATCCCAG 1101 CAAAACACTA CATAGAGTTT TGGAAAAAAA TTCCTTAGACT 1201 CAAAACACTA CATAGAGTTT TGGAAAAAAA TTCCTTTGAAC 1301 GTCTCGCTAT CTCTTAGCTC ATGGCAGTAC CTCTATCGTA CTCGTGAGCG 1301 GTCTCGCTAT CTCTTAGCTC ATGGCTATTC TGAAAATTCCT GAGGAAGCCA 1351 CATTCACCAA TGTTGATGAG TTCTTGGAAC CTCTATGAAC TAGGCACGA 1401 TCACTCTGTG CTTGTGAGTG TCGTGCGGTT TGGAACACCAA 1451 TTTCTTGAGG CAAGATTCCA CTTTTGGAAC CTCTTTGAACT ATGCTCACAGA 1451 TTTCTTGAGG CAAGATTCCA CTTTTGGAAC CTCTTTGAACT ATGCTCACAGA 1451 TTCTTTGAGG CAAGATTCCA CTTTTGGAAC CTCTTTGAACT ATGCTACAGA 1551 CATTTGCAACA TTCAGATCGT CACACGAACG TGATGGATGC CATTTACCAAA 1551 TAAGGCAGAG GTCAGATCGT CACACGAACG TGATGCAGAA 1601 ATGCTTTTG TCTGAGTTG TCTGAGACAC TAGAGATAG CCAACATCAAA 1601 ATGCCTCAAAC CGAACACACA CACACACACA GCCGCACTTTT GACACCACAA 1601 ATGCCTCAAC CGATGAAATT TAGAGACATT TCATGTCAACA 1751 TGCCCCGTCT GATGGAGAT TTTTGGAACT TTTTGAACACACACA 1751 TGCCCCGTCT GATGGAAAT TAGAACATT TCATGTCATA 1801 TCAAGAACC GATGGAACT TTTTGGAACT TTTTCGATAC TCAACACACA 1801 TCAAGAATC CTTAAGAGTT TCTGCACGTT TTTTCGATAC TCAACACACA 1801 TCAAGAATC CTTAAGAGTT TCTGCCGCTT TTTTCGATAC TCAACACACA 1801 TCAAGAATC CTTAAGAGTT TCTGCCCCT TTTTTCGATAC TCTCTAACAT TCAACACACA 1801 TCAAGAATC CTTAAGAGTT TCTGCCCCT TTTTCGATAC TCTCAACACACAAAA 1801 TCAAGAACTC CACACACAAAATAC GGTTCTAACAC GAATGCCTA ATGCTTCAACACACAAAACACAAAAACACAAAAAAAAAA						
701 GCATGGAAGG GTAAGGAACT GTTTATCTCA ATTGTATGCT AAAGACATCA 751 CTCCTGATAA TAAGCAAGAG CTCGACGAAG CTCTCCAGAG GGAGATTCAA 851 TGAGATGAAG GTACCGATGA AATCAAGAGG ACACTCCAA CACCACAGAG 851 TGAGATGAAG GCAGGGATGA ATCAAGAGG ACACTCCAA CACCACAGAGA 851 TGAGATGAAG GCAGGGATGA GTTACTCAC CGAAACAATT TGGAAGGTG 901 TCCCTAAAATT TCTTCGCCGT GTTGATACTG CGTTGAAGAA CATAGGGATT 1001 GGGGGGTGAT CGTGATGATAA TGCTCCTCTT ATCAGTTTT CTTCATGGAT 1001 GGGGGGTGAT CGTGATGGTA ATCCGAGAGG GACTCCTGAA GTAACGGAGG 1051 ATGTTAGCTT ACTAGCTAGA ATGATGCTG CAAATTTGTA TTATTCCCAG 1101 ATTGAAGATC TTATCTTTGA ACTGTCTATG TGGCGTTTGCA ATGATGAGCT 1151 GCGTGATCG GCAGAAGAAC TTCACAGGAA TTCCAAGAAAA GATGAAGTTT 1151 GCGTGATCC GCAGAGAGAAC TTCACAGGAA TTCCTAGAAAAA GATGAAGTTG 1201 CAAAACACTA CATAGAGTTT TGGAAAAAAA TTCCTTTGAA GAACCGTAC 1251 CGTGTTATAC TTGGTGATG AAGGGACAAG CTCTATAGGT CAAGAGAACACTAC 1251 CATTCACCAA TGTTGATGATG AAGGGACAAG CTCTATAGAAC CTCTTGAACT 1351 CATTCACCAA TGTTGATGATG AGGGCACAAG CTCTATACGTA CTCGTGAGCG 1451 TTTCTTGAGG CAAGTTTCCA CTTTTGGACT GCAGATTCCT GAAGAAACCCTAC 1451 TTTCTTGAGA TTTGGATC CTTTTGGACT GCCGATGGAA GCCTTCTTGA 1451 TTTCTTGAGA TTTGGATCT CTTTGGACT GCCGATGGAA GCCTTCTTGA 1451 TTTCTTGAGA TTTGGATCCT CTTTTGGACT GCCGATGGAA ACCGTAC 1551 CATTTGGAA TTGGATCCT CTTTGGACT GTCACTGATA AACCGTAC 1551 CATTTGGAAA TTGGATCCT CTTTGGACT TCTGAACTAGATA 1601 ATGGCTTTTT CTGAACTTGC TTTGGACT TCTGAACAAAAAAAAAA						
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901 TCCCTAAATT TCTCCCCTATA TGCTCCTCTT ATCAGTATT CTTCATGATT 1001 GGGGGGTGAT CGTGATGGTA ATCCGAGAGT GAACTCCTGAA GTAACGAGAG GTAACGAGAG ATGTGATGCT TATGTTTGA ACTGTCTATG TGGCGCTTGAA GTAACGAGAGAGAGAGACT TTATGTTTGA ACTGTCTATG TGGCGCTTGCA ATGATGAGCT GCAGAAGACA TTCAAGAGAT TCCACAGAAA GATGAACACTA CATAGAGTT TGGAAAAAAA TCCCTAGAAA GATGAACACTA CATAGAGTT TGGAAAAAAA TCCCTTGAA GATGAACCGTAC CATAGAGATT CACAGAAA TCCCAGAGAGA GATGAACCCTA CATAGAGTT TGGAAAAAAA TCCCTTGAA TGGACCGTAC CATAGAGCTA CATTGACTC ATGGCTATC CAGAAAAAAA TCCCTTGAACACACACACACACACACACACACACACACAC						
951 AACGAACGTG TTCCCTATAA TGCTCCTCTT ATTCAGTTTT CTTCATGGAT 1001 GGGGGGTGAT GGTGATGGTA ATCCGAGAGT GACTCCTGAA GTAACGAGAG GACTCTGAA ATGTTGATTCCAGAGAGT ATGTTGATGTT ACTAGCTAGA ATGATGGTG CAAATTTGTA TTATTCCCAG 1101 ATTGAAGATC TTATGTTTGA ACTAGCTAGA ATGATGGTG CAAATTGTA TTATTCCCAG 1101 ATTGAAGATC CAAGAAGAAC TTCACAGGAA TTCCAAGAAA GATGAAGTTG TAGAACCATA CATAGAGGTT TGGAAAAAAA TTCCTTAGAA GATGAAGTTG TAGAACCATA CATAGAGGTT TGGAAAAAAA TCCTTTGAA GAGAAGCCA TCTTTAGCTC AGGGAACCAA TCTTTAGCTC AGGGAACAA CTCTTAGCTC GAGAAGACCA TCTTTAGACC TTCTTAGCTC ATGGCTATTC TGAAAATTCCT GAGAAACCAGA TCTTTGAACC ATGGCTATTC TGAAAATTCCT GAGAAACCAGA TCTTTGAACC TAGACCAGAA TCTTTGAACC CTTTTGAACC TAGACCAGAA TCTTTGAACC TAGACCAGAC TCTTTGAACC AGGCAAGCAA CTTTTGAACC TAGACCAGAA TCTTGAACCA TGAAATTCCT GAGAAATCCAGA GCCGATGGAA GCCTTCTTGA CAAAGAACAA TTCCAAGAAACA GCCAAAGTTCC CAACAGACA TTTGGAACC TTTTGAACCA TAGACCAGAA GCCAACGGAC TCAAGACAA ACGACAGGA GCCGCTTTTT GAACCAAAAA ACGACAGGA GCCGCTTTTT GAACCAAAAA ACGACAGGA GCCGCTTTTT GAACCAAAAA ACGACAGGA GCCGCTTTTT GAACCAAAAA ACGACAGGA GCCGCTTTTT GAACCAACAA CTTTGGAACC TATGAACAAA TCTTGGAACT TCAAGAAAA ACGACAGGA GCCGCTTTTT GAACCAACAAAA ACGACAGGA GCCGCTTTTT GAACCAACAAAA ACGACAGGA TTTGCAGAAAT TAGAGAAAT TAGAGACAT TCAAGAAAAA ACGACAAGAA CTTTGGAACA TCTTGAACAAA ACGACAGAAAA ACGACAGAAAA ACGACAGAAAA ACGACAGACA						
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1051 ATGTTTGCTT ACTAGCTAGA ATGATGGCTG CAAATTGTA TTATTCCAG 1101 ATTGAAGATC TTATGTTTGA ACTGTCTATG 1251 GCGTGATCGC GCAGAAGAAC TTCACAGGAA TTCCCAAGAAA GATGAAGTTG 1251 CGAGAACACTA CATAGAGTTT TGGAAAAAAA TTCCTTTGAA TGAACCGTAC 1251 GGTGTTATAC TTGGTGATGT AAGGGCACAG CTCTATCGTA 1301 GTCTCGCTAT CTCTTAGCTC ATGGCTATTC TGAAAATACATCT GAGAAGACCA 1301 GTCTCGCTAT CTCTTAGCTC ATGGCTATTC TGAAATTCCT GAGGAAGCCA 1301 GTCTCGCTAT CTCTTAGCTC ATGGCTATTC TGAAATTCCT GAGAAGCCA 1301 TCACTCTGTG CTTGTGGTGA TCGTTGGAAC CTCTTGAACA 1401 TCACTCTGTG CTTGTGGTGA TCGTGCGGTT GCCGATGGAA GCCTTCTTGA 1451 TTTCTTGAGC CAAGTTTCCA CTTTTGGACC GCCGATGGAA GCCTTCTTGA 1451 TAAGGCAGGA GTCAGATCCT CACACGACC TGATGAGAGC CATTACCAAA 1501 TAAGGCAGGA GTCAGATCCT CCAAGGATGG TCCAAGAGAGC 1601 ATGGCTTTTG TCTGAGTCAT CCAAGGATGG TCCAGAGAGC 1601 ATGGCTTTTG TCTGAGTCAT CCAAGGATTG TCTGAAGAAA 1601 ATGGCTTTTG TCTGAGTACA CAAGGACTG TGATGGATGC CATTACCAAA 1601 ATGGCTTTTG TCTGAGTAAA TAGAGAACTTT TAGAGACATT TCATGTCATA 1701 GCAGAACCTC CAATGACAAA CTTTGGAGCC TATATCATT TCATGTCATA 1701 GCAGAACTCC GATGGAACT GTTCCATTGT TTGAAGAACT TCATGTCATA 1801 TCAAGAATC GATGGACAC CTTCCATTAT TCATGCAAAA 1801 TCAAGAATC GTTAAGAGTT TTCCATTAT TCGATGCAAC 1751 TGCCCCGTCT GATGGCGG CTTCCATTAT TTGAGAAACT TCCTGATCT 1851 GAGTCTGCTC CTGCTGCTTT GGCTCGGTTG TTTTCCATGG GAATGCAAAA 1801 TCAAGAACCC GTTAAGAGGT ATGCCACACAAAA TGCTCAGCAC 1751 GTAAAGATCC GTAAAAGGTT TCCACCACA GACACAATT TCCGTGACCAC 1751 CTACTTGTC TCAACCACCA GACACAATTC GGCTGCTATA TAAGGCTCAG 1751 CTACTTGTC TCAACCACCA GACACAATTC ACGGACCTATA TAACGCTCAG 1751 CTACTTGTC TCAAACCGC GAATGGGTC TCTTGAACAC GGAATGCGTC 1751 CCCCCAGTTT TCCAACACCA GACACAATTC ACGGACCTA ACTTCTTGCT 1751 CCCCCAGTTT TCCAACACCA GACACAATTC ACGGACCTA ACTTCTTGCT 1751 CCCCCAGGTTA TAAATGTTTCA CTGCTGCTC TCTAGAACAC GGAATGCTT 1751 CCCCCAGGTAT TCCAACACCA GACACACACA GACACACACA GACGCCTAA TAACACGTTT 1751 CCCCCAGGTTA TCCACCACA GACACACACA GACACACACA GACACACAC						
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1151 GCGTGATCGC GCAGAAGAAC TTCACAGGAA TTCCAAGAAA GATGAAGTTG 1201 CAAAACACTA CATAGAGTTT TGGAAAAAAAA TTCCTTTGAA TGAACCGTAC 1251 CGTGTTATAC TTGGTGATGT AAGGGACAAG CTCTATCGTA CTCGTGAGCG 1301 GTCTCGCTAT CTCTTAGCTC ATGGCTATTC TGAAAATCCT GAGGAAGCCA 1351 CATTCACCAA TGTTGATGAG TTCTTGGAAC CTCTTGAACT 1401 TCACTCTGTG CTTGTGGTGA TCGTGCGGTT GCCGATGAAC ATGCTTACAGA 1401 TACTCTGTGG CAAGTTCCA CTTTTGGACT GTCAACGGA GCCTTCTTGA 1501 TAAGGCAGGA GTCAGATCGT CACACGGACG TGATGGATGC CAAGTTCCA CTTTTGGACT GTCAACGGA GCCTTCTTGA 1501 TAAGGCAGGA GTCAGATCGT CACACGGACG TGATGGATGC CATTACCAAA 1601 ATGCTCTAAAC CGATGAAATT AGAGAAAGA GCCCTTTTT 1601 GCAGAACTC CATCAGACAA CTTTGGACT TAGAGACATT TCATGCATAC 1701 GCACGAACTC CATCAGACAA CTTTGGACT TAGAGACATT TCATGCATAC 1701 GCACGAACTC CATCAGACAA CTTTGGACT TAGAGACATT TCATGCATAC 1701 GCAGAACTC CATCAGACAA CTTTGGACC TATATCATTT CGACTGACT 1701 AAACCGTATC GATGGAGGA GTTCCATTGT TTGGAAACAT TCATGCATACAT 1801 TCAAGAATCC GTTAAGAGTT GTTCCATTGT TTTGGAAACAT TCCTGATCCAC 1851 GAGTCTGCTC GTGTGTTTT GGCCTCATGT TTTTCGATACG GAATGCAAAA 1801 TCAAGAATCC GTTAAGAGTT TCTGCCGCAT GTTTCCATTACACT TTGCAACACA 1951 GAGGACCTCA TAAATGTTGC TCAGAAATAC GGTGTTAACA TTCCGTCAG 1951 GTAAAGATC TGGAAGGTT TCTGCCGCAT GCAGCTATA TAACAATGTT 1901 AAACCGTATC TCAACCACCA GACACAATC GGCAGCTATA TAACAATGTT 1901 CATTCTTGTC CCAACCACCA GACACAATC GGCAGCTATA TAACAATGTT 1901 CAAGAACCC GAGGACTC TTGGAAACAC GGCAGCTATA TAACAATGTT 1901 CAACACGTC CAGCGTTCA CAGCACCAC AAATGCCTC CCAACCAGA CACTCCTTC 1951 GTCAAGGTC CAGCGTTCA CCGCACCAG GACTATA TAACAATGTT 1951 GTCAAGATC TCCAAAACCG GAACACACC GACACACAC GGAATGCCTC 1051 TAGAACGCT CCGCGCA AAAAGAGGC CATTGAAACAC GGAATGCCTC 1051 TAGAACGCT CCGCACCAGA AAAAGAGGC CATTGAAACAC GGAATGCCTC 1051 TCCAGTATGG TCCACCAGA AAAAGAGGC CATTGAAACAC GGAATGCCTC 1051 TCCAGTATGG TCCACAGAA ACCACACAA GCACACACA GACCACACAA GGAATGCCTC 1051 TCCAGTATGG TCCACCAGA AAAAGAGGC CACTGGAGGA CACTTCCTTC 1051 TCCAGTATGG TCCACCAGA AAAAAGAGC CACACACAA GGAATACC ACCCAGAAAA ACCACACACA GGAATACCC AACCACACA GACCACACA AAGAAACACA GGAATACC CCACACACAA GGAATACTC ACCCTTTCAACT ACCCCTTCAACCCTA AAGAACACCA AAA			TTATGTTTGA	ACTGTCTATG	TGGCGTTGCA	ATGATGAGCT
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1501 TAAGGCAGGA GTCAGATCGT CACACGGACG TGATGGATGC CATTACCAAA 1551 CATTTGGAAA TTGGATCCTA CCAAGATTGG TCTGAAGAAA AACGACAGGA 1601 ATGGCTTTTG TCTGAGTTGG TTGGCAAAAG GCCGCTTTTT GGACCTGATC 1651 TACCTCAAAC CGATGAAATT AGAGAAGTTT TAGAGGACATT TCATGTCATA 1701 GCAGAACTTC CATCAGACAA CTTTGGAGCC TATATCATTT CGATGGCACA 1751 TGCCCCGTCT GATGTGCTGG CGGTTGAACT TCTTCAACGT GAATGCAAAA 1801 TCAAGAATCC GTTAAGAGTT GTTCCATTGT TTGAGAAACT TCGTGATCC 1851 GAGTCTGCTC CTGCTGCTTT GGCCCGGTTG TTTTCGATAGA CTGCTGACAA 1901 AAACCGTATC GATGGGAAGC TCTTCAACGT GAATGCAAAA 1901 AAACCGTATC GATGGGAAGC TCTTCAACGT GAATGCAAAA 1901 AAACCGTATC GATGGGAAGC TCTTCAACGT GAATGCAAAA 1901 AAACCGTATC GATGGGAAGC TCTTCAACGT GATTGGATAT TCGATTCAG 1901 AAACCGTATC TGGAAGGTTT TCTGCCGCAT GCCACCCATT TAAAGGCTCAG 2001 GAGGACCTCA TAAATGTTGC TCAACAACAC GACACAATTC ACGGATCTCT TCGTGTACCG 2101 CTATCTTGTC TCAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2101 GTCATTGCTA CAGGTTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2201 TAGAACGCTG CAGGGTTT ACACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2201 GTCATTGCTA CCGAGGAGTA CCGTTCCAC TCTAGAACAC GGAATGCGTC 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGC TCAGAAGCG TCCACACAGA GATGGAGTA CCGTTTCA 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG ACCACAGTA ACCACCGTT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG ACCACAGACAA GATGGAGTAC CATTGGAGC CATTGAACCA GAATGGCTC ACCACAGA AAAAGAAGC CATTGAACAC GGAATGGCT 2401 ACATTGGAG TCGACCGGCA AAAAGAAGC CATTGAACAC GGAATGGCT 251 TGTTGAGGA TCCACAGGAA TTTTGCATGG ACCACAGACAA GGTTTCATCT 2501 TCCAGTTGGG ACCACGAAA TGGACCGTT TAAACCACCA GGTTTCATCT 2601 TTTAGGGTCA CTTTGATTT GAGCACCTT TAAACAAGTT ATTGCGAAGAC CATTGAACAC 2651 TGGTATTGCA CCTTTCATATG CTGCAACACAA ACCACACAAA ACAGTTAAGA ACAGTTAAT AAGGCTAC AGTTTCCAG GAACACACAA AAAGAACTAA AAGAACTAA AAGAACTAA AAGAACTAA AACAACTAA AACACCCTT AACCTTTTCC						
1551 CATTTGGAAA TTGGATCCTA CCAAGATTGG TCTGAAGAAA AACGACAGGA 1601 ATGGCTTTTG TCTGAGTTGG TTGGCAAAAG GCCGCTTTTT GGACCTGATC CGATGAAATT AGAGAAGTT TAGAGACATT TCATGTCATA CGATGAAATT AGAGAAGTT TAGAGACATT CGATGGCAAC CTTTGGAGCC TATATCATT CGATGGCAAC CTTTGGAGCC TATATCATT CGATGGCAAC CTTTGGAGAACT TCTTCAACGT GAATGCAAAA GGCTCGTTT GGCCCGTCT GTTAAGAGTT GTTCCATTGT TTGAGAAACT TCTTCAACGT GAATGCAAAA ACTGGTACTC CTGCTGCTTT GGCTCGGTTG TTTTCGATAG ACTGGTACAT TCTGATCACT TTGAGAAACT TCTGATCACT TTGAGAAACT TCTGATCACT TTGAGAAACT TCTGATCACT TTGAGAAACT TCTGATCACT TTGAGAAACT TCTGATCACT TCTGATCACT TTGAGAAACT TCTGATCACT TCTGATCACT TTGAGAAACT TCTGATCACT TAAACGATCAC GGCAGCTATA TAAGGCTCAG TCAGAAATAC GGTGTTAAGC TAACAATGTT TCTGAAGAACA GGTGTTAAGC ACTCATCTTG TCAACCACCA GACACAATTC ACGGATCTC TCTGTGACGC AAGACAATTC ACGGATCTCT TCGTGTGACG ACACAAATCC GGAGAGGAGC ACTTGTGCTT TCCAAAACCG GAATGGCGTG AATTGATGAC GGAATGCTT TCCAGAAACCG GAATGGCGTG AATTGATGAC GGAATGCTT TCCAAAACCG GAATGGCGTG AATTGATGAC TCCAAAACCG GAATGGCGTG AATTGATGAC GGAAGATGA ACCACGTTT TCCGTCTACT TCCAGAAACAC GAACCAACAAT GTGTTCAAGG AACCACGTTT TCCAGAAGAC AAAAGAAGGC CATGTGGAGTA TCCGACAGACAA GAACACAAATG GAACCACACAACA GAACACAAACA GGAACAAACAA AACAACACAA GGAACAAATG AACAACAACAA AACAACAACAA AACAACAACAA GGAACAAATAG ACACAGAACAA AACAACAACAA GGAACAAACAA AACAACAACAA AACAACAACAA AACAAC						
1601 ATGGCTTTTG TCTGAGTTGG TTGGCAAAAG GCCGCTTTTT GGACCTGATC 1651 TACCTCAAAC CGATGAAATT AGAGAAGTT TCATGTCATA 1701 GCAGAACTTC CATCAGACAA CTTTGGAGCAC 1751 TGCCCCGTCT GATGTCTGG CGGTTGAACT TCTTCAACGT GAATGCAAAA 1801 TCAAGAATCC GTTAAGAGTT GTTCCATTGT TTGAGAAACT TCTTCAACGT GAATGCAAAA 1801 TCAAGAATCC GTTAAGAGTT GTTCCATTGT TTGAGAAACT TGCTGATCTC 1851 GAGTCTGCTC CTGCTGCTTT GGCTCGGTTG TTTTCGATAA ACTGGTACAT 1901 AAACCGTATC GATGGGAAGC AAGAAGTTAT GATTGGATAAC 1951 GTAAAGATGC TGGAAGGTTT TCTGCCGCAT GATTGGATCAT 2051 CCATGGTCGT GGTGGAACTG TCAGAAAAAC GGTGTTAAGC TAACAATGTT 2051 CCATGGTCGT GGTGGAACTG TCAGAAAAAC GGTGTTAAGC TAACAATGTT 2051 CCATGGTCGT CAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2101 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2251 CCCCAAGTTC CCGAGAGATA CCGTTCAACT GTGTTCAACT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAACT GTGTTCAAGG ACCACATT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAACT GTGTTCAAGG ACCACATT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAACT GTGTTCAAGG ACCACGTT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAACT GTGTTCAAGG ACCACGTT 2301 GTCATTGCAA TCCCGTCG CCACCACAA GATGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGA AAAAGAAGGC CATGTGAGG CATTGAACA 2401 ACATTGGAA TCCATGGAT TTTTGCATGG ACCACACAAA GGAAGAACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTT TAAACAACA 2451 CTGCGTGCA TACCATGGAT TTTTGCATGG ACCACACACA GATGAACAA ACCACCGTTT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 251 ATGTTAAGAA TCTTCATATG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 251 TGGTATTGCA GCCCTGAATG ATGCAAACAA AGGAACAAA GGTTTCATCT 2601 TTTAGGGTCA CTATTGATTT AGTCGAAACA AGCAACAAA GGTTTCATCT 2611 TTTTGGGTA GCCCGCA AAAAGAAGGC CATGTGAACA AGGTTCCTTC 2611 TCCAGGTGG AACACACAAA GGAAATATG AGAACACAA AGAACTACA AGAACTCCTA AGGAACTAC AAGAACTAC AAGAACTCCTT AACACCCTT AACACTCTT AACACCCTT AACGTTTTCC						
1701 GCAGAACTTC CATCAGACAA CTTTGGAGCC TATATCATTT CGATGGCAAC 1751 TGCCCCGTCT GATGTGCTGG CGGTTGAACT TCTTCAACGT GAATGCAAAA 1801 TCAAGAATCC GTTAAGAGTT GTTCCATTGT TTGAGAACCT TGCTGATCTC 1851 GAGTCTGCTC CTGCTGCTTT GGCTCGGTTG TTTTCGATAG ACTGGTACAT 1901 AAACCGTATC GATGGGAAGC AAGAAGTTAT GATTGGATAT TCTGATTCAG 1951 GTAAAGATGC TGGAAGGTTT TCTGCCGCAT GGCAGCTATA TAAGGCTCAG 2001 GAGGACCTCA TAAATGTTGC TCAGAAAAAC GGTGTAAAC TAACAATGTT 2051 CCATGGTCGT GGTTGAACTG TTGGAAGAATAC GGTGTAAAC ACTCATCTTG 2101 CTATCTTGTC TCAACCACCA GACACAATTC GGAGGAGCCT ACTCATCTTG 2201 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2251 CCCCAAGTTC TCCAAAACCG GAATGGCGTG AATTGATGA ACCACCACTA TCAGAACAC GGAATGCGTC 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG ACCACCAGA GATGGATC TCAGAAGCGT TCCAAAACCG GAATGGCGT AATTGATGA ACCACCGTTT 2351 TGTTGAGTAT TCCGTCTGG CCACACCAGA GATGGATAC GGAAGGATAC 2401 ACATTGGAAG TCCGACCGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCACCTTT TAAACAAGTT ATGCGAAGG 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCACCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCCTTCATTTG CTGCAAAACG GTTTCATCT 2601 TTTAGGGTCA CTTTTATT AGTCGAAATG GTGTTCCAG GATCTTTCCAGGTGA ACCACAAAA GGAACACAAA GGAAATATA AGGACTCAA AGGTGACCC 2651 TGGTATTGCA CCCTGAATG ATGCCACAA AGGTTTCTCAG GAACCTCTA AGGTCACCA 2701 CATTTGGGGA ACACACAAA GGAAATATC AGGAAACTAA GAAACTCCTA 2701 CATTTGGGGA ACACACAAA GGAAATATC AAGAACTAA GAAACTCCTA 2701 CATTTGGGGA ACACACAAA GGAAATATC AAGAACTAA GAAACTCCTA 2701 CATTTGGGGA ACACACAAA GGAAATATC AAGAACTAA AACAACTCCTA AACACCCCTT AACACCCTT AACACCCCTT	1601	ATGGCTTTTG	TCTGAGTTGG	TTGGCAAAAG	GCCGCTTTTT	GGACCTGATC
1751 TGCCCCGTCT GATGTGCTGG CGGTTGAACT TCTTCAACGT GAATGCAAAA 1801 TCAAGAATCC GTTAAGAGTT GTTCCATTGT TTGAGAACT TGCTGATCTC 1851 GAGTCTGCTC CTGCTGCTTT GGCTCGGTTG TTTTCGATAG ACTGGTACAT 1901 AAACCGTATC GATGGGAAGC AAGAAGTTAT GATTGGATAT TCTGATTCAG 1951 GTAAAGATGC TGGAAGGTTT TCTGCCGCAT GGCAGCTATA TAAGGCTCAG 2001 GAGGACCTCA TAAATGTTGC TCAGAAATAC GGTGGTACAT TAAACAATGTT 2051 CCATGGTCGT GGTGGAACTG TTGGAAGAGA AGGTGGACCT ACTCATCTTG 2101 CTATCTTGTC TCAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2151 GTCAAGGTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2251 CCCCAAGTTC TCCAAAACCG GAATGGCGTC AATTGATGA ACCACGTTT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG ACCACGTTC 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG ACCACGTTT 2351 TGTTGAGTAT TCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCCGACGGCA AAAAGAAGGC CATGTGGAGG CATTGAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTT GAGCAGCTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATTGCGAAGG 2551 ATGTTAAGGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATTGCGAAGG 2561 TGGTATTGCA CCCTGAATG ATGCGAAATG GTGTTCCAG GATCTTTC 2661 TTTAGGGTCA CTTTTGATTT AGTCGAAATG GTGTTCCAG GATCTTTC 2671 CATTTGGGA ACACACAAA GGAAGTTCT GAAGGAGATC CCTACTTTGC 2701 CATTTGGGA ACACACAAA GGAAGTTCTT GAAGAACTAA GAAACTCATA 2751 CTTCAGGTG CAACACACAA GGAAGTTCTT GAAGAACTAA AAGAACTCATA 2761 CTTCAGGTG CAACACACAA GGAAGTTCTT GAAGGAGTC CCTACTTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACCCTT AACGTTTTCC				AGAGAAGTTT	TAGAGACATT	TCATGTCATA
1801 TCAAGAATCC GTTAAGAGTT GTTCCATTGT TTGAGAAACT TGCTGATCTC 1851 GAGTCTGCTC CTGCTGCTTT GGCTCGGTTG TTTTCGATAG ACTGGTACAT 1901 AAACCGTATC GATGGGAAGC AAGAAGTTAT GATTGGATAT TCTGATTCAG 1951 GTAAAGATGC TGGAAGGTTT TCTGCCGCAT GGCAGCTATA TAAGGCTCAG 2001 GAGGACCTCA TAAATGTTGC TCAGAAAATAC GGTGTTAAGC TAACAATGTT 2051 CCATGGTCGT GGTGGAACTG TTGGAAGAGG AGGTGGACCT ACTCATCTTG 2101 CTATCTTGTC TCAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2151 GTTCAAGGTG AAGTTATTGA ACAGTCGTTC GGAGAGGAGC ACTTGTGCTT 2201 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG ACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG GACCAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTAT AAACAAGTT ATTGCGAAGG 2451 TGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATTGCGAAGG 2451 TCTGCGTGCA TACCATGGAT TTTTGCATGG GACCAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTA TAAACAAGTT ATTGCGAAGG 2451 TGTTAAGGA TCTTCATATG CTGCAAGAGA TGTACAATCA ATTGCCTACT 2501 TCCAGTATGG CTTTGATTT AGTCGAAGAG GTTTCATCT 2601 TTTAGGGTCA CTATTGATT AGTCGAAGAG GTGTTCCCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGGTTTCCCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGGAAACCAA GAACCCCTA 2701 CATTTGGGG AACAGCACAA GGAAGTTCTT GAAGAACCTAA GAACCCCTA 2701 CATTTGGGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	1701	GCAGAACTTC	CATCAGACAA	CTTTGGAGCC	TATATCATTT	CGATGGCAAC
1851 GAGTCTGCTC CTGCTGCTTT GGCTCGGTTG TTTTCGATAG ACTGGTACAT 1901 AAACCGTATC GATGGGAAGC AAGAAGTTAT GATTGGATAT TCTGATTCAG 1951 GTAAAGATGC TGGAAGGTTT TCTGCCGCAT GGCAGCTATA TAAGGCTCAG 2001 GAGGACCTCA TAAATGTTGC TCAGAAATAC GGTGTTAAGC TAACAATGTT 2051 CCATGGTCGT GGTGGAACTG TTGGAAGAGG AGGTGGACCT ACTCATCTTG 2101 CTATCTTGTC TCAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2151 GTTCAAGGTG AAGTTATTGA ACAGTCGTTC GGAGAGGAGC ACTTGTGCTT 2201 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2251 CCCCAAGTTC TCCAAAACCG GAATGGCGT AATTGATGAACAC GGAATGCGTC 2301 GTCATTGCTA CCGAGAGATA CCGTTCAATT GTGTTCAAGG AACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2451 CTGCGTGCGA TCGACCGCA AAAAGAAGC CATGTGAGCA CATTGAAACA 2451 CTGCGTGCGA TCGACCGGCA AAAAGAAGC CATGTGAGAC CATTGAAACA 2451 TCTCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACCAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACCAAGCA ACGCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAAGGA TGTACCAATCA ATGGCCTTTC 2611 TGTTTTCAGGAA ACAGTTGAAACA GACCACACAA ATGGCCTTTC 2611 TGTTAAGAA ACAGTTGAAACA GACCACACAA ATGGCCTTTC 2611 TGTTAAGGA ACAGTTGAAACA GACCACACAA ATGGCCTTTC 2611 TGTTAAGGA ACAGTTGAAACA GACCACACAA AGGAGAATCA AGGGTGACCC 2611 TGTTAGGGTCA CTATTGATTT AGTCGAAATG AGGTTCCTA AGGGTGACCC 2611 TGTTAGGGTA ACAGTTGAAA AGAAATATG AGGAAACTAA GAAACTCCTA 2611 TCCAGGTGG CAACACACAA GGAAGTTCTT GAAACAACTAA GAAACTCCTA 2701 CATTTGGGGA ACAGTTGAAA AGGAAACTAA AGGAAACTAA AAGAAACTAA AAGA	1751	TGCCCCGTCT	GATGTGCTGG	CGGTTGAACT	TCTTCAACGT	GAATGCAAAA
1901 AAACCGTATC GATGGGAAGC AAGAAGTTAT GATTGGATAT TCTGATTCAG 1951 GTAAAGATGC TGGAAGGTTT TCTGCCGCAT GGCAGCTATA TAAGGCTCAG 2001 GAGGACCTCA TAAATGTTGC TCAGAAAATAC GGTGTTAAGC TAACAATGTT 2051 CCATGGTCGT GGTGGAACTG TTGGAAGAGG AGGTGGACCT ACTCATCTTG 2101 CTATCTTGTC TCAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2151 GTTCAAGGTG AAGTTATTGA ACAGTCGTTC GGAAGAGACACAGCCA GACACAATTC ACGGATCTCT TCGTGTGACG 2251 CCCCAAGTTC TCCAAAACCG GAATGCGTC ACTTGTGCTT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG ACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGC 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGAC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAAGG GTGTTCCTAA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCCTAAGG ACACAGACAA GGTTTCTTCGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG ATGGCCTTTC 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	1801	TCAAGAATCC	GTTAAGAGTT	GTTCCATTGT	TTGAGAAACT	TGCTGATCTC
1951 GTAAAGATGC TGGAAGGTTT TCTGCCGCAT GGCAGCTATA TAAGGCTCAG 2001 GAGGACCTCA TAAATGTTGC TCAGAAATAC GGTGTTAAGC TAACAATGTT 2051 CCATGGTCGT GGTGGAACTG TTGGAAGAGG AGGTGGACCT ACTCATCTTG 2101 CTATCTTGTC TCAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2151 GTTCAAGGTG AAGTTATTGA ACAGTCGTTC GGAGAGGAGC ACTTGTGCTT 2201 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2251 CCCCAAGTTC TCCAAAACCG GAATGCGGTG AATTGATGGA TCAGATGGCT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG AACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAAGG GTGTTCCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTCGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	1851	GAGTCTGCTC	CTGCTGCTTT	GGCTCGGTTG	TTTTCGATAG	ACTGGTACAT
2001 GAGGACCTCA TAAATGTTGC TCAGAAATAC GGTGTTAAGC TAACAATGTT 2051 CCATGGTCGT GGTGGAACTG TTGGAAGAGG AGGTGGACCT ACTCATCTTG 2101 CTATCTTGTC TCAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2151 GTTCAAGGTG AAGTTATTGA ACAGTCGTTC GGAGAGGAGC ACTTGTGCTT 2201 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2251 CCCCAAGTTC TCCAAAACCG GAATGGCGT AATTGATGGA TCAGATGGCT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG AACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAAGG GTGTTCCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA	1901	AAACCGTATC	GATGGGAAGC	AAGAAGTTAT		
2051 CCATGGTCGT GGTGGAACTG TTGGAAGAGG AGGTGGACCT ACTCATCTTG 2101 CTATCTTGTC TCAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2151 GTTCAAGGTG AAGTTATTGA ACAGTCGTTC GGAGAGGAGC ACTTGTGCTT 2201 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2251 CCCCAAGTTC TCCAAAACCG GAATGCGTG AATTGATGGA TCAGATGGCT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG AACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAAGG GTGTTCCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	1951	GTAAAGATGC	TGGAAGGTTT	TCTGCCGCAT	GGCAGCTATA	TAAGGCTCAG
2101 CTATCTTGTC TCAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG 2151 GTTCAAGGTG AAGTTATTGA ACAGTCGTTC GGAGAGGAGC ACTTGTGCTT 2201 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2251 CCCCAAGTTC TCCAAAACCG GAATGCGTG AATTGATGGA TCAGATGGCT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG AACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2001	GAGGACCTCA	TAAATGTTGC	TCAGAAATAC	GGTGTTAAGC	TAACAATGTT
2151 GTTCAAGGTG AAGTTATTGA ACAGTCGTTC GGAGAGGAGC ACTTGTGCTT 2201 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2251 CCCCAAGTTC TCCAAAACCG GAATGCGTG AATTGATGGA TCAGATGGCT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG AACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2051	CCATGGTCGT	GGTGGAACTG	TTGGAAGAGG	AGGTGGACCT	
2201 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC 2251 CCCCAAGTTC TCCAAAACCG GAATGCGTG AATTGATGGA TCAGATGGCT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG AACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2101	CTATCTTGTC	: TCAACCACCA	GACACAATTC		
2251 CCCCAAGTTC TCCAAAACCG GAATGCGTG AATTGATGGA TCAGATGGCT 2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG AACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2151	GTTCAAGGTG				
2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG AACCACGTTT 2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC						
2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA 2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2251	CCCCAAGTTC	TCCAAAACCG	GAATGGCGTG	AATTGATGGA	TCAGATGGCT
2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA 2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACACTCAAA GGAAGTTCTT GAAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2301	GTCATTGCTA	CCGAGGAGTA	CCGTTCAATT	GTGTTCAAGG	AACCACGTTT
2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT 2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACACTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2351	. TGTTGAGTAI	TTCCGTCTGG	CCACACCAGA	GATGGAGTAC	GGAAGGATGA
2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG 2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2401	. ACATTGGAAG	TCGACCGGCA	AAAAGAAGG C	CATGTGGAGG	CATTGAAACA
2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC 2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2451	. CTGCGTGCGA	A TACCATGGAT	TTTTGCATGG	ACACAGACAA	GGTTTCATCT
2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC 2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2501	. TCCAGTATGO	CTTGGCTTTG	GAGCAGCTTT	TAAACAAGTI	ATTGCGAAGG
2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC 2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2551	ATGTTAAGAA	A TCTTCATATO	CTGCAAGAGA	TGTACAATCA	ATGGCCTTTC
2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA 2751 CTTCAGGTGG CAACACACA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2601	TTTAGGGTC	A CTATTGATT	AGTCGAAATC	GTGTTCGCTA	AGGGTGACCC
2751 CTTCAGGTGG CAACACACA GGAAGTTCTT GAAGGAGATC CCTACTTGAA 2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2651	TGGTATTGC	A GCCCTGAATO	ATAGGCTACT	AGTTTCTCAG	GATCTTTGGC
2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC	2701	CATTTGGGG	A ACAGTTGAGA	A AGCAAATATO	AAGAAACTAA	GAAACTCCTA
2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC 2851 AAGCATACAC ATTGAAACGG ATCCGTGATC CAAACTATAA GGTGGAGGTG	2751	CTTCAGGTG	CAACACACA?	A GGAAGTTCTT	GAAGGAGATO	CCTACTTGAA
2851 AAGCATACAC ATTGAAACGG ATCCGTGATC CAAACTATAA GGTGGAGGTG	2801	L ACAAAGACTO	C AGACTCCGTC	3 ATTCTTACAT	TACAACCCTT	AACGTTTTCC
	2851	L AAGCATACA	C ATTGAAACGO	ATCCGTGATC	CAAACTATA	A GGTGGAGGTG

2901	CGCCCCCGCG	TATCGAAAGA	ATCTGCTGAA	ACAAGTAAAT	CGGCTGATGA
2951	ACTTGTAACA	TTGAATCCAA	CAAGTGAATA	TGCTCCTGGT	TTGGAAGACA
				CTGGCATGCA	
3051	TAATTTTTGG	TGATTTTTT	CACTTGTATT	TGTTTCTTTT	ATGTTAAGTG
3101	TGTGCTAAGA	TATCATAAAT	ACTAGATGAA	TCTAGTTGCA	AGCACTTCAA
				CCTTTTTCAT	
3201	CATCAGGTTT	TGTTGATGTT	TTTCCTTACT	TTGTTACCAT	ACAAACGAGT
3251	TAATGCAATT	GATGTTATGT	TTCAATGCAT	AGATTTTATC	TCCTTTCTTC
3301	TAAAAAAAAA	AAAAAAAAA	AAAAAAAAA	AGTACTCTGC	GTTGTTACCA
3351	ርጥርርጥጥ ልጥር	Δ СΤΔGΤGΔΔΤ	TC		

220/241

1	MATNKMEKMA	SIDAQLRQLV	PAKVSEDDKL	IEYDALLLDR	FLDILQDLHG
51	EDLKDSVQEV	YELSAEYERK	HDPKKLEELG	NLITSLDAGD	SIVVAKSFSH
101	MLNLANLAEE	VQIAHRRRNK	LKKGDFRDES	NATTESDIEE	TLKRLVFNMK
151	KSPQEVFDAL	KNQTVDLVLT	AHPTQSVRRS	LLQKHGRVRN	CLSQLYAKDI
201	TPDDKQELDE	ALQREIQAAF	RTDEIKRTPP	TPQDEMRAGM	SYFHETIWKG
251	VPKFLRRVDT	ALKNIGINER	VPYNAPLIQF	SSWMGGDRDG	NPRVTPEVTR
301	DVCLLARMMA	ANLYYSQIED	LMFELSMWRC	NDELRDRAEE	LHRNSKKDEV
351	AKHYIEFWKK	IPLNEPYRVI	LGDVRDKLYR	TRERSRYLLA	HGYSEIPEEA
401	TFTNVDEFLE	PLELCYRSLC	ACGDRAVADG	SLLDFLRQVS	TFGLSLVRLD
451	IRQESDRHTD	VMDAITKHLE	IGSYQDWSEE	KRQEWLLSEL	VGKRPLFGPD
501	LPQTDEIREV	LETFHVIAEL	PSDNFGAYII	SMATAPSDVL	AVELLQRECK
551	IKNPLRVVPL	FEKLADLESA	PAALARLFSI	DWYINRIDGK	QEVMIGYSDS
601	GKDAGRFSAA	WQLYKAQEDL	INVAQKYGVK	LTMFHGRGGT	VGRGGGPTHL
651	AILSQPPDTI	HGSLRVTVQG	EVIEQSFGEE	HLCFRTLQRF	TAATLEHGMR
701	PPSSPKPEWR	ELMDQMAVIA	TEEYRSIVFK	EPRFVEYFRL	ATPEMEYGRM
751	NIGSRPAKRR	PCGGIETLRA	IPWIFAWTQT	RFHLPVWLGF	GAAFKQVIAK
801	DVKNLHMLQE	MYNQWPFFRV	TIDLVEMVFA	KGDPGIAALN	DRLLVSQDLW
851	PFGEQLRSKY	EETKKLLLQV	ATHKEVLEGD	PYLKQRLRLR	DSYITTLNVF
901	QAYTLKRIRD	PNYKVEVRPR	VSKESAETSK	SADELVTLNP	TSEYAPGLED
951	TLILTMKGIA	AGMQNTG			

FIGURE 111



pPZP221:TrPEPC sense



TrCSa

1	GAATTCGATT	AAGCAGTGGT	AACAACGCAG	AGTACGCGGG	GAGCACAACA
51	TTACGTTAAT	TACATTTTCT	CTTTCGCCAT	TGTTCTTTCT	CTTCTCAATA
101	TAAAGACCAA	TTCAATTCCC	AATTCTTTTG	GATCCGAAAT	CATTCATTCT
151	ACGCTTCTTC	TCTCTTCTCT	GCGTTTCAAA	CCCTAGTTGT	TTTGTTGATT
201	GATCTTAATG	GCGTTCTTTC	GAAGCGTTTC	TGCGCTTTCA	AAACTACGAT
251	CTCGTGTGGG	TCAACAACCT	AGTCTTGCTA	ATTCAGTTAG	ATGGCTCCAA
301	ACTCCAAGCT	CCAGTAACAC	TGATCTTTAT	TCTGAGATGA	AGGAGCTAGT
351	TCCAGAGTAT	CAGGAACGTG	TTAAGAAGTT	GAAGAAAGAC	CATGGAAGTG
401	TTGAATTGGG	AAAAATCACA	GCTGATATGG	TACTTGGTGG	AATGAGAGGA
451	ATGACTGCTT	TAGTGTGGCT	AGGCTCAGCT	GTTGACCCAG	ATGAGGGAAT
501	TCGCTTTAGG	GGCATGACAA	TTCCTGACTG	CCAGAAAACA	CTTCCAGGTG
551	CTTTTCCTGG	TGGGGAGCCT	TTGCCCGAGG	CTATACTGTG	GCTTCTATTG
601	ACCGGAAAGG	TACCAAGTAA	AGAGCAAGTA	GATTCATTAG	CTCACGAATT
651	GCGAAGTCGT	GCAAAAATCC	CAGAGTATGC	TTACAAGGCA	ATTGATGCAC
701	TGCCTGTTTC	TGCTCATCCA	ATGACACAAT	TTAGTACTGG	TGTAATGGCC
751	CTCCAGGTGG	AGAGTGAGTT	TACAAAGGCA	TACGAGGGTG	GGATACATAA
801	GTCAAGGTAT	TGGGAGCCAA	CTTATGAGGA	TAGCTTGAAT	TTAATTGCTC
851	GTTTGCCTGG	AATTGCTGCC	TATATTTATC	GACGGATATA	CAAGGATGGA
901	AAAATCATAC	CATTGGATGA	TTCTTTGGAT	TATGGTGCAA	ACTATGCTCA
951	CATGTTAGGA	TTTGATGATC	CAGAAACGCT	GGAGTTTATG	AGGCTGTATA
1001	TTTCTATCCA	TAGTGATCAT	GAAGGTGGCA	ACGTTAGTTC	TCACACAGCT
1051	CACCTAGTTG	CTAGTTCACT	ATCAGATCCT	TATCTTGCAT	TCGCAGCTGC
1101	TCTGAATGGT	TTAGCTGGCC	CACTGCATGG	TTTAGCCAAT	CAGGAAGTTC
1151	TACGATGGAT	CAGAAACATA		TTGGAACTCC	AAACATAAGT
1201	ACAGAACAAT	TGAGCGACTA		ACATTGAACA	GTGGCCAGGT
1251	TGTGCCTGGA	TATGGACATG		CAATACAGAC	CCAAGATACA
1301	CTTGCCAGAG	GGAGTTTGCA	TTGAAGCATT	TGCCTAATGA	TCCACTTTTC
1351	CAGCTGGTGT	CCAAAATTAA	AGAAGTCGTG	CCTCCCATTC	TGACCAAGTT
1401	AGGAAAGGTT	AAAAATCCAT		TGATGCTCAT	AGTGGAGTAC
1451	TACTAAACTA	. CTATGGTCTA	. ACTGAAGAAA	-	CGTTCTTTT
1501	GGTGTCGCGA	. GGAGTATTGG			GGGACCGTGC
1551	TCTTGGAATG				GAGAAACTTG
1601	. AGAAACTGGT				TTATCTGTGG
1651	. ATTACTAAAA	TACACTCTGC			
1701	. TGGTGCAATT				
1751	. TTTCTGGTTG	TTTTGTCAGC			
1801				_	
1851	CAGCATAAAT				
1901	GGGGGTAATC	CCTCTGTATI			
1951	AAAATACAAA			- - ·	
2001	AAAAAAAAA	AAAAAAAAA	AAAAAGTACT	CTGCGTTGTT	ACCACTGCTT
2051	AATCACTAGT	GAATTC			

1	MAFFRSVSAL	SKLRSRVGQQ	PSLANSVKWL	ÖTÉPPPMIDE	TODI: HOMAT AT D
51	YQERVKKLKK	DHGSVELGKI	TADMVLGGMR	GMTALVWLGS	AVDPDEGIRF
101	RGMTIPDCQK	TLPGAFPGGE	PLPEAILWLL	LTGKVPSKEQ	VDSLAHELRS
151	RAKIPEYAYK	AIDALPVSAH	PMTQFSTGVM	ALQVESEFTK	AYEGGIHKSR
201	YWEPTYEDSL	NLIARLPGIA	AYIYRRIYKD	GKIIPLDDSL	DYGANYAHML
251	GFDDPETLEF	MRLYISIHSD	HEGGNVSSHT	AHLVASSLSD	PYLAFAAALN
301	GLAGPLHGLA	NQEVLRWIRN	IVKEFGTPNI	STEQLSDYIH	KTLNSGQVVI
351	GYGHGVLRNT	DPRYTCQREF	ALKHLPNDPL	FQLVSKIKEV	VPPILTKLG
401	VKNPWPNVDA	HSGVLLNŸYG	LTEENYYTVL	FGVARSIGVG	PQLIWDRALC
<i>1</i> E 1	MDIÆRPKSVT	LEKLEKLVGA	SS		



pPZP221:TrCSa sense



TrCSb

1	GAATTCGATT	AAGCAGTGGT	AACAACGCAG	AGTACGCGGG	GAGCACAACA
51	TTACGTTAAT	TACATTTTCT	CTTTCGCCAT	TGTTCTTTCT	CTTCTCAATA
101	TAAAGACCAA	TTCAATTCCC	AATTCTTTTG	GATCCGAAAT	CATTCATTCT
151	ACGCTTCTTC	TCTCTTCTCT	GCGTTTCAAA	CCCTAGTTGT	TTTGTTGATT
201	GATCTTAATG	GCGTTCTTTC	GAAGCGTTTC	TGCGCTTTCA	AAACTACGAT
251	CTCGTGTGGG	TCAACAACCT	AGTCTTGCTA	ATTCAGTTAG	ATGGCTCCAA
301	ACTCCAAGCT	CCAGTAACAC	TGATCTTTAT	TCTGAGATGA	AGGAGCTAGT
351	TCCAGAGTAT	CAGGAACGTG	TTAAGAAGTT	GAAGAAAGAC	CATGGAAGTG
401	TTGAATTGGG	AAAAATCACA	GCTGATATGG	TACTTGGTGG	AATGAGAGGA
451	ATGACTGCTT	TAGTGTGGCT	AGGCTCAGCT	GTTGACCCAG	ATGAGGGAAT
501	TCGCTTTAGG	GGCATGACAA	TTCCTGACTG	CCAGAAAACA	CTTCCAGGTG
551	CTTTTCCTGG	TGGGGAGCCT	TTGCCCGAGG	CTATACTGTG	GCTTCTATTG
601	ACCGGAAAGG	TACCAAGTAA	AGAGCAAGTA	GATTCATTAG	CTCACGAATT
651	GCGAAGTCGT	GCAAAAATCC	CAGAGTATGC	TTACAAGGCA	ATTGATGCAC
701	TGCCTGTTTC	TGCTCATCCA	ATGACACAAT	TTAGTACTGG	TGTAATGGCC
751	CTCCAGGTGG	AGAGTGAGTT	TACAAAGGCA	TACGAGGGTG	GGATACATAA
801	GTCAAGGTAT	TGGGAGCCAA	CTTATGAGGA	TAGCTTGAAT	TTAATTGCTC
851	GTTTGCCTGG	AATTGCTGCC	TATATTTATC	GACGGATATA	CAAGGATGGA
901	AAAATCATAC	CATTGGATGA	TTCTTTGGAT	TATGGTGCAA	ACTATGCTCA
951	CATGTTAGGA	TTTGATGATC	CAGAAACGCT	GGAGTTTATG	AGGCTGTATA
1001	TTTCTATCCA	TAGTGATCAT	GAAGGTGGCA	ACGTTAGTTC	TCACACAGCT
1051	CACCTAGTTG	CTAGTTCACT	ATCAGATCCT	TATCTTGCAT	TCGCAGCTGC
1101	TCTGAATGGT	TTAGCTGGCC	CACTGCATGG	TTTAGCCAAT	CAGGAAGTTC
1151	TACGATGGAT	CAGAAACATA	GTTAAGGAGT	TTGGAACTCC	AAACATAAGT
1201	ACAGAACAAT	TGAGCGACTA	CATTCATAAA	ACATTGAACA	GTGGCCAGGT
1251	TGTGCCTGGA	TATGGACATG	GAGTTTTGCG	CAATACAGAC	CCAAGATACA
1301	CTTGCCAGAG	GGAGTTTGCA	TTGAAGCATT	TGCCTAATGA	TCCACTTTTC
1351	CAGCTGGTGT	CCAAAATTAA	AGAAGTCGTG	CCTCCCATTC	TGACCAAGTT
1401	AGGAAAGGTT	AAAAATCCAT	GGCCTAATGT	TGATGCTCAT	AGTGGAGTAC
1451	TACTAAACTA	CTATGGTCTA	ACTGAAGAAA	ACTATTATAC	CGTTCTTTTT
1501	GGTGTCGCGA	GGAGTATTGG	AGTTGGCCCT	CAGCTGATAT	GGGACCGTGC
1551	TCTTGGAATG	CCACTTGAAA	GGCCAAAAAG	TGTCACACTG	GAGAAACTTG
1601	AGAAACTGGT	CGGCGCATCG	TCCTAAAATT	GAAAGCGCGG	TTATCTGTGG
1651	ATTACTAAAA	TACACTCTGC	GGTTGTAGGT	TGTTGGTAAC	TCTAAACATT
1701	TGGTGCAATT	GCAATGAGAA	ATATTTTGCC	CAAATCCCCC	TTCCCTTATT
1751	TTTCTGGTTG	TTTTGTCAGC	ATTTTTTGAT	TGAGGAGATT	TTGGTATTTA
1801	GGAAAAGGGT	GGGATTATCA	CCCTCACAGT	TGTCTTTCCA	TTTTTCTACA
1851	CAGCATAAAT	TAGGTCCCAA	GGGAGCATCA		ATTATGTTTT
1901	GGGGGTAATC	CCTCTGTATT	CTTTCTAAAT	AGGATTGACC	CCTTTGACAA
1951	AAAATACAAA	TTATCAATAT	CACTCGTCTA		CGACTAAAAA
2001	AAAAAAAAA		AAAAAGTACT	CTGCGTTGTT	ACCACTGCTT
2051	AATCACTAGT	GAATTC			

1	MAFFRSVSAL	SKLRSRVGQQ	PSLANSVRWL	OLESSENIDE	ISEMKEDVPE
51	YQERVKKLKK	DHGSVELGKI	TADMVLGGMR	GMTALVWLGS	AVDPDEGIRF
.01	RGMTIPDCQK	TLPGAFPGGE	PLPEAILWLL	LTGKVPSKEQ	VDSLAHELRS
.51	RAKIPEYAYK	AIDALPVSAH	PMTQFSTGVM	ALQVESEFTK	AYEGGIHKSR
201	YWEPTYEDSL	NLIARLPGIA	AYIYRRIYKD	GKIIPLDDSL	DYGANYAHMI
251	GFDDPETLEF	MRLYISIHSD	HEGGNVSSHT	AHLVASSLSD	PYLAFAAALN
301	GLAGPLHGLA	NQEVLRWIRN	IVKEFGTPNI	STEQLSDYIH	KTLNSGQVVP
351	GYGHGVLRNT	DPRYTCQREF	ALKHLPNDPL	FQLVSKIKEV	VPPILTKLG
101	VKNPWPNVDA	HSGVLLNYYG	LTEENYYTVL	FGVARSIGVG	PQLIWDRALG
151	MPLERPKSVT	TEKTEKT.VGA	SS		



pPZP221:TrCSb sense



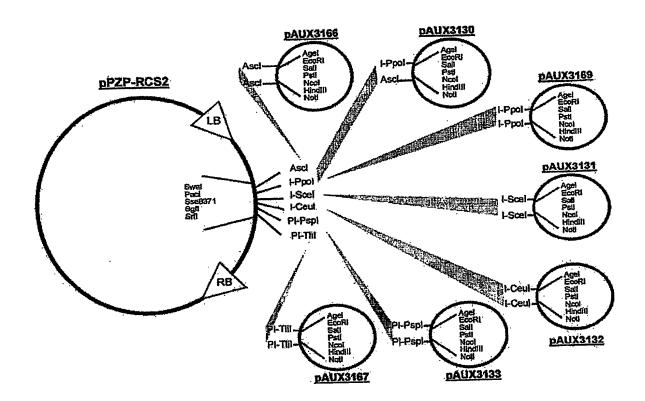
TrCSd

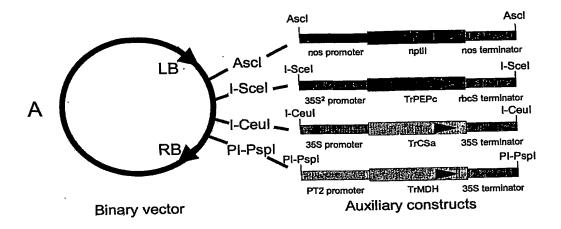
1	GAATTCGATT	AAGCAGTGGT	AACAACGCAG	AGTACGCGGG	GATCCGAAAT
51	CATTCATTCT	ACTTTTCAAC	CTGTTGTTTT	GTTGATTGAT	CTAAATGGCG
101	TTCTTTCGAA	GCGTTTCTGC	GCTTTCAAAA	CTACGATCTC	GTGTGGGTCA
151	ACAACCTAGT	CTTGCTAATT	CAGTTAGATG	GCTCCAAACT	CCAAGCTCCA
201	GTAACACTGA	TCTTTATTCT	GAGATGAAGG	AGCTAGTTCC	AGAGTATCAG
251	GAACGTGTTA	AGAAGTTGAA	GAAAGACCAT	GGAAGTGTTG	AATTGGGAAA
301	AATCACAGCT	GATATGGTAC	TTGGTGGAAT	GAGAGGAATG	ACTGCTTTAG
351	TGTGGCTAGG	CTCAGCTGTT	GACCCAGATG	AGGGAATTCG	CTTTAGGGGC
401	ATGACAATTC	CTGACTGCCA	GAAAACACTT	CCAGGTGCTT	TTCCTGGTGG
451	GGAGCCTTTG	CCCGAGGCTA	TACTGTGGCT	TCTATTGACC	GGAAAGGTAC
501	CAAGTAAAGA	GCAAGTAGAT	TCATTAGCTC	ACGAATTGCG	AAGTCGTGCA
551	AAAATCCCAG	AGTATGCTTA	CAAGGCAATT	GATGCACTGC	CTGTTTCTGC
601	TCATCCAATG	ACACAATTTA	GTACTGGTGT	AATGGCCCTC	CAGGTGGAGA
651	GTGAGTTTAC	AAAGGCATAC	GAGAGTGGGA	TACATAAGTC	AAGGTATTGG
701	GAGCCAACTT	ATGAGGATAG	CTTGAATTTA	ATTGCTCGTT	TGCCTGGAAT
751	TGCTGCCTAT	ATTTATCGAC	GGATATACAA	GGATGGAAAA	ATCATACCAT
801	TGGATGATTC	TTTGGATTAT	GGTGCAAACT	ATGCTCACAT	GTTAGGATTT
851	GATGATCCAG	AAACGCTGGA	GTTTATGAGG	CTGTATATTT	CTATCCATAG
901	TGATCATGAA	GGTGGCAACG	TTAGTTCTCA	CACAGCTCAC	CTAGTTGCTA
951	GTTCACTATC	AGATCCTTAT	CTTGCATTCG	CAGCTGCTCT	GAATGGTTTA
1001	GCTGGCCCAC	TGCATGGTTT	AGCCAATCAG	GAAGTTCTAC	GATGGATCAG
1051	AAACATAGTT	ACGGAATTTG	GAACTCCAAA	CATAAGTACA	GAACAATTGA
1101	GCGACTACAT	TCATAAAACA	TTGAACAGTG	GCCAGGTTGT	GCCTGGATAT
1151	GGACATGGAG	TTTTGCGCAA	TACAGACCCA	AGATACACTT	GCCAGAGGGA
1201	GTTTGCATTG	AAGCATTTGC	CTAATGATCC	ACTTTTCCAG	CTGGTGTCCA
1251	AAATTAAAGA	AGTCGTGCCT	CCCATTCTGA	CCAAGTTAGG	AAAGGTTAAA
1301	AATCCATGGC	CTAATGTTGA	TGCTCATAGT	GGAGTACTAC	TAAACTACTA
1351	TGGTCTAACT	GAAGAAAACT	ATTATACCGT	TCTTTTTGGC	GTCGCGAGGA
1401	GTATTGGAGT	TGGCCCTCAG		ACCGTGCTCT	TGGAATGCCA
1451	CTTGAAAGGC	CAAAAAGTGT	CACACTGGAG	AAACTTGAGA	AACTCGTCGG
1501	TGCATCATCC	TAAAATTGAA			ACTAAAATAC
1551	ACACTGCGGT	TGTAGGTTGT	+	AAACATTTGG	TGCAATTGCA
1601	ATGAGAAATA		ACATCCCCTT	CCCTTATTTT	TCTGGTTGTT
1651	TTGTCAGCAT				AAAGGGTGGG
1701	ATTATCACCC				CATAAATTAG
1751	GTCCCAAGGG				
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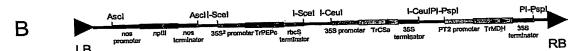
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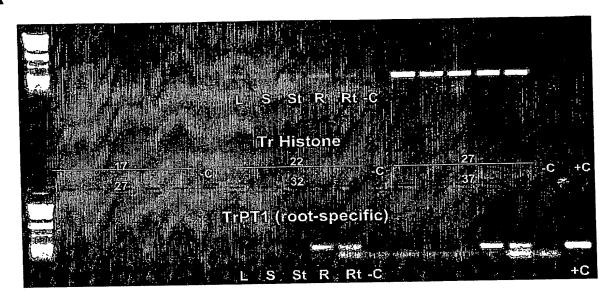




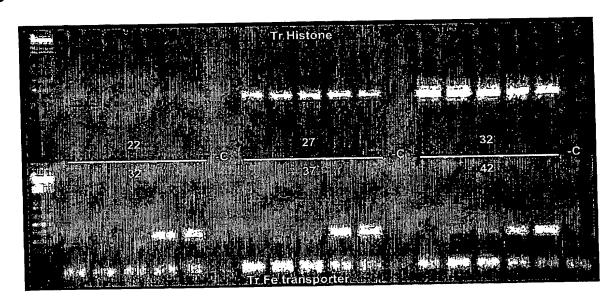
Binary vector construct

236/241

Α

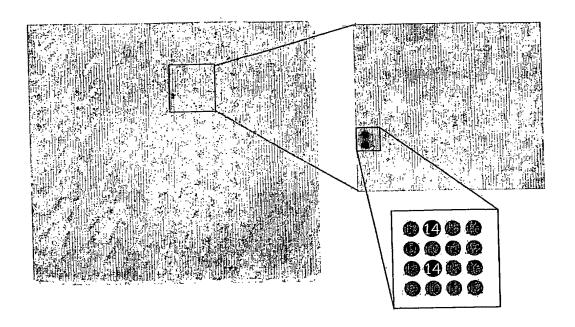


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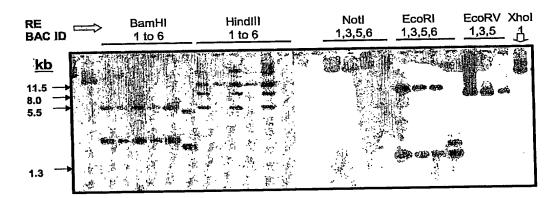


237/241

A



В



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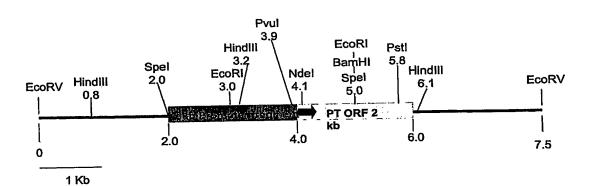
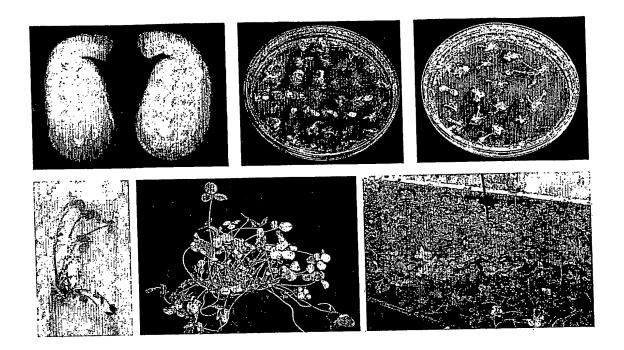
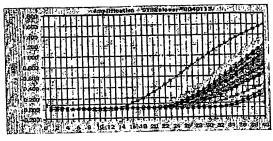
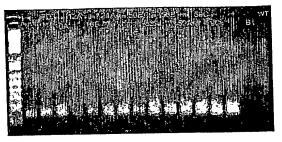


FIGURE 128



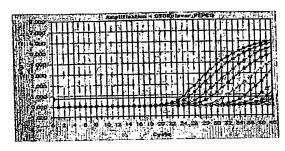


QPCR plots

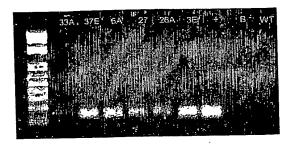


QPCR Result

240/241



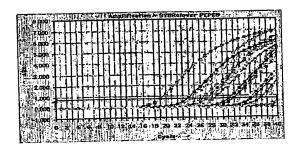


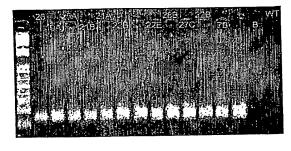


QPCR Result

FIGURE 131

241/241





QPCR plots

QPCR Result

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Lolium perenne

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G7u 145	val	Ile	Glу	Leu	G]y 150	Glu	Leu	Ser	Ala	Phe 155	Glu	Lys	Glu	Gly	Leu 160

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45 40 35

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PCT/AU2004/000493 WO 2004/089066

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PRT

Lolium perenne

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Ala Glu Ala Leu Asn Gly Val Lys Met Glu Leu Val Asp Ala Ala Phe 50 60

Pro Leu Leu Lys Gly Val Val Ala Thr Thr Asp Val Val Glu Ala Cys 65 70 75 80

Thr Gly Val Asn Val Ala Val Met Val Gly Gly Phe Pro Arg Lys Glu 85 90 95

Gly Met Glu Arg Lys Asp Val Met Ser Lys Asn Val Ser Ile Tyr Lys $100 \hspace{1cm} 105 \hspace{1cm} 110$

Ser Gln Ala Ser Ala Leu Glu Ala His Ala Ala Pro Asn Cys Lys Val 115 120 125

Leu Val Val Ala Asn Pro Ala Asn Thr Asn Ala Leu Ile Leu Lys Glu 130 135 140

Phe Ala Pro Ser Ile Pro Glu Lys Asn Ile Ser Cys Leu Thr Arg Leu 145 150 155 160

Asp His Asn Arg Ala Leu Gly Gln Ile Ser Glu Arg Leu Asp Val Gln 165 170 175

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Lys Pro Val Arg Glu Leu Val Lys Asp Asp Glu Trp Leu Asn Ala Gly 210 220
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PCT/AU2004/000493 WO 2004/089066

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Lolium perenne

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180

240 300

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480

540

600

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PCT/AU2004/000493 WO 2004/089066

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DNA

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                                                                       600
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PCT/AU2004/000493 WO 2004/089066

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ľ

95

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90

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Lolium perenne

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туг	Arg	g Ser	· Ile	Va1 85.	Phe	Gln	Glu	Pro	Arg 90	Phe	٧a٦	Glu	туг	Phe 95	Arg
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Asn Phe His Met Leu Gln Glu Met Tyr Asn Glu Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Val Glu Met Val Phe Ala Lys Gly Asn Pro Gly Ile Ala Ala Leu Tyr Asp Arg Leu Leu Val Ser Glu Glu Leu Gln Pro Leu Gly Asp Lys Leu Arg 205 <210> 674 <211> <212> DNA Trifolium repens <220> <221> misc_feature (15)..(15)<222> n is a, c, g, or t <223> <220> misc_feature <221> (623)..(623) <222> n is a, c, g, or t <223> <220> misc_feature (645)..(645) <221> <222> n is a, c, g, or t <223> <220> <221> misc_feature
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N

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Ser Asp Val Lys Asn Val Ile Ile Trp Gly Asn His Ser Ser Thr Gln 180 185 190

Tyr Pro Asp Val Asn His Ala Thr Val Asn Thr Pro Ala Gly Glu Lys 195 200 205

Pro Val Arg Glu Leu Val Ser Asp Asp Ala Trp Leu Asn Gly Glu Phe 210 215 220

Ile Ser Thr Val Gln Gln Arg Gly Ala Ala Ile Ile Lys Ala Arg Lys 225 230 240

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540593

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 gtcctgatca acctgtgatc cttcacatgc ttgatattcc tccagcagca gagtcattga
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  caactgatgt tgttgaggca tgcactggag tcaatattgc agtcatggtt ggtggattcc
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  caagaaaaga aggtatggag aggaaggatg tgatgtctaa gaacgtctct atttacaagt
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  cccaggcttc tgcccttgaa aagcatgctg ctgccaactg caaggttttg gttgttgcta
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acccagcaac accaatgcat tgatcttgaa ggaatttgct ccatctattc cagagaaaaa
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ggtgctgcag ggcaaattgg ttatgcactt gtccctatga ttgctagggg agtgatgctt
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ggtcctgatc aacctgtgat cctacacatg cttgatattc cacccgcagc agagtcattg
                                                                          240
aatggagtta agatggagtt ggtcgatgct gcatttccac ttcttaaagg tgttgttgct
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acaactgatg ttgttgaggc atgcactgga gtcaatatcg cagtcatggt tggtggattc
                                                                          360
 ccaagaaaag aaggtatgga gaggaaggat gttatgtcta agaacgtctc tatttacaag
                                                                          420
 tcccaagctt ctgcccttga aaagcatgct gctgccaact gcaaggtttt ggttgttgct
                                                                          480
 aacccagcaa acaccaatgc attgatcttg aaggaatttg ctccatctat tccagagaaa
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gcaggccaaa ttggttatgc acttgtccct atgattgcta ggggagtgat gcttggtcct
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gatcaacctg tgatccttca catgcttgat atccctccag cagcagagtc attgaatgga
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gttaaaatgg agttggtgga tgctgcattt ccacttctta aaggcgttgt tgctacaact
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gatgttgttg aagcatgcac tggagtcaat attgcagtca tggttggtgg attcccaaga
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aaagaaggta tggagaggaa ggatgtgatg actaagaatg tctctattta caagtcccag
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gcttctgccc ttgaaaagca tgctgctgcc aactgcaagg ttttggttat tgctaaccca
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gccaaattgg ttatgcactt gtccctatga ttgctagggg agtgatgctt ggtcctgatc
aacctgtgat ccttcacatg cttgatattc ctccagcagc agagtcattg aatggagtta
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aaatggagtt ggtggatgct gcatttccac ttcttaaagg tgttgttgct acaactgatg
                                                                       300
ttgttgaagc atgcactgga gtcaatattg cagtcatggt tggtggattc ccaagaaaag
                                                                       360
                                                                       420
aaggtatgga gaggaaggat gtgatgacta anaatgtctc tatttacaag tcccaggctt
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                                                                        360
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                                                                        420
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gctgcagggc aaattggtta tgcacttgtc cctatgattg ctaggggagt gatgcttggt
                                                                         180
 cctgatcaac ctgtgatcct acacatgctt gatattccac ccgcagcaga gtcattgaat
                                                                         240
 ggagttaaga tggagttggt cgatgctgca tttccacttc ttaaaggtgt tgttgctaca
                                                                         300
 actgatgttg ttgaggcatg cactggagtc aatatcgcag tcatggttgg tggattccca
                                                                         360
 agaaaagaag gtatggagag gaaggatgtt atgtctaaga acgtctctat ttacaagtcc
                                                                         420
 caagettetg ceettgaaaa geatgetget gecaactgea aggttttggt tgttgetaae
                                                                         480
 ccagcaaaca ccaatgcatt gatcttgaag gaatttgctc catctattcc agagaaaaac
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 atcaacctgt gatccttcac atgcttgata ttcctccagc agcagagtca ttgaatggag
                                                                         240
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ttaagatgga gttggtcgat gctgcatttc cacttcttaa aggtgttgtt gctacaactg
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atgttgttga ggcatgcact ggagtcaata ttgcagtcat ggttggtgga ttcccaagaa
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cttctgccct tgaaaagcat gctgctgcca actgcaaggt tttggttgtt gctaacccag
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caacaccaat gcattgatct tgaaggaatt tgctccatct attccagaga aaaacatttc
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 ttggtggatg ctgcatttcc acttcttaaa ggtgttgttg ctacaactga tgttgttgaa
                                                                            300
 gcatgcactg gagtcaatat tgcagtcatg gttggtggat tcccaagaaa agaaggtntg
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                                                                     480
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                                                                      180
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                                                                      240
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                                                                      300
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                                                                   180
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Trifolium repens

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Arg Cys Glu Ser Glu Ser Ser Phe Phe Gly Asn Glu Thr Ser Ala Ala 50 55 60
Leu Arg Ala Thr Phe Ala Pro Lys Ala Gln Lys Glu Asn Gln Asn Ile
65 70 75 80
Asn Arg Asn Leu His Pro Gln Ala Ser Tyr Lys Val Ala Val Leu Gly
85 90 95
Ala Ala Gly Gly Ile Gly Gln Pro Leu Ala Leu Leu Ile Lys Met Ser
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Pro Leu Val Ser Asp Leu His Leu Tyr Asp Ile Ala Asn Val Lys Gly
115 120 125
Val Ala Ala Asp Ile Ser His Cys Asn Thr Pro Ser Lys Val Leu Asp
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Ala Ile Leu Gly Ala Ala Gly Gly Ile Gly Gln Ser Leu Ser Leu Leu 50 60

Leu Lys Ile Asn Pro Leu Val Ser Val Leu His Leu Tyr Asp Val Val 65 70 75 80

Asn Thr Pro Gly Val Thr Ala Asp Val Ser His Ile Asp Thr Gly Ala 85 90 95

Val Val Arg Gly Phe Leu Gly Gln Ala Gln Leu Glu Asn Ala Leu Thr

110

100 105

Gly Met Asp Leu Val Val Ile Pro Ala Gly Val Pro Arg Lys Pro Gly 115 120 125

Met Thr Arg Asp Asp Leu Phe Lys Ile Asn Ala Gly Ile Val Arg Thr 130 140

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Lys Lys Ala Gly Thr Tyr Asp Pro Lys Arg Leu Leu Gly Val Thr Thr 180 185

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Asp Pro Arg Glu Val Asp Val Pro Val Val Gly Gly His Ala Gly Val 210 215 220

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Gln Val Val Glu Ala Lys Ala Gly Ala Gly Ser Ala Thr Leu Met Ala 260 . 265 270

Tyr Ala Ala Ala Lys Phe Ala Asn Ala Cys Leu Arg Gly Leu Lys Gly 275 280 285

Glu Ala Gly Ile Val Glu Cys Ala Phe Val Asp Ser Gln Val Thr Glu 290 295 300

Leu Pro Phe Phe Ala Ala Lys Val Arg Leu Gly Arg Gly Gly Ala Glu 305 310 320

Glu Ile Tyr Gln Leu Gly Pro Leu Asn Glu Tyr Glu Arg Ile Gly Leu 325 330 335

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Gly Met Thr Arg Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Lys 130 140

Thr Leu Cys Glu Ala Ile Ala Lys Arg Cys Pro Lys Ala Ile Val Asn 145 150 160

Val Ile Ser Asn Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Val 165 170 175

Phe Lys Arg Ala Gly Thr Tyr Asp Pro Lys Arg Leu Leu Gly Val Thr 180 185 190

Met Leu Asp Val Val Arg Ala Asn Thr Phe Val Ala Glu Val Leu Gly 195 200 205

Leu Asp Pro Arg Asp Val Asp Val Pro Val Val Gly Gly His Ala Gly 210 215

Ile Thr Ile Leu Pro Leu Leu Ser Gln Val Lys Pro His Ser Ser Phe 225 230 235

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Trifolium repens

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PCT/AU2004/000493 WO 2004/089066

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Trifolium repens

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Ile Asp Gly Ala Phe Pro Leu Leu Arg Gly Val Val Ala Thr Thr Asp 65 70 75 80

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Ser Pro Arg Lys Glu Gly Met Glu Arg Lys Asp Val Met Ser Lys Asn 100 105 110

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PCT/AU2004/000493 WO 2004/089066

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Leu Met Lys Met Asn Pro Leu Val Xaa Val Leu His Leu Tyr Asp Val 65 70 75 80

Val Asn Thr Pro Gly Val Thr Ser Asp Ile Ser His Met Asp Thr Ala 85 90 95

Ala Val Val Arg Gly Phe Leu Gly Gln Asn Gln Leu Glu Asp Ala Leu 100 105 110

Thr Gly Met Asp Leu Val Ile Ile Pro Ala Gly Val Pro Arg Lys Pro 115 120 125

Gly Met Thr Arg Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Lys 130 135

Thr Leu Cys Glu Ala Ile Ala Lys Arg Cys Pro Lys Ala Ile Val Asn 145 150 150 160

Val Ile Ser Asn Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Val 165 170 175

Phe Lys Arg Ala Gly Thr Tyr Asp Pro Lys Arg Leu Leu Gly Val Thr 180 185

Met Leu Asp Val Val Arg Ala Asn Thr Phe Val Ala Glu Val Leu Gly 195 200 205

Leu Asp Pro Arg Asp Val Asp Val Pro Val Val Gly Gly His Ala Gly 210 215 220

Ile Thr Ile Leu Pro Leu Leu Ser Gln Val Lys Pro His Ser Ser Phe 225 230 235 240

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Trifolium repens

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Asp Gly Ile Gly Pro Glu Val Val Ser Val Ala Lys Asp Val Leu Leu 50 60

Leu Thr Gly Ser Ile His Gly Ile Lys Leu Glu Phe Gln Glu Lys Leu 65 70 . 75 80

Leu Gly Gly Ala Ala Leu Asp Ala Thr Gly Val Pro Leu Pro Asp Asp 90 95

Thr Leu Ser Val Ala Lys Gln Ser Asp Ala Val Leu Leu Gly Ala Ile 100 105 110

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20 25 30
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Asp Glu Phe Leu Glu Pro Leu Glu Leu Cys Tyr Arg Ser Leu Cys Ala 35 40 45

Cys Gly Asp Arg Ala Ile Ala Asp Gly Ser Leu Leu Asp Phe Leu Arg 50 55 60

Gln Val Ser Thr Phe Gly Leu Ser Leu Val Arg Leu Asp Ile Arg Gln 65 70 75 80

Glu Ser Asp Arg His Thr Asp Val Met Asp Ala Ile Thr Lys His Leu 85 90 95

Glu Ile Gly Ser Tyr Gln Asp Trp Ser Glu Glu Lys Arg Gln Glu Trp 100 105

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Pro Gln Thr Asp Glu Ile Arg Glu Val Leu Glu Thr Phe His Val Ile 130 135 140

Ala Glu Leu Pro Ser Asp Asn Phe Gly Ala Tyr Ile Ile Ser Met Ala 145 150 150

Thr Ala Pro Ser Asp Val Leu Ala Val Glu Leu Leu Gln Arg Glu Cys 165 170 175

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Leu His Gly Glu Asp Ile Arg Gln Thr Val Gln Asp Cys Tyr Glu Leu 50 60
Ser Ala Glu Tyr Glu Gly Glu Leu Lys Pro Glu Lys Leu Glu Glu Leu
65 70 75 80
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300

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Trifolium repens

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DNA

Trifolium repens

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Thr Thr Ser Ala Ala Leu Leu His Pro Ile His Leu Ser Ser Ser Ser 35

Gly Ile Ser Pro Pro Ser Asn Val Lys Gly Thr Leu Thr Val Val Asp 50 60 Glu Arg Thr Gly Lys Lys Tyr Thr Ile Glu Val Ser Pro Asp Gly Thr 65 70 75 80 Val Lys Ala Asn Asp Phe Lys Lys Ile Ser Thr Gly Lys Asn Asp Lys 90 95 Gly Leu Lys Leu Tyr Asp Pro Gly Tyr Leu Asn Thr Ala Pro Val Arg 100 105 110Ser Thr Ile Ser Tyr Ile Asp Gly Asp Glu Gly Ile Leu Arg Tyr Arg 115 120 125 Gly Tyr Pro Ile Glu Glu Leu Ala Glu Lys Ser Thr Phe Pro Glu Val 130 135 140 Ala Tyr Leu Ile Leu Tyr Gly Asn Leu Pro Ser Ala Asn Gln Leu Gln 145 150 150 160 Glu Trp Glu Phe Ala Ile Ser Gln His Ser Ala Leu Pro Gln Gly Val 165 170 175 Leu Asp Leu Ile Gln Ser Met Pro Gln Asp Ala His Pro Met Gly Val 180 185 190 Leu Val Asn Ala Ile Ser Ala Leu Ser Val Phe His Pro Asp Ala Asn 195 200 205 Pro Ala Leu Arg Gly Leu Asp Ile Tyr Asn Ser Lys Gln Val Arg Asp 210 215 Lys Gln Ile Ala Arg Ile Ile Gly Lys Ile Thr Thr Ile Ala Ala 225 230 235 240 Ile Asn Leu Arg Met Ala Gly Arg Pro Pro Val Leu Pro Ser Asn Lys 245 250 255 Leu Ser Tyr Thr Glu Asn Phe Leu Tyr Met Leu Asp Ser Leu Gly Asn 260 265 270 Arg Ser Tyr Lys Pro Asn Pro Gln Leu Thr Arg Ala Leu Asp Ile Ile 275 280 285 Phe Ile Leu His Ala Glu His Glu Met Asn Cys Ser Thr Ser Ala Val 290 295 300 Arg His Leu Ala Ser Ser Gly Val Asp Val Tyr Thr Ala Ile Ala Gly 305 310 315 Gly Val Gly Ala Leu Tyr Gly Pro Leu His Gly Gly Ala Asn Glu Ala Val Leu Lys Met Leu Ser Glu Ile Gly Ser Val Asp Asn Ile Pro Glu 340 345 Phe Ile Glu Gly Val Xaa <210> 338 <211> 609 <212> DNA Trifolium repens <213> <220> misc_feature <221> <222> (2)..(2)n is a, c, g, or t <220> misc_feature <221> <222> (7)..(7) n is a, c, g, or t <223> <220> misc_feature (609)..(609) <221> <222> n is a, c, g, or t <223> <400> 338 cntttcnttt ccacagcatc ctaatcctaa tcctaatcct aatcctatta ctaattacta 60 attactaatt actagtacta attagtaata ccgatccctt tttctcgaac ccattcattc 120 . aattcaaaga aggaaaaaca aaatcacaca aacaaacatc ttacaacaat gtcaacgaca 180 actactacaa ccgacgaatc caagctgcac gacgctgcac ggaaccgttt ggctaccctc 240 tcagctcact tgcttccttc ctccacaaac tccgctgcgc ttctccatcc tatccacctt 300 tcttcttcct ctgggatctc cccaccgtct aatgtcaaag gaacactcac cgttgttgat 360 gaacgtaccg ggaagaagta taccattgag gtctctcctg atggcaccgt taaagccaat 420 gatttcaaga agatatcaac tgggaagaat gataaggggc tcaaacttta tgatcctgga 480 tatttaaaca ctgctcctgt gcgatcaaca atttcttata ttgatggtga tgagggaatc 540 cttagatata gaggataccc cattgaagag ttggccgaga aaagcacctt tccggaagtg 600 609 acatatctn 339 <210> 589 <211> <212> DNA <213> Trifolium repens <220> <221> misc_feature <222> (2)..(2)n is a, c, g, or t

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Asn Arg Asn Leu His Pro Gln Ala Ser Tyr Lys Val Ala Val Leu Gly 85 90 95

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PCT/AU2004/000493 WO 2004/089066

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WO 2004/089066

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International application No. PCT/AU2004/000493

A.	CLASSIFICATION OF SUBJECT MATTER].		
Int. Cl. 7: A01H 5/00, C12N 15/29					
According to International Patent Classification (IPC) or to both national classification and IPC					
В.	FIELDS SEARCHED				
Minimum docu	mentation searched (classification system followed by class	sification symbols)			
Documentation	searched other than minimum documentation to the extent	that such documents are included in the fields search	ed		
WPIDS, CA grass, rye gr	base consulted during the international search (name of day, MEDLINE, AGRICOLA: phosphoenolpyruvateass, lolium, fescue, festuca, clover, trifolium, melify, krebs, TCA, organic acid, soil	e carboxylase, PEPC, malate dehydrogenas	e, MDH, plsmt, c engineer,		
C.	DOCUMENTS CONSIDERED TO BE RELEVANT				
Category*	Citation of document, with indication, where appro	priate, of the relevant passages	Relevant to claim No.		
x					
x	WO 2000/073475 A1 (Pioneer Hi-Bred International) 7 December 2000				
<u> </u>		of Box C X See patent family ann	ex		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) "Y" Special categories of cited documents: "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone document of particular relevance; the claimed invention cannot be considered to					
or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family					
Date of the actual completion of the international search Date of mailing of the international search report Z 4 JUN 7004					
18 June 2004 Name and mailing address of the ISA/AU Authorized officer					
AUSTRALIA PO BOX 200 E-mail addres	Ining address of the ISA/AU IN PATENT OFFICE , WODEN ACT 2606, AUSTRALIA ss: pct@ipaustralia.gov.au . (02) 6285 3929	GARETH COOK Telephone No: (02) 6283 2541	<u>.</u>		

International application No. PCT/AU2004/000493

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	Samac DA et al, "Plant improvement for tolerance to aluminum in acid soils - a review", Plant Cell, Tissue and Organ Culture, December 2003, 75(3):189-207 see pages 202-203	9, 18
Е, Х	US 2004/116682 A1 (Cheikh et al) 17 June 2004 whole of document	9, 18
Á	Häusler RE et al, "Single and double overexpression of C4-cycle genes had differential effects on the pattern of endogenous enzymes, attenuation of photorespiration and on contents of UV protectants in transgenic potato and tobacco plants", Journal of Experimental Botany, 2001, 52(362):1785-1803 whole of document	
A	Häusler RE et al, "Overexpression of C4-cycle enzymes in transgenic C3 plants to improve C3-photosynthesis", Journal of Experimental Botany, 2002, 53(369):591-607 whole of document	
Α.	Tesfaye M et al, "Overexpression of Malate Dehydrogenase in Transgenic Alfalfa Enhances Organic Acid Synthesis and Confers Tolerance to Aluminum", Plant Physiology, 2001, 127:1836-1844 whole of document	·
A	EP 1 122 316 A1 (Centro de Investigacion y Estudios Avanzados del Instituto nacional Irapuato) 8 August 2001 whole of document	
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International application No.

PCT/AU2004/000493

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sh	neet)
This international search report has not been established in respect of certain claims under Article 17(2)(a) for the reasons:	following
1. Claims Nos.:	
because they relate to subject matter not required to be searched by this Authority, namely:	
2. Claims Nos.:	
because they relate to parts of the international application that do not comply with the prescribed requ	uirements to such
an extent that no meaningful international search can be carried out, specifically:	
3. Claims Nos.:	
because they are dependent claims and are not drafted in accordance with the second and third sentence	ces of Rule'6.4(a)
Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)	
This International Searching Authority found multiple inventions in this international application, as follows:	
See supplemental sheet.	
As all required additional search fees were timely paid by the applicant, this international search report	rt covers all
searchable claims.	
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority depayment of any additional fee.	id not invite
3. As only some of the required additional search fees were timely paid by the applicant, this internation	al search report
covers only those claims for which fees were paid, specifically claims Nos.:	
·	
4. X No required additional search fees were timely paid by the applicant. Consequently, this international restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 9, 10, 18, 19 as a	search report is requested by the
Applicant.	
Remark on Protest The additional search fees were accompanied by the applicant's protest.	
No protest accompanied the payment of additional search fees.	

International application No.

PCT/AU2004/000493

Supplemental Box

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No III: Observations where unity of invention is lacking.

The problem addressed by the current application is the modification of organic acid biosynthesis in plants. The solution is provided through the use of polypeptides involved in the organic acid biosynthesis, and their encoding polynucleotides, from clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*), specifically polypeptides and their encoding polynucleotides from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*). These polypeptides have been placed into three broad groupings by the Applicant: malate dehydrogenases (MDH), citrate synthases (CS) and phosphenol pyruvate carboxylases (PEPC).

The general concept underlying the application appears to reside in enzymes involved in organic acid biosynthesis. However the enzymes involved in the organic acid biosynthetic pathway through the tricarboxylic acid cycle (TCA) are known in the prior art, as has been admitted by the Applicant page 2 lines 18 to 22 of the specification. Therefore the involvement of the enzymes in organic acid biosynthesis cannot be considered a special technical feature. The enzymes themselves may be from clover, medic, ryegrass or fescue, with the specifically disclosed sequences being from either from white clover or perennial ryegrass. However the species of origin can only constitute a special technical feature if the species of origin makes a contribution over the prior art. There is nothing in the application to indicate that isolation of peptides from white clover makes an inventive contribution over the prior art, therefore the species of origin cannot be considered a special technical feature.

Since there is no obvious special technical feature, it is appropriate to use the Markush approach to analyse the application for unity of invention.

- (A) The common property is the involvement of the enzymes in the organic acid biosynthesis in plants.
- (B) (1) There is no common structure that is a significant structural element shared by all the polypeptides. A significant structural element is one that forms the contribution of the polypeptides over the prior art, and is disclosed in the application.
- (B) (2) There is no single recognised class of compounds embracing all the polypeptides, as the polypeptides belong to different classes of proteins, ie. MDH, CS and PEPC, each carrying out different biological functions.

Unity of invention is therefore lacking in the application.

The Applicant has placed the enzymes into three groups: MDH, CS and PEPC. Each of these groups needs to be analysed to determine if there is unity within the Applicant's groupings. Taking MDH, this group of enzymes is known in the prior art, as has been admitted by the Applicant at page 2 lines 18 to 22 of the specification. As this is a known grouping, Markush practice again needs to be applied to determine if unity exists.

- (A) The common property is the involvement of the MDHs in the reversible conversion of malate to oxaloacetate.
- (B) (1) There is no common structure that is a significant structural element shared by all the MDH enzymes that has been disclosed in the specification.
- (B) (2) There is no single recognised class embracing all MDHs, the recognised class being one where there is an expectation that all members of the class will behave in the same way in the context of the claimed invention. According to the application in the paragraph bridging pages 2 and 3, MADH is important in several metabolic pathways and plants contain multiple forms that differ in coenzyme specificity and subcellular location. The diversity of function of MDHs is also reflected in that there are multiple enzyme classification (EC) numbers into which the enzymes are placed according to function, the numbers being 1.1.1.37, 1.1.1.38, 1.1.1.39, 1.1.1.40, 1.1.1.82 and 1.1.1.83.

International application No.

PCT/AU2004/000493

Supplemental Box

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No III: Observations where unity of invention is lacking.

Unity in the Applicant's grouping of MDH enzymes is therefore lacking. Each polypeptide sequence within the Applicant's MDH grouping is considered to be a separate invention. Similarly with PEPC each polypeptide sequence is considered a separate invention as no significant structural element has been identified in the application, and there is no single recognised class embracing all PEPCs - the application states at page 3 lines 4 to 10 that PEPCs are widely distributed through most plant tissues filling various physiological roles, and these enzymes have different EC numbers depending on their coenzymes, the EC numbers being 4.1.1.31, 4.1.1.32, 4.1.1.49. The CS group is considered to be a single group for the purposes of unity, there being only one class embracing all CS enzymes.

The application is therefore considered to be to 37 separate inventions. The 37 separate inventions are:

1. citrate synthases (CS)

2 to 37. each separate polypeptide sequence of the Applicant's groupings MDH and PEPC (ie. each polypeptide of SEQ IDs 22, 31, 35, 37, 39, 41, 45, 47, 112, 114, 116, 184, 186, 188, 190, 198, 200, 202, 204, 206, 219, 253, 272, 277, 289, 294, 297, 303, 307, 309, 311, 316, 320, 324, 326 and 348 is a separate invention).

The Applicant requested the search be limited to claims 9, 10, 18 and 19. Claims 9 and 10 are directed to a construct comprising sequences encoding MDH, PEPC and optionally CS. Claims 18 and 19 are directed to a method of modifying organic acid synthesis by transforming a plant with sequences encoding MDH, PEPC and optionally CS. Both a construct comprising sequences encoding MDH and PEPC and a plant transformed with such a construct are disclosed in:

Beaujean A et al, "Integration and expression of Sorghum C4 phosphoenolpyruvate carboxylase and chloroplastic NADP+-malate dehydrogenase separately or together in C3 potato plants", *Plant Science*, 2001, 160:1199-1210

Hence these claims lack unity, a posteriori.

Information on patent family members

International application No.

PCT/AU2004/000493

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member				,	
WO	200/073475	AU	51593/00	CA	2 361 912	US	6 653 535
		BR	0010975	EP	1 181 380	US	2004/078839
EP	1 122 316	AU	45533/98	BR	9815878	wo	1999/063100
Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.							